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RESULT 1
BD268215
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BD021936 Packaging
BD268212 Adenoviru
AX356045 Sequence
BD021944 Packaging
BD261944 Sequence
BD01943 Packaging
I09270 Sequence 34
I09270 Sequence 37
I0928 Sequence 35
I0926 Sequence 35
I0925 Sequence 36
I0925 Sequence 18
A95117 Sequence 1
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                                                        July 14, 2005, 04:39:07; Search time 2449.65 Seconds (without alignments) 6468.225 Million cell updates/sec
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                     - nucleic search, using sw model
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AR343138 Sequence
AX382187 Sequence
CO854906 Sequence
AR323988 EGPP expr
AY370909 Expressio
       J01917 Adenovirus
AF534906 Human ade
                     AR091540 Sequence
AR102233 Sequence
AR230731 Sequence
AX103430 Sequence
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AX084506 Sequence
AX084515 Sequence
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AX30727 Sequence
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Partent: JP 2002534130-A 8 15-OCT-2002;
NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
OS Artificial Sequence
PD 15-OCT-2002
PF 14-JAN-2000 JP 2000593765
PR 14-JAN-1999 US 60/115920
PF 14-JAN-1999 US 60/115920
PF GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO
PC CL2N15/09, AG1K35/76, AG1K48/00, AG1P33/00, AG1P43/00, AG1P4
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synthetic construct
other sequences;
1 (base 1 to 7469)
Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C.
Skripchenko,Y.
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    ; Score 327; DB 6;
; Pred. No. 2.8e-66;
0; Mismatches 0;
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| Aorganism="synthetic construct"
|mol_type="genomic DNA"
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Vectors for ocular transduction and use thereof for genetic thera
Patent: WO 0183729-A 8 08-NOV-2001;
Novartis AG (CH) ; The Scripps Research Institute (US) ; Nemerow,
Glen R. (US) ; Von Seggern, Daniel J. (US) ; Friedlander, Marty
(US)
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                                                                      GAGCGAGTCCGCATCGACCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA
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                                               CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT
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1. 7469
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/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.4%; Score 325; DB 6; I
100.0%; Pred. No. 7.7e-66;
tive 0; Mismatches 0;
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ACCESSION

RESULT 4 BD021936

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COMMENT

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4049 GATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC 4108
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                                                         synthetic construct
synthetic construct
other sequences artificial sequences.
1 (bases 1 to 10610)
Memerow, G.R., Seggern, D.J.V., Hallenbeck, P.L., Stevenson, S.C. Skripchenko, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%; Score 325; DB 6; Length 10610; 100.0%; Pred. No. 7.6e-66; ive 0; Mismatches 0; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism='Artificial Sequence'
Location/Qualifiers
                                                                                                                                                Adenovirus vector, packaging cell line, comproduction and use Patent: JP 200254130-A 16 15-OCT-2002; NOVARTIS AG,THE SCRIPPS RESEARCH INSTITUTE PN JP 2002534130-A/16

PD 15-OCT-2002
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/mol_type="genomic DNA"
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                             BD268212.1 GI:33077980 JP 2002534130-A/16.
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synthetic construct
production and use.
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                                                                                                         PAT 27-AUG-2002
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24-SEP-1997 JP 1998515273
25-SEP-1996 US 087719806
GLEN R MEMEROW, DANIEL J VON SEGGERN
C12NS/10, COTK14/075, C12N15/09//A61K31/711, A61K35/76, A61K48/00,
A61P35/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1148 GGCGGAGGTGCTGCTGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA 1207
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                                                                                                                                                                                                                                                 1 (bases 1 to 7469)
Memerow, G.R. and Seggern, D.J.V.
Packaging cell systems for use in promotion of the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                         7469 bp DNA linear PAT 27-AUG-20 systems for use in promotion of the development of
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                                                                                                                                                                                                                                                                                               high-capacity adenoviral vectors
Patent: JP 2001505047-A 8 17-APR-2001;
NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
PN JP 2001505047-A/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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100.0%; Pred. No. 7.7e-66
ive 0; Mismatches 0
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              1208 GGTGAGGTGTGGCAGGCTTGAGATC 1232
                                                                                                                                         vectors
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GGTGAGGTGTGGCAGGCTTGAGATC 326
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                                                                                                                                        high-capacity adenoviral
BD021936
                                                                                                                                                                BD021936.1 GI:22563159
JP 2001505047-A/8.
unidentified
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Topology: Circular;
Key
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Matches 325, Conservative
                                                                                                                       Packaging cell
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BD268212
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KEYWORDS
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AUTHORS
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FEATURES

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4168

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Gaps

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PAT 06-FEB-2002

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241

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14-JAN-2000 JP 2000593765

14-JAN-1999 US 60/115920

GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI

SUSAN C STEVENSON, YELENA SKRIPCHENKO

C CI2NIE/09, A61K35/76, A61K48/00, A61P35/00, A61P43/00, A61P43/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adenovirus vector, packaging cell line, composition and method for BD268211
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NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
PN JP 2002534130-A/15
PD 15-OCT-2002
PP 14-JAN-2000 JP 2000593765
PR 14-JAN-1999 US 60/115220
PR 14-JAN-1999 US 60/115220
PR GLEN ROBERT NEMBROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK. PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00,
C12N5/10,
PC C12N5/10,
PC C12N5/10,
PC C12N5/10,
PC C12N5/10,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC
Description of Artificial Sequence: plasmid
FF Key Location/Qualifiers
I cource I coarion/Qualifiers
FT source I coarion/A455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other sequences; artificial sequences.

1 (bases 1 to 14455)
Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and Skripchenko,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                         4169 GAGGGAGTCCGCATCGACCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA
                                                                                                                                                                                                                                                         4049 GATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC
                                                                                                                                                                                                                                                                                                               62 CAGTACTCTTGGATCGGAAACCGTCGGCCTCCGAACGGTACTCCGCCACGAGGACCT
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                                                                                                                                             Length 10610;
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Location/Qualifiers
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                                                                                                                                             99.4%; Score 325; DB 6; I
100.0%; Pred. No. 7.6e-66;
ive 0; Mismatches 0;
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/organism="synthetic construct"

    10610
    organism="unidentified"

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/db_xref="taxon:32630"
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  Location/Qualifiers
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synthetic construct
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Matches 325; Conservative
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KEYWORDS
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  FEATURES
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S JP 2001505047-A/16.
unidentified
Unidentified
unidentified
unidentified
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unclassified.
CE 1 (bases 1 to 10610)
RS Memerow, G.R. and Seggern, D.J.V.
Packaging cell systems for use in promotion of the development of high-capacity adenoviral vectors
AL Packaging cell systems for use in promotion of the development of high-capacity adenoviral vectors
NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
RN JP 2001505047-A/16
RD 17-APR-2001
PF 24-SEP-1997 JP 1998515273
PR 25-SEP-1997 JP 1998515273
PR 25-SEP-1996 US 08/719806
PI GLEN R MEMEROW, DANIEL J VON SEGGENN
PC CLINS/10, CO7K14/075, CI2NIS/09//A6IK31/711, A6IK35/76, A6IK48/00, PC CLINS/10, CO7K14/075, CI2NIS/09//A6IK31/711, A6IK35/76, A6IK48/00, PC Strandedness: Double;
CC Topology: Circular;
FH Key Location/Qualifiers.
                                     Nemerow, G.R., von Seggern, D.J. and Friedlander, M. Vectors for ocular transduction and use thereof for genetic therapy Patent: WO 0183729-A 16 08-NOV-2001;
Novartis AG (CH); The Scripps Research Institute (US); Nemerow, Glen R. (US); Von Seggern, Daniel J. (US); Friedlander, Marty (US)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="texon:32630"
/note="plasmid"
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99.4%; Score 325; DB 6;
Best Local Similarity 100.0%; Pred. No. 7.6e-66;
Matches 325; Conservative 0; Mismatches 0;
other sequences; artificial sequences.
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Packaging cell systems for use in promotion of the development of high-capacity adenoviral vectors

Patent: JP 2001505047-A 15 17-APR-2001;

NOVARTIS AG.THE SCRIPPS RESEARCH INSTITUTE

DD 17-APR-2001

PP 24-SEP-1997 JP 1998515273

PR 25-SEP-1996 US

PR 25-SEP-1996 US

GLEN R MEMEROW, DANIEL J VON SEGGERN

PI GLEN R MEMEROW, DANIEL J VON SEGGERN

C CLISE/10, COTK14/075, C12N15/09//A61K31/711, A61K35/76, A61K48/00,
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Best Local Similarity 100.0%; Pred. No. 7.6e-66;
Matches 325; Conservative 0; Mismatches 0;
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/organism="unidentified"
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/db_xref="taxon:32644"
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/organism="synthetic construct" |
/mol_type="unassigned DNA" |
/db xref="taxon:32630" |
/noTe="plasmid" |
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Fisher,R.A., Gilbert,W., Sato,V.L., Flavell,R.A., Maraganore,J.M. and Liu,T.R.
DAN SEQUENCES, RECOMBINANT DNA MOLECULES AND PROCESSES FOR PRODUCING SOLUBLE T4 PROTEINS
Patent: WO 8901940-A 35 09-MAR-1989;
                                                                                                                                                                                GATCGGAAACCCGTCCGCACCGAACGGTACTCCGCCACCGAGGGACCTGAGCGAGTCCG
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                                                                                                                                                 611 GGGCCAGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTACTCTTG
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                                              Score 309.2; DB 6,
Pred. No. 3.9e-62;
0; Mismatches 3;
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Pred. No. 3.9e-62;
0; Mismatches 3
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Sequence 35 from Patent WO 8901940.
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/organism="unknown"
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                                              94.6%;
ilarity 99.0%;
Conservative 0
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Sato, V.L., Flavell,R.A., Maraganore,J.M. and Liu,T.R.
and Liu,T.R.
DNA SEQUENCES, RECOMBINANT DNA MOLECULES AND PROCESSES FOR PRODUCING SOLUBLE T4 PROTEINS
PACHEL: WO 8901940-A 37 09-MAR-1989;
Location/Qualifiers
1. 5413
                                                                                                                                                                                                                   1 (bases 1 to 5365)
Fisher,R.A., Gilbert,W., Sato,V.L., Flavell,R.A., Maraganore,J.M.
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DNA SEQUENCES, RECOMBINANT DNA MOLECULES AND PROCESSES FOR PRODUCING SOLUBLE T4 PROTEINS
PATENT: WO 8901940-A 34 09-MAR-1989;
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Sequence 34 from Patent WO 8901940.
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1. .5365
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WO 8901940.
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Sequence 37 from Patent '
109270
109270.1 GI:588054
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                                                                                                                                                                                                                               1 (bases 1 to 5566)
Fisher,R.A., Gilbert,W., Sato,V.L., Flavell,R.A., Maraganore,J.M. and Liu,T.R.
and Liu,T.R.
bnd SEQUENCES, RECOMBINANT DNA MOLECULES AND PROCESSES FOR PRODUCING SOLUBLE T4 PROTEINS
PACHEL: WO 8901940-A 36 09-MAR-1989;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 6149)
Fisher,R.A., Gilbert,W., Sato,V.L., Flavell,R.A., Maraganore,J.M.
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                                                                                                                             Sequence 36 from Patent WO 8901940.
109269
109269.1 GI:588053
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Sequence 19 from Patent WO 8901940.
109252.
109252.1 GI:588036
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and Liu,T.R.

MAD SEQUENCES, RECOMBINANT DNA MOLECULES AND PROCESSES FOR PRODUCING SOLUBLE T4 PROTEINS
PARENT: WO 8901940-A 19 09-MAR-1989;
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                                                                                                                                                 1. .6149
/organism="unknown"
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                                                                                                                 Location/Qualifiers
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Aaa59054 Nucleotid Aba94266 Adenoviru Add78132 Adenoviru Adf48736 Adenoviru Ad4832372 Complete Aaa59043 Nucleotid Aba94252 Nucleotid Add75149 Plasmid p Ad4832375 Complete Aaa59051 Nucleotid Aba94260 Nucleotid Aba94260 Nucleotid Ada75157 Plasmid p Ad48802 Esf fibre Aav32374 Complete Aaa59050 Nucleotid Aba94259 Nucleotid Ada75156 Plasmid p Adf48801 Esf fibre Aav32374 Complete Aav32374 Complete Aav32375 Complete Aav32375 Complete Aav32375 Complete Aav32375 Complete Aav32375 Plasmid p
SUMMARIES	AAA59054 ABA94266 ADB75112 ADB75112 AAA59043 AAA59043 AAA59043 AAA59043 AAA59051 AAA3775 AAA3775 AAA3776 AAA359050 ABB75157 AAA59050 ABB75157 AAA59050 ABB75156 AAA59050 ABB75156 AAA59050 ABB75156 AAA59050 ABB75156 AAA59050 ABB75156 AAA59050 ABB75156 AAA6801
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                                                                                                                                    Gaps
vectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a gulless adenoviral vector particle. The present sequence represents sequence, which is used to construct nucleic acid molecules of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adenovirus 5 tripartite leader (TPL) partial nucleotide sequence.
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                                                                                                        Length 327;
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                                                                              Sequence 327 BP; 63 A; 79 C; 116 G; 69 T; 0 U; 0 Other;
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                                                                                                       ; Score 327; DB 3;
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Best Local Similarity 100.0%;
Matches 327; Conservative 0;
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(SCRI ) SCRIPPS RES INST.
(NEME/) NUMBRROW G R.
(VSEG/) VON SEGGERN D J.
(FRIE/) FRIEDLANDER M.
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                                                      invention
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The invention provides an isolated polynucleotide comprising adenovirus (AV) inverter terminal repeat sequences (ITRS), AV packaging signal coperativaly linked to ITRS and a photoreeptor-specific promocer. A recombinant AV vector (AVV) comprising the polynucleotide is useful for tereating an ocular disease, e.g., retinal control occidence control occid
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                          e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat
sequences, packaging signal and photoreceptor-specific promoter.
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Polynucleotide for making vectors, useful for treating ocular diseases
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                                                                                                      Example 1; Page 122; 149pp; English
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inverted terminal repeat sequence; Human adenovirus type 5 retinitis pigmentosa. WPI; 2003-657234/62. US2002193327-A1 19-DEC-2002 Nemerow GR, 

adenovirus packaging signal; photoreceptor-specific promoter; adenovirus type 37; adenovirus type 13; adenovirus type 2, adenovirus type 37; adenovirus type D serotype; adenovirus type 2; adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor; rhodopsin; wild-type Stargardt disease gene; STDG1; anti-cancer agent; retinal degenerative disease; retinitis pigmentosa; Stargardt's disease; diabetic retinopathy; retinal vascularisation; choroideraemia; photoreceptor-restricted transgene expression; recombinant adenovirus vector; adenovirus type 5; Ad5; Friedlander M; tripartite leader sequence; TPL; ds Von Seggern DJ, 01-MAY-2001; 2001US-00847101. 01-MAY-2000; 2000US-00562934 (SCRI ) SCRIPPS RES INST.

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CCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACC 120

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CCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACC 120

1 AGATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAACTCTTCGCGGTCTTT

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Length 327;

Score 327; DB 10; Pred. No. 4.8e-80;

100.0%; bcc. 100.0%; Pred. No. 1... 0; Mismatches

Matches 327; Conservative

Similarity

Query Match Best Local &

121 TGAGCGAGTCCGCATCGAAACCTCTCGAGAAAGCCGTCTAACCAGTCAC 180

TGAGCGAGTCCGCATCGACCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCAC

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241 TGGCGGAGGTGCTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCG 300

AGGTGAGGTGTGCCAGGCTTGAGATCT 327

301

TGGCGGGAGGTGCTGCTGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCG 300

AGTCGCAAGGIAGGCIGAGCACCGIGGCGGGCGGCAGCGGGIGGCGGICGGGTTGITIC

181 181 241

> sequences, adenovirus packaging signals operatively linked to the sequences and photoreceptor-specific promoters, useful for treating Novel nucleic acids comprising adenovirus inverted terminal repeat

Example 1; Page 62; 106pp; English.

The invention describes an isolated mucies and alphoroceptor-specific adenovirus inverted terminal repeat sequence, and a photoreceptor-specific signal operatively linked to the sequence, and a photoreceptor-specific signal operatively linked to the sequence, and a photoreceptor-specific for targeted delivery of a gene product to the eye of a mammal which involves administering (II) that comprises heterologus DNA encoding the crecombinant virus comprises a fibre protein that specifically or selectively binds to receptors that are expressed on cells which are photoreceptors in the eye. The recombinant virus comprises a fibre protein which is an adenovirus type 37, from an adenovirus type 10 serotype. The fibre is a chimeric protein containing a sufficient portion of the N-terminus of an adenovirus type 2 or type 5 fibre protein for interaction with an adenovirus type 2 or type 5 fibre protein for of the N-terminus of an adenovirus type 2 or type 5 fibre protein for interaction with an adenovirus type 2 or type 5 fibre protein for of the N-terminus of an adenovirus type 2 or type 5 fibre protein for interaction with an adenovirus type 2 or type 5 fibre protein for contrion of an adenovirus type 2 or type 5 fibre protein for a selective binding to photoreceptors in the eye of a mammal. The contrion of an adenovirus factor, and selective binding to photoreceptors in the eye of a mammal. The coperatively linked to a nucleic acid comprising the therapeutic product operatively linked to a nucleic acid comprising the therapeutic product concer agent and a protein that regulates expression of a photoreceptor-specific gene product. The delivery is effected for treatment of an ocular disease such as retinal degenerative disease e.g., retinitis coular diseases uch as retinal degenerative disease e.g., retinitis coular diseases. The viral nucleic acid comprises an adenovirus diseases in the viral nucleic acid comprises an adenovirus retinity and any adenovirus in the ethorogeneral product. The degenerative disease such as r inverted terminal repeat (ITR) sequences, and an adenovirus packaging signal operatively linked to the sequence. The ITRs and packaging signal are derived from an adenovirus serotype B or C, or adenovirus type 2 or photoreceptor-restricted transgene expression. This sequence represents TPL (tripartite leader sequence) from the adenovirus type 5 genome, used are derived from an adenovirus serotype B or C, or adenovirus type 2 or 5. The viral nucleic acid further comprises a photoreceptor-specific promoter. (II) includes photoreceptor promoters providing a means not only for specific targeting of expression in these cells, but also for The invention describes an isolated nucleic acid (I) comprising enhance the expression of complementing adenoviral proteins.

Novel isolated nucleic acid molecule useful for delivering heterologous gene to human or any animal, or for producing gutless adenoviral vector WPI; 2003-843463/78.

Sequence 327 BP; 63 A; 79 C; 116 G; 69 T; 0 U; 0 Other;

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packaging cell line; pseudotyping; adenovirus vector; gene therapy; hereditary disorder; tumour; HIV infection; fibre; fibre-gene-deleted adenoviruses; hygromycin resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; anti-HIV; gene therapy; HIV gene expression inhibitor; HIV gene expression activation; adenovirus tripartite leader; TPL; gulless adenoviral vector particle; helper-independent fiberless recombinant adenovirus vector;
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AGGIGAGGIGIGGCAGGCITGAGAICI 327
                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tripartite leader sequence; ds.
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                                                                                                                                                                                                     ADF48736 standard; DNA; 327
                                                                                                                                                                                                                                                                                                                                               12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adenovirus type 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKRIPCHENKO Y
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(SKRI/)
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                                                                                                                          RESULT 4
ADF48736
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The invention describes an isolated mucleic acid molecule (I) comprising an adenovirus tripartite leader (TPL) nuclectide, the TPL nuclectide an adenovirus tripartite leader (TPL) nuclectide, the TPL nuclectide an adenovirus tripartite leader (TPL) nuclectide exons or first, second and third same or different TPL exons chosen from the complete or partial TPL exon 1. Complete TPL exon 2 and complete TPL exon 3. (I) is useful for delivering a patterologous gene to a human or any animal, or for producing a gutless adenoviral vector particle. A recombinant adenovirus particle (II) is useful for delivery of an exogenous gene to a target cell which involves contacting the cell with an adenovirus vector genome (III) is useful for producing an adenovirus vector particle containing (III) is useful for producing an adenovirus vector particle containing (III) which involves (III) is useful for packaging of the genome and (III) which is deficient in expressing of the genome and (III) which is deficient in expressing of the genome and (III) which is deficient in expressing sufficient functional fiber protein to support assembly of fiber containing particles and harvesting the particle produced by the cell involves complementing a missing fiber gene of (III) or helper-dependent fiber gene from a different adenovirus vector genome by expressing in packaging cells a fiber gene from a different adenovirus vector to a cell of choice. (I) is useful for recombinant adenovirus vector to a cell of choice. (I) is useful for recombinant adenovirus vector to a cell of choice. (I) is useful for cecombinant particle leader sequence represents a partial adenovirus containing diseases such as hereditary condisored to disrupt HIV infection. This sequence represents a partial adenovirus equence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGTACTCTTGGATCGGAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGACGGACC
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Pred. No. 4.8e-80;
0; Mismatches 0;
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                                              Claim 14; SEQ ID NO 26; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete sequence of the pCLF plasmid.
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(first entry)
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Best Local Similarity 100.
Matches 327; Conservative
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29-SEP-1998
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    particle
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The present sequence is that of a pCLF plasmid used in the method of the invention. The pCLR plasmid ass derived from the pCDNA3/Fibrar plasmid (AAV32371) containing an additional adenovirus type 2 (AD2) tripartite leader sequence to enhance expression. The pCLF plasmid also contains an adenovirus type 5 (AD2) fiber gene controlled by a CMV promoter and a neo cresistant gene. The invention provides adenoviral vectors having adenovirus type 5 (AD2) fiber gene controlled by a CMV promoter and a neo cresistant gene. The invention provides adenoviral vectors having deletions of all or part of various gene sequences encoding adenoviral structural proteins and/or early region proteins. Deletions in these proteins and/or early region proteins. Deletions in these content and the structural and/or early gene regions are produced by of diagnostic and therapeutic applications. The adenoviral vectors having deletions in the structural and/or early gene regions are produced by cellular complementation of these adenoviral genes. Therefore, the pCLF plasmid was used as a complementation plasmid which was introduced into a host cell line where parts of the fiber gene region would be stably characterised by hyper-proliferative cells (e.g. tumours), genetic characterised by hyper-proliferative cells (e.g. tumours), genetic diseases (e.g. Huntington's disease, Tay-Sachs disease, or sickle cell disease), or infections (e.g. HIV infection). They can also be used for in vitro production of biologically active proteins. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908 GATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC 967
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Circular; adenovirus type 5; pCDNA3/Fiber plasmid; structural protein; complementation; fiber protein; gene therapy; HIV; tumour; early gene; Huntington's disease; Tay-Sachs disease; sickle cell disease; pCLF plasmid; AD2; adenovirus type 2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adenoviral vectors - which lack DNA encoding for structural protein or fibre protein used particularly for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC
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                                                                                                                                                                                   /*tag= a
/note= "AD2 tripartite leader sequence"
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                                                                                                                                                                                                                                             /*tag= b
/product= "AD5 fiber protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 85-94; 170pp; English.
                                                                                                                                             cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               96US-00719806
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Matches 325; Conserv
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                                                                                                                                                                                                                                                                                                                                                                           Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL exons. The nucleic acid is used to produce an adenovirus vector particle, deliver an exogenous gene to a target cell, pseudotype recombinant viral vectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a gutless adenovirus vector particle. The present sequence represents a partial TPL sequence, which is used to construct nucleic acid molecules of the invention. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid comprising an adenovirus tripartite leader nucleotide producing high-capacity and targeted vectors for adenovirus-based
               GAGCGAGTCCGCATCGGATCGGAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA
                                                                      GTCGCAAGGTAGGCTGAGCACCGTGGCGGGCGCCAGCGGGGTGGCGGCTTGTTTCT
                                                                                                     GGCGGAGGTGCTGCTGATGTAATTAAAGTAGGCGGTCTTGAGACGCCGGATGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7469 BP; 1850 A; 1937 C; 1810 G; 1872 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.4%; Score 325; DB 3; Length 7469; 100.0%; Pred. No. 3.7e-79; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a partial tripartite leader sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERPINDUNGEN VERW GES MBH.
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                        Claim 10; Page 154-156; 212pp; English.
                                                                                                                                                          GGTGAGGTGTGCCAGGCTTGAGATC 326
                                                                                                                                                                                                                                                     AAA59043 standard; DNA; 7469 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Von Seggern DJ,
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Best Local Similarity 100.0
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                  Human adenovirus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skripchenko Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200042208-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-1999;
                                                                                                                                                                                                                                                                                                         15-SEP-2003
07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nemerow GR,
122
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1148 GGCGGAGGTGCTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA 1207
                                                                       1028 GAGCGAGTCCGCATCGACCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA 1087
                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides an isolated polymucleotide comprising adenovirus (AV) inverter terminal repeat sequences (ITRS), AV packaging signal operatively linked to ITRS and a photoreceptor-specific promoter. A recombinant AV vector (AVV) comprising the polymucleotide is useful for trargeted delivery of a gene product to the eye (especially to the vitreous cavity), for treating an ocular disease, e.g., retinal degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic
               196
                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide for making vectors, useful for treating ocular diseases, e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat sequences, packaging signal and photoreceptor-specific promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenovirus, inverter terminal repeat sequence; ITRS; ocular disease; fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STDG1; opthalmological; antiinflammatory; antidiabetic; cytostatic;
CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGGAACGGTACTCCGCCACCGAGGGACCT
                                                                                                                     GAGCGAGTCCGCATCCGATCGGAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA
                                                                                                                                                                                             GTCGCAAGGTAGGCTGAGCACCGTGGCGGGCGGCAGCGGGTGGCGGTCGGGGGTTGTTTCT
                                                                                                                                                                                                                                                                   242 GGCGGAGGTGCTGCTGATGAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of expression plasmid pCLF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friedlander M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 108-110; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                             GGTGAGGTGTGGCAGGCTTGAGATC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA94252 standard; DNA; 7469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nemerow GR, Von Seggern DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-2001; 2001WO-EP004863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000; 2000US-00562934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVS ) NOVARTIS AG.
(SCRI ) SCRIPPS RES INST.
(NEMS/) NEMEROW G. R.
(VEEG/) VON SEGGEN D.J.
(FRIE/) FRIEDLANDER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-082846/11.
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preferably human. The AAV comprises a fiber protein that specifically or selectively binds to receptors that are expressed on cells (preferably photoreceptors in the eye). Preferably, the recombinant virus comprise a fiber protein from an adenovirus type D subgroup or is a chimeric protein containing a portion of the N-terminus of an adenovirus type 2 or type 5 penton, and the therapeutic product is a trophic factor, an anti-apoptotic factor, gene encoding a rhodopsin protein, a wild-type stargardt disease gene (STDG1), an anti-cancer agent and a protein that regardt disease gene (STDG1), an anti-cancer agent and a protein that nucleic acid of AAV comprises ITRS and packaging signal derived from AAV subgroup B or C, especially an AV type 2 or type 5. AAV is also useful for targeted gene therapy, where the vector comprises an AV type 37 fiber protein or its portion, and selectively transduces photoreceptors and delivers a gene product encoded by AAV. The present sequence represents an expression plasmid pCLF containing the adenovirus 5 fiber gene
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Sequence 7469 BP; 1850 A; 1937 C; 1810 G; 1872 T; 0 U; 0 Other; Length 7469; Score 325; DB 6; I Pred. No. 3.7e-79; 99.4%; Scor. 100.0%; Pred. No. 5... 0; Mismatches Query Match

1087 1207 1027 1147 121 181 241 301 908 GATCTGAATTCGAGCTCGCTGTTGGGCTTGAGGACAAACTCTTCGCGGTCTTTC 967 968 CAGTACTCTTGGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT 242 GGCGGAGGTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGGATGGTCGA 1148 GGCGGAGGTGCTGCTGATGATGAAGTAAGTAAGGCGCGTCTTGAGACGGCGGATGGTCGA GATCTGAATTCGAGCTCGCTGTTGGGCTTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT GAGCGAGTCCGCATCGACCGGATCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA 1028 GAGCGAGTCCGCATCGACCGGATCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA 182 GTCGCAAGGTAGGCTGAGCACCGTGGCGGGCGGCAGCGGGTGGCGGTCGGGGTTGTTTCT 1088 drogcaaddraddraddradcaccdrodddadadadadddadddaddaddaddaddadaradradaracrodddararrar 1208 GGTGAGGTGTGGCAGGCTTGAGATC 1232 GGTGAGGTGTGGCAGGCTTGAGATC 326 62 122 302 셤 ઠે 셤 ઠે 셤 ò 셤 à g ઠે 셤

ADB75149 standard; DNA; 7469 BP (first entry) Plasmid pCLF DNA sequence. 04-DEC-2003 ADB75149; RESULT 8 ADB75149 

ophthalmological, antiinflammatory; antidiabetic; gene therapy; adenovirus inverted terminal repeat sequence; adenovirus packaging signal; photoreceptor-specific promoter; adenovirus packaging signal; photoreceptor-specific promoter; adenovirus type 37; adenovirus type 10; adenovirus type 11; adenovirus type 12; adenovirus type 12; adenovirus type 13; photoreceptor; trophic factor; anti-apoptotic factor; rhodopsin; wild-type gragardt disease gene; STDd1; anti-cancer agent; retinal adenovirus disease; disease; gimentosa; Stargardt's disease; gyrate atrophy; retinal vascularisation; choroideraemia; gyrate atrophy; macular dystrophy; retinoblastoma; photoreceptor-restricted transgene expression; recombinant adenovirus vector; adenovirus type 5; fibre coding region; pCDNA3/Fibre; plasmid; cyclic; circular; ds;

CMV promoter cucmber mosaic virus promoter; Synthetic

sequences, adenovirus packaging signals operatively linked to the sequences and photoreceptor-specific promoters, useful for treating Novel nucleic acids comprising adenovirus inverted terminal repeat Friedlander M; 01-MAY-2001; 2001US-00847101. Von Seggern DJ, 01-MAY-2000; 2000US-00562934 (SCRI ) SCRIPPS RES INST. Human adenovirus type 5. Cucumber mosaic virus. retinitis pigmentosa. WPI; 2003-657234/62. US2002193327-A1 Nemerow GR, 19-DEC-2002 

Example 1; Page 41-44; 106pp; English.

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Gaps

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0; Indels

Matches 325; Conservative Local Similarity

control operatively linked to the sequence, and a photoreceptor-specific adenovirus inverted terminal repeat sequence, and a photoreceptor-specific promoter. A Recombinant adenovirus vector (II) comprising (I) is useful corrected delivery of a gene product to the eye of a mammal which is involves administering (II) that comprises heterologous DNA encoding the gene product or reculting in expression of the gene product, where the gene product or reculting in expression of the gene product, where the cerombinant virus comprises a fibre protein that specifically or selectively binds to receptors that are expressed on cells which are photoreceptors, in the eye The recombinant virus comprises a fibre correction which is an adenovirus type 37, from an adenovirus type D serotype. The fibre is a chimeric protein containing a sufficient portion of the fibre is a chimeric protein containing a sufficient portion of an adenovirus type 2 or type 5 penton, and a sufficient portion of an adenovirus type 2 or type 5 penton, and a sufficient portion of an adenovirus serotype D knob portion of the fiber for encapsulated nucleic acid comprises a photoreceptor-specific promoter operatively linked to a nucleic acid comprising the therapeutic product which is chosen from trophic factor, anti-apoptotic factor, gene encoding a rhodopsin protein, wild-type Stargardt disease gene (STDG1), an anti-cancer agent and a protein that requires expression of a photoreceptor-specific gene product. The disperse tripopatises and adenovirus packaging signal operatively linked to the sequence. The ITRs and packaging signal are derived from an adenovirus serotype B or C, or adenovirus packaging signal are derived from an adenovirus serotype B or C, or adenovirus packaging are product transminal repeat (ITR) sequences, and adenovirus packaging are product transmined from an adenovirus serotype B or C, or adenovirus proper or photoreceptor-reprices or adenovirus second transment each or restricted for transgent each or proper each or restricted transge pnotoreceptor-restricted transgene expression. This sequence represents plasmid comprising an adenovirus fibre gene under the control of a The invention describes an isolated nucleic acid (I) comprising cucmber mosaic virus (CMV) promoter.

908 GATCTGAATTCGAGCTCGCTGTTGGCCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC 967 2 GATCTGAATTCGAGCTCGCTGTTGGGGTTGGCGGTTGAGGACAAACTCTTCGCGGTCTTTC Gaps Sequence 7469 BP; 1850 A; 1937 C; 1810 G; 1872 T; 0 U; 0 Other; ; 0 Score 325; DB 10; Length 7469; Pred. No. 3.7e-79; Indels ö 100.0%; Prec. ... 99.48; Best Local Similarity 100. Matches 325; Conservative Query Match

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121 CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT 62

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1147
                                                             1087
                                                                                                                                                                              968 CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes an isolated nucleic acid molecule (I) comprising an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide sequence comprising a first and second different TPL exons or first, second and third same or different TPL exons, the TPL exons chosen from complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon 3. (I) is useful for delivering a heterologous gene to a human or any animal, or for producing a gutless adenoviral vector particle. A
                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule useful for delivering heterologous gene to human or any animal, or for producing gutless adenoviral vector
                                              1028 GAGCGAGTCCGCATCGACCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA
                                                                                                            1088 GTCGCAAGGTAGGCTGAGCACCGTGGCGGGCGGCAGCGGCGGCGGCGGCGGTCGCGGTTGTTTCT
                                                                                                                                                           GGCGGAGGTGCTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA
                                                                                            GTCGCAAGGTAGGCTGAGCACCGTGGCGGGCGGCAGCGGGTGGCGGTCGGGGTTGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 packaging cell line; pseudotyping; adenovirus vector; gene therapy; hereditary disorder; tumour; HIV infection; fibre; fibre-gene-deleted adenoviruses; hygromycin resistance; tripartite leader sequence; ds; pCLF; pCDN3/fibre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV gene expression activation; adenovirus tripartite leader; TPL; gutless adenoviral vector particle; helper-independent fiberless recombinant adenovirus vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; anti-HIV; gene therapy; HIV gene expression inhibitor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibre expressing/tripartite leader sequence plasmid pCLF.
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                                                                                                                                                                                                                                          GGTGAGGTGTGGCAGGCTTGAGATC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; SEQ ID NO 8; 157pp; English.
                                                                                                                                                                                                                                                                                                                                      ADF48794 standard; DNA; 7469 BP
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Skripchenko Y;
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26-JUN-2000; 2000US-00423783.
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adenovirus type 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEGGERN D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEMEROW G R. HALLENBECK P. STEVENSON S. SKRIPCHENKO Y.
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(SKRI/) S
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coordenous gene to a target cell which involves contacting the cell with an amount of (II) sufficient to infect the cell. A helper-independent fiberless recombinant adenovirus vector genome (III) is useful for producing an adenovirus vector particle containing (III) which involves provaining a packaging cell line which complements replication and packaging of the genome and (III) which is deficient in expressing sufficient functional fiber protein to support assembly of fiber containing particles and harvesting the particle produced by the cell involves complementing a missing fiber gene of (III) or helper-dependent convolves recombinant adenovirus vector genome by expressing in packaging cells a fiber gene from a different adenoviral serotype than the recombinant adenovirus vector genome by expressing in packaging cells a fiber gene from a different adenoviral serotype than the recombinant adenovirus vector (III) is also useful for specifically targeting an adenovirus vector to a cell of choice. (I) is useful for gene therapy. (II) is useful for treating diseases such as hereditary disorder, and for reducing proliferation of tumour cells in a subject, or cultaritic leader sequence added to plasmid poly. (C) gene-deleted adenovirus expressing plasmid for complementation of E4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1028 GAGCGAGTCCGCATCGACCGGATCGGAAAACCTCTCGAGAAAGCGCGTCTAACCACAACA 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1148 GGCGGAGGTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      908 GATCTGAATTCGAGCTCGTCTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGGTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1088 GTCGCAAGGTAGGCTGAGCACCGTGGCGGCGGCAGCGGGGTGGCGGTCGGGGTTGTTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 GGCGGAGGTGCTGCTGATGATGAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
recombinant adenovirus particle (II) is useful for delivery of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7469 BP; 1850 A; 1937 C; 1810 G; 1872 T; 0 U; 0 Other;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.4%; Score 325; DB 10;
100.0%; Pred. No. 3.7e-79;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete sequence of the pE4/Fiber plasmid.
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(first entry)
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misc feature
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29-SEP-1998
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4289 GGCGGAGGTGCTGCTGATGAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA 4348

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4349 Géréagérerescasecrreagare 4373

BP

AAA59051 standard; DNA; 10610

RESULT 11

AAA59051

07-NOV-2000 (first entry)

AAA59051;

tripartite leader; adenovirus vector particle; gene delivery;

E4 gene, fiber gene, ss.

Adenovirus;

Human adenovirus type 5.

Synthetic

WO200042208-A1.

20-JUL-2000.

Nucleotide sequence of the E4/fiber-expressing plasmid pE4/Fiber.

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The present sequence is that of a pE4/Fiber plasmid used in the method of the invention. The plasmid contains an adenovirus type 5 (AD5) fiber gene controlled by a CMV promer, an AD5 Ed gene and an adenovirus type 2 (AD2) tripartite leader sequence upstream of the fiber gene. The controlled by a CMV promer, an AD5 Ed gene and an adenovirus type 2 (AD2) tripartite leader sequence upstream of the fiber gene. The covarious gene sequences encoding adenoviral structural proteins and/or early region proteins. Deletions in these proteins would allow a reduced cover isk of wild-type virus contamination and would also allow packaging of coreign DNA in such vectors for a variety of diagnostic and therapeutic applications. The adenoviral vectors having deletions in the structural and/or early gene regions are produced by cellular complementation of these adenoviral general produced by cellular complementation of these adenoviral generally rectors having deletions in the structural complementation plasmid which was introduced into a host cell line where parts of the fiber and E4 gene region would be stably inserted into the parts of the fiber and E4 gene region would be stably inserted into the complementation plasmid which was introduced into a host cell line where complement and E4 gene region would be stably inserted into the part of the fiber and E4 gene region would be stably inserted by presence or gene therapy, e-g. for treating conditions characterised by hypercorporal referance cells (e-g. tumours), genetic diseases (e-g. Huntington's clisease, Tay-Sachs disease, or sickle cell disease), or infections (e-g. Hiv infection). They can also be used for in vitro production of the production of the production of the parts of the parts of the parts of the parts of the production of the parts of the parts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adenoviral vectors - which lack DNA encoding for structural protein or fibre protein used particularly for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10610 BP; 2807 A; 2821 C; 2446 G; 2536 T; 0 U; 0 Other;
  a
= "AD5 E4 regulatory gene"
.4366
                                                                                               /note= "AD5 leader sequence"
4372. 6124
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                                                                                                                                                 /*tag= c
/note= "AD5 fiber gene"
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                                                                                                                                                                                                                                                                                                                                  97WO-EP005251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Von Seggern DJ;
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                       /note= '
                                                                            *tag=
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                                                                                                                                                                                                                                                                                                                                  24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1996;
                                                                                                                            misc_feature
                                                                                                                                                                                                                             WO9813499-A2
                                                                                                                                                                                                                                                                               02-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nemerow GR,
                                               sig_peptide
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4109 CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT 4168 The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL exons. The nucleic acid is used to produce an adenovirus vector particle, 4049 GATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC 2 GATCTGAATTCGAGCTCGCTGGTTGGCGTTGAGGACAAACTCTTCGCGGTCTTTC 62 CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT deliver an exogenous gene to a target cell, pseudotype recombinant virvectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a quiless adenoviral vector particle. The present sequence represents pE4/Fiber, a complementing plasmid containing E4 and fiber Adenoviral Gaps Sequence 10610 BP; 2807 A; 2821 C; 2446 G; 2536 T; 0 U; 0 Other; ö 99.4%; Score 325; DB 3; Length 10610; 100.0%; Pred. No. 4e-79; 0; Mismatches 0; Indels 0; Example 1; Page 164-167; 212pp; English. Matches 325; Conservative Similarity Query Match Local genes 음 ò g ઠ 4108 4168 4228 ö 181 1169 GAGCGAGTCCGCATCGGACCGGAAAACCTCTCGAGAAAGGCGTCTAACCGTCAACA 2 GATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGGTCTTTC 4049 GATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT 4109 CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT 122 GAGCGAGTCCGCATCGGCATCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA GTCGCAAGGTAGGCTGAGCACCGTGGCGGGCGGCAGCGGGTGGCGGTCGGGGTTGTTTCT 1229 GTCGCAAGGTAGGCTGAGCACCGTGGCGGCGCCAGCGGGTGGCGGTCGGGTTGTTTCT Gaps ô Length 10610; 0; Indels DB 2; 4e-79; Conservative

Best Local Similarity Matches 325; Conserv

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Query Match

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New nucleic acid comprising an adenovirus tripartite leader nucleotide for producing high-capacity and targeted vectors for adenovirus-based

Stevenson SC;

Hallenbeck PL,

Von Seggern DJ,

GR,

Nemerow

WPI; 2000-476068/41.

gene therapy

Skripchenko Y;

(NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH. (SCRI ) SCRIPPS RES INST.

14-JAN-2000; 2000WO-EP000265.

99US-0115920P

14-JAN-1999;

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01-MAY-2001; 2001US-00847101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides an isolated polynucleotide comprising adenovirus operatively linked to ITRS and a photoreceptor-specific promoter. A recombinant AV vector (AVV) comprising the polynucleotide is useful for targeted delivery of a gene product to the eye (especially to the vitreous cavity), for treating an ocular disease, e.g., retinal degenerative disease, retinitis pigmentosa, Stargard's disease, diabetic retinopathies, retinal vascularizations, and retinoblastoma, of a mammal preferably human The AAV comprises a fiber protein that specifically or selectively binds to receptors that are expressed on cells (preferably photoreceptors in the eye). Preferably, the recombinant virus comprise a fiber protein from an adenovirus type D subgroup or is a chimeric protein containing a portion of the N-terminus of an adenovirus type 2 or type 5 penton, and the therapeutic product is a trophic factor, an anti-
                                                                                                            301
                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide for making vectors, useful for treating ocular diseases, e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat sequences, packaging signal and photoreceptor-specific promoter.
                                                                                                                                                                                                                                                                                                                                                          Adenovirus; inverter terminal repeat sequence; ITRS; ocular disease; fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STDG1; opthalmological; antiinflammatory; antidiabetic; cytostatic;
                                   1169 GAGCGAGTCCGCATCGACCGGAAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA
                                                             GTCGCAAGGTAGGCTGAGCACCGTGGCGGGCGGCAGCGGGTGGCGGTCGGGGGTTGTTTCT
                                                                                   4229 GICGCAAGGIAGGCIGAGCACCGIGGCGGCGGCGGCGGCGGCGGCGGCGGCGGTCGGGCTTCT
                                                                                                              GGCGGAGGTGCTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA
                                                                                                                                      1289 GGCGGAGGTGCTGCTGATGAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA
                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of expression plasmid pE4/Fiber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Friedlander M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 118-121; 149pp; English
                                                                                                                                                                                       4349 GGTGAGGTGTGCCAGGCTTGAGATC 4373
                                                                                                                                                                GGTGAGGTGTGCCAGGCTTGAGATC 326
                                                                                                                                                                                                                                                     ABA94260 standard; DNA; 10610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-2001; 2001WO-EP004863
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(SCRI ) SCRIPPS RES INST.
(NEME/) NEMEROW G R.
(VSEG/) VON SEGGERN D J.
(FRIE/) FRIEDLANDER M.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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apoptotic factor, gene encoding a rhodopsin protein, a wild-type stargardt disease gene (STDG1), an anti-cancer agent and a protein that regulates expression of a photoreceptor specific gene product. The viral nucleic acid of AAV comprises ITRS and packaging signal derived from AAV subgroup B or C, especially an AV type 2 or type 5. AAV is also useful for targeted gene therapy, where the vector comprises an AV type 37 fiber protein or its portion, and selectively transduces photoreceptors and delivers a gene product encoded by AAV. The present sequence represents an expression plasmid p84/Fiber containing the adenovirus E4 and Fiber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4049 GAICTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10610 BP; 2807 A; 2821 C; 2446 G; 2536 T; 0 U; 0 Other;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 325; DB 6; Length 10610; Pred. No. 4e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%; Score ...
100.0%; Pred. No. 4e-75
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Matches 325; Conservative
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The invention describes an isolated nucleic acid (I) comprising adenovirus inverted terminal repeat sequence, an adenovirus packaging condenovirus inverted terminal repeat sequence, and aphororeceptor-specific promoter. A Recombinant adenovirus vector (II) comprising (I) is useful for targeted delivery of a gene product to the eye of a mammal which comprisives beterologous DNA encoding the gene product or resulting (II) that comprises heterologous DNA encoding the gene product or receptors that are expressed on cells which are recombinant virus comprises a fibre protein that specifically or comprises, in the eye. The recombinant virus comprises a fibre protein which is an adenovirus type 37, from an adenovirus type D to protein which is a chimmeric protein containing a sufficient portion of the N-terminus of an adenovirus type 2 or type 5 fibre protein for interaction with an adenovirus type 2 or type 5 fibre protein for interaction with an adenovirus serotype D knob portion of the fibre for comprises a photoreceptor specific promoter selective binding to photoreceptors in the eye of a mammal. The encapsulated nucleic acid comprising the therapeutic promoter compensatively linked to a nucleic acid comprising the therapeutic promoter which is chosen from trophic factor, anti-apoptotic factor, gene encoding a rhodopsin protein, wild-type stargardt disease gene (STDGI), an anti-concent agent and a protein that regulates expression of a photoreceptor-specific gene product. The delivery is effected for treatment of an encled specific gene product. The delivery is effected for treatment of an event and a protein that regulates expression of a photoreceptor-specific gene product. The delivery is effected for treatment of an event and a protein that regulates expression of a photoreceptor-specific gene product. The delivery is effected for treatment of an event of specific acid comprises in the event and acquired and acquired at extinoplastions inherited and acquired retinal and neovascular degenerative diseases. The v
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nd fibre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inverted terminal repeat (ITR) sequences, and an adenovirus packaging signal seguence. The ITRs and packaging signal are derived from an adenovirus sequence. C, or adenovirus types is the viral nucleic acid further comprises a photoreceptor-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter. (II) includes photoreceptor promoters providing a means not only for specific targeting of expression in these cells, but also for photoreceptor-restricted transgene expression. This sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4049 GATCTGAATTCGAGCTCGCTGTTGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC
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                                                                                                                                                                                                                                                                            sequences, adenovirus packaging signals operatively linked to the sequences and photoreceptor-specific promoters, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid expressing adenovirus type 5 fibre gene and E4 gene that ca
used to complement one or more delivery plasmids expressing E4 and
                                                                                                                                                                                                                                                     Novel nucleic acids comprising adenovirus inverted terminal repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10610 BP; 2807 A; 2821 C; 2446 G; 2536 T; 0 U; 0 Other;
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                                                                                                                                       Friedlander M;
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                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 57-61; 106pp; English.
                                                                                                                                       Seggern DJ,
                            01-MAY-2000; 2000US-00562934
                                                                           (SCRI ) SCRIPPS RES INST
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GTCGCAAGGTAGGCTGAGCACCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGTTGTTTCT

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The invention describes an isolated nucleic acid molecule (I) comprising an adenovirus tripartice leader (TPL) nucleotide, the TPL nucleotide sequence comprising a first and second different TPL exons or first, second and third same or different TPL exons, the TPL exons chosen from complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon 2 and complete TPL exon 3. (I) is useful for delivering a heterologous gene to a human or any animal, or for producing a gutless adenoviral vector particle. A recombinant adenovirus particle (II) is useful for delivery of an exogenous gene to a target cell which involves concacting the cell with an amount of (II) sufficient to infect the cell. A helper-independent fiberless recombinant adenovirus vector genome (III) is useful for producing an adenovirus vector particle containing (III) which involves producing a packaging cell line which complements replication and packaging the genome and (III) which is deficient in expressing sufficient functional fiber protein to support assembly of fiber
                                                        4229 GTCGCAAGGTAGGCTGAGCACCGTGGCGGCGGCGGCAGCGGGTGGCGGTCGGGGTTGTTTCT 4288
                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                              packaging cell line; pseudotyping; adenovirus vector; gene therapy;
hereditary disorder; tumour; HIV infection; E4 transcription unit; fibre;
hygromycin resistance; ds; circular; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule useful for delivering heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to human or any animal, or for producing gutless adenoviral vector
                                    GGCGGAGGTGCTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                         cytostatic, anti-HIV, gene therapy, HIV gene expression inhibitor, HIV gene expression activation; adenovirus tripartite leader; TPL,
                                                                                                                                                                                                                                                                                                                                                                                                          HÍV gene expression activation, adenovirus tripartite leade:
gutless adenoviral vector particle,
helper-independent fiberless recombinant adenovirus vector;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 16; 157pp; English.
                                                                                                                               GGTGAGGTGTGGCAGGCTTGAGATC 4373
                                                                                                            302 GGTGAGGTGTGGCAGGCTTGAGATC 326
                                                                                                                                                                                                                                                                                                                                                      E4/fibre expressing plasmid pE1/fibre.
                                                                                                                                                                                                                                         ADF48802 standard; DNA; 10610 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nemerow GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2000; 2000US-00482682.
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                                                                                                                                                                                                                                                                                                               12-FEB-2004 (first entry)
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SKRIPCHENKO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human adenovirus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEMEROW G R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-843463/78.
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Skripchenko Y;
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                                                                                                                                                                                                                                                                            ADF48802;
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(STEV/) 8
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containing particles and harvesting the particle produced by the cell line. [III] is useful for pseudotyping recombinant viral vectors which involves complementing a missing fiber gene of [III] or helper-dependent fiberless recombinant adenovirus vector genome by expressing in packaging cells a fiber gene from a different adenoviral serotype than the recombinant adenovirus vector. [III] is also useful for specifically targeting an adenovirus vector to a cell of choice. [I] is useful for equence the range therapy. [II] is useful for treating diseases such as hereditary disorder, and for reducing proliferation of tumour cells in a subject, or to disrupt HIV infection. This sequence represents the complementing plasmid pB4/fibre that expresses the adenoviral E4 and fibre genes.
                                                                                                                                                                                                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Circular, adenovirus type 5; pEl/Fiber plasmid; structural protein; complementation; fiber protein; gene therapy; HIV; tumour; AD5; early gene; Huntington's disease; Tay-Sachs disease; sickle cell disease; El regulatory protein; ds.
                                                                                                                                                                                                                                                                                                CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "ADS fiber gene consisting of a CMV promoter at this gene"
                                                                                                                                                                                                                                             2 GATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC
                                                                                                                                                                                                                                                            1049 GAICTGAATTCGAGCTCGCTGTTGGCTCGCGGTTGAGGACAAACTCTTCGCGGTTTTC
                                                                                                                                                                                                                                                                                                                         4109 CAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT
                                                                                                                                                                                                                                                                                                                                                     GAGCGAGTCCGCATCGACCCGCATCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA
                                                                                                                                                                                                                                                                                                                                                                             4169 GAGCGAGTCCGCATCGGACCGGATCGGAAAACCTCTCGAGAAAGGCGTCTAACCAGTCACA
                                                                                                                                                                                                                                                                                                                                                                                                         GTCGCAAGGTAGGCTGAGCACCGTGGCGGCGGCAGCGGGTGGCGGTCGGGGTTGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                  1229 GTCGCAAGGTAGGCTGAGCACCGTGGCGGGCGGCAGCGGGTGGCGGTCGGGGTTGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGGAGGTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGA
                                                                                                                                                                                                                   Gaps
                                                                                                                                                            Sequence 10610 BP; 2807 A; 2821 C; 2446 G; 2536 T; 0 U; 0 Other;
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                                                                                                                                                                                      99.4%; Score 325; DB 10; Length 10610; 100.0%; Pred. No. 4e-79;
                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                               100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete sequence of the pE1/Fiber plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1349 GGTGAGGTGTGGCAGGCTTGAGATC 4373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGAGGTGTGGCAGGCTTGAGATC 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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nes 325; Conservative
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Matches
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The present sequence is that of a pEI/Fiber plasmid used in the method of the invention. The plasmid contains an adenovirus type 5 (AD5) fiber gene controlled by a CMV promoter, an AD5 I gene and a pMAM backbone. The invention provides adenoviral vectors having deletions of all or part of various gene sequences encoding adenoviral structural proteins and/or early region proteins. Deletions in these proteins would allow a reduced risk of wild-type virus contamination and would also allow packaging of creign DNA in such vectors for a variety of diagnostic and therapeutic applications. The adenoviral vectors having deletions in the structural and/or early gene regions are produced by cellular complementation of these adenoviral genes. Therefore, the pEI/Fiber plasmid was used as a complementation plasmid which was introduced into a host cell line where parts of the fiber and El gene region would be stably inserted into the host cell chromosomes. The resulting El/fiber gene deficient plasmid can be used as a gene delivery vector. The vectors can be used for diagnosis or gene therapy, e.g. for treating conditions characterised by hypercy proliferative cells (e.g. tumours), genetic diseases (e.g. Huntington's diseases, Tay-Sachs disease, or sickle cell diseases), or infections (e.g. HIV infection). They can also be used for in vitro production of the piologically active proteins. (Updated on 25-MAR-2003 to correct PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13315 GATCTGAATTCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTC 13256
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                                                                                                                                                                                                                                                                                                                                                                   Adenoviral vectors - which lack DNA encoding for structural protein or fibre protein used particularly for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13255 CAGTACTCTTGGATCGGAAACCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT
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Pred. No. 4.4e-79;
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   97WO-EP005251
                                                                   96US-00719806
                                                                                                                                                                                                                                   Von Seggern DJ;
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Matches 325; Conservative
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(SCRI ) SCRIPPS RES INST.
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24-SEP-1997;
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CL467818 SAIL 1276
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CC258768 CH261-164
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BF972939 GC2241236
AG02111 AJ602111
CA711965 WJDIC.pk0
CA378248 657011 NC
CC258473 TH261-29F
CC258473 TH261-29F
CC5473782476 WJLIC.pk0
CA724476 WJLIC.pk0
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CA726479 CGAT34TC
EX900296 EX900296
CR665091 OSJNEDIZI
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Query
Match Length DB
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9b htc::
9b htc::
9b est4::
9b est6::
9b est6::
9b 9s81::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST:*
                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                    Scoring table:
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421.6
441.6
440.2
40.2
40.2
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AG101098 CF711474

BJ280072 BJ280072 CD897521 AZO3.105J CD897524 AZO3.104K AG125251 Pan trog1 CL491442 SALL_1271 CL491442 SALL_555 CL256246 FHCRC_GT- CL46949 ELOIT0206 CD439437 ELOIN0524 BX84406 AZADIN524 BX82406 AZADIN524 BX82406 AZADIN524 BX31486 BX31486 AJ477938 AJ437938 BE2306759 HS1 15 G0 BK823637 GM700021A CB627516 OSIIEB021	'S DNA linear GSS 31-MAR-2004 Arabidopsis thaliana genomic clone	<pre>survey sequence. e cress) Streptophyta, Embryophyta, Tracheophyta, ta; eudicotyledons; core eudicots; icales; Brassicaceae; Arabidopsis.</pre>	Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D., Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J. D., Cotton, D., Bullis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S. A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002)	th Triangle Park, NC 27709, USA Lacom T-DNA left border flanking sequences of on Library (SAIL) lines are available ogical Resource Center (ABRC).	B posis thaliana" : DNA" (02" (09.v1" :ollection" border sequences were isolated using a	DB 9; Length 1086;
22 4 BJ280072	ALIGNMENT  1086 bp  AIL Collection	GI:45870723  GI:45870723  thaliana (thale cress) traniana	rke, E., Presting, G., P., Bacwaden, J., G., Maguel, T., H. Gizzebroout Arabidopsis revisity, 7.2985-2994 (20	Conteact: Sessions A Applied Trait Genetics Syngement Biotechnology Inc. 3054 Cornwallis Rd., Research Triangle Park, NC Small: allen.sessionsosyngenta.com ABRC Stock Number CS647449; T-DNA left border fl Syngenta Arabidopsis Insertion Library (SALL) lithrough the Arabidopsis Biological Resource Cent Sequences represent a pool of amplified genomic class: TDNA tagged.	location/Qualifiers  11086 /organism="Arabidopsis thalian /mol_type="genomic DNA" /ecotype="Golumbia" /db_xref="taxon:3702" /clone="SAIL 1276 G09.v1" /clone="T-DNA left border seque modified TAIL-PCR strategy"	13.2%; Score 43.2; 56.1%; Pred. No. 0
38.6 11.8 642 38.6 11.8 649 38.6 11.8 670 38.2 11.7 909 38.2 11.7 1276 38 11.6 896 38 11.6 896 38 11.6 1978 37.8 11.6 1978 37.8 11.6 1058 37.8 11.6 1058 37.8 11.6 1058 37.8 11.6 11.5 397 37.6 11.5 568 37.6 11.5 568	CL467818 SAIL_1276_G09.v1 Si		Sessions, J. Bullis, J. Bullis, D., Snel Bullis, D., Snel Mitzel, T., Kata A high-throughp Plant Cell 14 (2235987)	Contact: Sessio Applied Trait G Syngente Blotec 3054 Cornwallis Email: allen.se ARC Stock Numb Syngenta Arabid through the Ara Sequences repre Single contiguo Class: TDNA tag	o.	/ Match Local Similarity 5
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 CL467818/c LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AUTHORS TITLE JOURNAL MEDLINE PUBMED	COMMENT	FEATURES SOUTG	
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us-09-482-682-26.rst

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1097 TGGGGCCGGC 1088
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Matches 71;
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CC258769/c
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3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Bmail: allen.sessions@syngenta.com
Bmail: allen.sessions@syngenta.com
ABRC Stock Number CS826573; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
Location/Qualifiers
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                                                                                                                                                                                                                                                              1262 bp DNA linear GSS 01-APR-2004
SAIL_620_G10.v3 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_620_G10.v3, genomic survey sequence.
CL496190
                                                                                                                                                                                                                                                                                GSS 01-APR-2004
                                                                  511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l (bases 1 to 1262)
Sessions.A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Boxaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
A high-throughput Arabidopais reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
                                   238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 GGTAGGCTGAGCACCGTGGCGGGCGGCAGCGGGTGGCGGTCGGGGGTTGTTTCTGGCGGAG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 GTGCTGCTGATGAAGTAAAGTAAGCGGGTCTTGAGACGGCGGATGGTCGAGGTGAGG 308
                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="genomic DNA"
/ecotype="Columbia"
/db xref="taxon:3702"
/clone="XaIL 520 G10.v3"
/clone lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using modified TAIL-PCR strategy"
                                   239 TCTGGCGGAGGTGCTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGT
   Gaps
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   61; Indels
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   0; Mismatches
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Arabidopsis thaliana
                                                                                                                                                                                                450 GGÁGGGGAGGGGGGGAGG 432
                                                                                                                                                                  299 CGAGGTGAGGTGTGGCAGG 317
                                                                                                                                                                                                                                                                                                                                                 CL496190.1 GI:45988256
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Applied Trait Genetics
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   Conservative
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Matches 75; Conserv
   78;
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                                                                                                                                                                                                                                                RESULT 2
CL496190/c
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JOURNAL
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CH261-164A7_RM1.1 CH261 Gallus gallus genomic clone CH261-164A7, survey sequence.
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CH261-164A7_RM1.2 CH261 Gallus gallus genomic clone CH261-164A7, genomic survey sequence.
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Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Extosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianine; Gallus.
1 (bases 1 to 1164)
                                                                                                                                                                                                          Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1164)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Garlus, gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 GTGGCGGCGGCGCGCGGCGGTCGCGGGTTGTTTCTGGCGGAGGTGCTGCTGATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 TAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGAGGTGAGGTGTGGCAGGCTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Center
Washington University School of Medicine
Bmail: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGGAGA
Class: BAC ends
High quality sequence start: 186
High quality sequence stop: 475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_line="UCD001, inbred 256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.7%; Score 41.6; DE
59.2%; Pred. No. 1.1;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/strain="Red_Jungle_Fowl"
/db_xref="taxon:9031"
/clone="CH261-164A7"

    .1164
    /organism="Gallus gallus"

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                                                                                                               CC258768.1 GI:3059939
                                                                                                                                                                Gallus gallus (chicken)
Gallus gallus
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Gaps

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/tissue type="leiomyosarcoma cell line"
/lab_host="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="MIH MGC 46"
/note="Organ: uterus; Vector: poTB7; Site 1: XhoI; Site_2:
BCORI; CDNA made by oligo-dT priming. Directionally cloned
into BcoRI/KhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pooldeae; Triticeae; Triticum.

Pooldeae; Triticae; roaceae;

Zhang, D., Klueva, N., Barker, G.L.A., Wilson, I.D., Edwards, K.J.,

Close, T.J., Zheng, H., McCartor, K., Soaree, B.M. and Nguyen, H.T.

Combining expressed-sequence-tags sequencing and subtractive hybridization for rapid identification of differentially expressed genes under heat stress in wheat (Triticum aestivum (L.) Moench)

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCGGGGTTGTTTCTGGCGGAGGTGCTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 GTGGAGCCGGACGCGGCGCGCGGTGTCGCTGATGAATTCAAGAACCCCCCAGTGAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 GGACCTGAGCGAGTCCGCATCGACCGGATCGGAAAACCTCTCGAGAAAGGCGTCTAACCA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGGAGCGGGCGGCGGGGGGGGGCGCGCGCGCTTCGGGAGCCAGCGGGTGCTG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ602111 364 bp mRNA linear EST 03-NOV-20
AJ602111 T05 Triticum aestivum cDNA clone C10_T05_plate_33, mRNA
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/tissue_type="Heat stressed whole seedlings"
/dev_stage="2 weeks old"
/clone_lib="T05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 364;
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University of Bristol
Woodland Road Bristol, BSB 1UG, United Kingdom.
Location/Qualifiers
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55.8%; Pred. No. 2...,
... 0; Mismatches
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0; Mismatches
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Pred. No. 2.5
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/cultivar="Mustang"
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Best Local Similarity 56.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/strain="Red Jungle Fowl"
/db_xref="laxon:901"
/clone="CH261-164A7"
/sex="female"
/cell_line="UCD001, inbred 256"
/colne_lib="UCD001, inbred 256"
/clone_lib="UCD001, inbred 256"

S Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
L Unpublished (2003)
Conteard X. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: RM1 TACGACTCATTAGGGAAA
Class: BAC ends
High quality sequence start: 186
High quality sequence stop: 475.
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602241236F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4329656 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 TAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGAGGTGAGGTGTGGCAGGCTTGAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 710)

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gow.h column: 09
Plate: LLCM1191 row: h column: 09
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.

Email: capbbs-remail.nih.gov

Tissue Procurement. Arcc

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Location/Qualifiers
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/db_xref="taxon:9606"
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                      632 bp mRNA linear EST 26-NOV-2002 wlplc.pk002.j18 wlplc Triticum aestivum cDNA clone wlplc.pk002.j18 5. end, mRNA sequence.
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247 GGGCTTGACCCACTCGACGAGGAGGGGCGTTCTTGGGGAAGGCGACGTTCTG 188
                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Spermatophyta, Spermatophyta, Poates, Friticae, Triticae, Tritic
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Hi Line) lemma and palea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 GGGCTTGACCCACTCGACGAGGAGCGTCGGAGGCGTTCTTGGGGGAAGGCGACGTTCTG 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dolan, M., Hainey, C., Yuan, Z.,
                                                                                               GTCACAGTCGCAAGGTAGGCTGAGCACCGTGGCGGCGCGCCAGCGGGTGGCGGTCGGGGTT
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E. I DuPont de Nemours and Company
E. I DuPont de Nemours and Company
Tel: 302-631-2607
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
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/db_xref="taxon:4565"
/clone="wlplc.pk002.j18"
/lab_host="PH108"
/lone=lib="wlplo"
/note="Vector: pBluescript SK+; Si
Xhol; Wheat (Triticum aestivum, Hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
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Miao, G., Caraher, N. and Hanafey, M.K.
DuPont Wheat CDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum (bread wheat)
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Location/Qualifiers
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CA731965.1 GI:25547563
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CA378248/c
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SOURCE
ORGANISM
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CA731965/c
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CA378248 598 bp mRNA linear EST 06-NOV-2002 657011 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT42L01\_B\_F01 5', mRNA sequence.

LOCUS

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CH261-29F4 RM1.1 CH261 Gallus gallus genomic clone CH261-29F4, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus. I (bases I to 598)

Rexroad, C. E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G., Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.
Sequence analysis of a rainbow trout cDNA library and creation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 crérocrescoadocrudoridecodocidariones rendades de contra a contra de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoseuria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross match v0.990329.
Seq primer: AGCGGATAACAATTTCACAGGA.
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/tissue_rype="pooled"
/lab host="WH108"
/clone_lib="NCCCWA_IRT"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from Pooled tissue from brain, gill, liver, spleen, muscle, and kidney."
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Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
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/mol_type="mRNA"
/db_xref="taxon:8022"
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                                                                                                                                                                Oncorhynchus mykiss (rainbow trout)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                   CC286173.1 GI:30655433
CA378248.1 GI:24697932
                                                                                                                                                                                                                                                    Oncorhynchus mykiss
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Best Local Similarity 50.03
Matches 100; Conservative
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AJ437840 ADDIR2 Helianthus annuus cDNA clone HaDDIR205H12, mRNA
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1 (bases 1 to 511)
                                                                                                                                                                                                                            /db_xref="taxon:3702"
/clone="SAIL 877 H06.v1"
/clone lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"
    Syngenta Arabidopsis Insertion Library (SAIL) lines are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratoire de Biotechnologie et Amelioration des Plantes
Institut National Polytechnique de Toulouse - Ecole National
Superieure Agronomique de Toulouse
IFR40, Pole de Biotechnologie Vegetale, 18 chemin de Borde Rouge,
Auzeville, CASTANET TOLOSAN 31326, France.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 AGGTAGGCTGAGCACCGTGGCGGCGGCGGCGGGTGGCGGTCGGGGTTGTTTCTGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and single contiguous sequences.
Class: TDNA tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tamborindeguy,C., Ben,C., Liboz,T. and Gentzbittel,L. Sequence evaluation of four specific cDNA libraries for developmental genomics of sunflower Mol. Genet. Genomics of Sunflower Contact: Gentzbittel L
                                                                                                                                                                                                                                                                                                                                                                                              Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                               /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Helianthus annuus"
                                                                                                                                                                                                                                                                                                                                                                                           Score 39.6; DB Pred. No. 4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helianthus annuus (common sunflower)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="hypocotyls"
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/dev_stage="1-5 days"
                                                                                                                                                                                      /mol_type="genomic DNA"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4232"
/clone="HaDp1R205H12"
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/cultivar="Emil"
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--hes 75; Conservative
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3944 Cornwallis Rd., Research Triangle Park, NC 27709, USA
2054 Email: allen.sessions@ayngenta.com
ABRC Stock Number CS839484; T-DNA left border flanking sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CL513605
936 bp DNA linear GSS 01-APR-2004
SALL 877 H06.v1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL 877-H06.v1, genomic survey sequence.
CL513605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 GGTAGGCTGAGCACCGTGGCGGCGGCAGCGGGTGGCGGTCGGGGGTTGTTTCTGGCGGAG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 GTGCTGCTGATGATGTAATTAAAGTAGGCGGTCTTGAGACGGCGGATGGTCGAGGTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_line="UCD001, inbred 256"
/clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_l: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - For library and clone
ordering information: http://www.chori.org/bacpac"
Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R. Gallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Lenght: 182000 Std Error: 0.00
Seq prime: RMI TACGACTCACTATAGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 GGGAGGGGTGGGATGGGGGGTAATGGGGGGGGGTAGAGAGGGGCGCGGAGGGTGGGGAGAG
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                                                                                                                                                                                                                                                                                                                                            /organism="Gallus gallus"
/mol type="genomic DNA"
/strain="Red Jungle Fowl"
/db xref="taxon:9031"
/clone="CH261-29F4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Arabidopsis thaliana
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High quality sequence start: 135
High quality sequence stop: 281.
Location/Qualiflers
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Applied Trait Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
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Matches 76; Conservative
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BX900296

847 bp mRNA linear EST 16-JAN-2004
BX900296 Oryza sativa library (Han B) Oryza sativa cDNA clone
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Enrhartoideae; Oryzae.

Enrhartoideae; Oryzae.

I (basea: 1 to 847)

Han, B., Feng, C., Huang, Y.C., Ying, K., Li, Y., Guan, J.P., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Weng, Q.J., Zhang, L., Liu, Y.L., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, L., Liu, Y., Li, C., Li, T., Zhang, Y., Li, C., Li, T., Zhang, Y., Li, C., Li, T., Zhang, Y., Hu, H., Jia, P.X., Zhang, L., Lan, L. F., Chen, W., Wu, S.A. and Xue, Y.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 719)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 TCGGCCAAGCGGAGAAGTTCGCGGGAGGCGTCGACTTGCTCGTGGTCGGGCCCGGGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 TGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCTGAGCGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 TCGAGCTCGCTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="zmmBma0219F20"
/clone lib="zm 0.7 1.5 KB"
/note="Vector: pBGSK-; Site 1: Hincl1; 0.7-1.5
/methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 719;
                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-6208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
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BX900296
BX900296.1 GI:40492487
                                                                                                                                                                                                                                                                              Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                      Other_GSSs: OGEAT34TM
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Class: sheared ends
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Matches 104; Conservative
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1 (bases; Triticeae; Triticum.

2 (bases; Triticeae; Triticum.

3 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.

Dupont Wheat cDNA Sequence

Unpublished (2002)

Contact: Scott V. Tingey

Contact: Scott V. Tingey

E. I. DuPont de Nemours and Company

I Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2602

Email: Scott. V. Tingey@USA.dupont.com

Seq primer: Mil.,
                                                                                                                                                                                       wdilc.pk002.d2 wdilc Triticum aestivum cDNA clone wdilc.pk002.d2 5' end, mRNA sequence.
CA728476
CS728476.1 GI:25450461
EST.
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BZ715587.1 GI:28498659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   557 GGGCTTGACCCACTCGACGAGGGGGTCNGAGGCGTTCTTGGGGAAGGCGACGTTCTG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 GACCTGGTCGCCGCGGCGTCGATGCCGGTGTAGAGCATGACAGGCTGCCGTCGGGGAG 438
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Hi Line) developing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 59; Indels
                        Indels
                                                                   22 GTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGT
                        3,
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/note="Vector: pBluescript SK+; Si
Xhol; Wheat (Triticum aestivum, Hi
inflorescence +/- 4 cm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
12.0%; Score 39.2; DB 6;
Best Local Similarity 55.6%; Pred. No. 5;
Matches 74; Conservative 0; Mismatches 59;
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  Pred. No. 4.9;
); Mismatches
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Triticum aestivum
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l Similarity 93.2%;
41; Conservative (
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  Best Local Similarity
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                   Matches
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/clone="OSJNEf15K06"

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Search completed: July 14, 2005, 23:22:42
Job time : 3123.52 secs
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrharcoideae; Oryzeae; Oryza.

1 (bases 1 to 378)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Rudrana, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of Ests involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB685324 378 bp mRNA linear EST 09-APR-20 OSJNEf15K06.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA clone OSJNEf15K06 5', mRNA sequence.
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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/ Organism="Oryza sativa (japonica cultivar-group)"
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/db_xref="taxon:39947"
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12.0%; Score 39.2; DB 5; Length 847;
Best Local Similarity 53.7%; Pred. No. 5.1;
Matches 80; Conservative 0; Mismatches 69; Indels
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/mol_wore="mRNA"
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/clone="y658903p5"
/clone_lib="Oryza sativa library (Han B)"
                                                                                       China
                    Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 200233, Ch
Email: bhan@ncgr.ac.cn
Clone requests: bhan@ncgr.ac.cn
This is rice cdna est clone
Web site: http://www.ncgr.ac.cn
Location/Qualifiers
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BACKWARD: gga aac agc tat gac cat g
Plate: 15 row: K column: 06
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CB685324.1 GI:29689049
    Unpublished (2003)
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Tel: 520 626 3967
Fax: 520 621 9288
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"
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                                                                                                                                                                          111 CCGAGGGACCTGAGCGAGTCCGCATCGACCGGATCGGAAAACCTCTCGAGAAAGGCGTCT 170
                                                                                                                                                                                             Gaps
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                                                                                                                 DB 6; Length 378;
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                                                                                                                11.9%; Score 39; DB 6 ilarity 55.6%; Pred. No. 5.4; Conservative 0; Mismatches
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July 14, 2005, 04:39:07; Search time 9289.17 Seconds (without alignments) 6468.225 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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SUMMARIES	Description	BD268221 Adenoviru	BD268252 Adenoviru	BD268233 Adenoviru	BD268236 Adenoviru	BD268232 Adenoviru	BD268253 Adenoviru	A83180 Sequence 13	BD082846 Method an	X02996 Adenovirus	CQ854904 Sequence	CQ854905 Sequence	BD268216 Adenoviru	AR343138 Sequence	AX382187 Sequence	CQ854906 Sequence	AF323988 EGFP expr	AY370909 Expressio	AX084504 Sequence	AX084506 Seguence
	ΩI	BD268221	BD268252	BD268233	BD268236	BD268232	BD268253	A83180	BD082846	AD5001	CQ854904	CQ854905	BD268216	AR343138	AX382187	CQ854906	AF323988	AY370909	AX084504	AX084506
	DB	9	9	9	9	9	9	9	9	14	9	9	9	9	9	9	12	12	9	9
df	* Query Match Length DB	1240	7231	7960	7989	8383	8484	10332	10332	11570	31976	31976	32480	32798	32798	32802	33007	33476	33592	33699
	* Query Match	100.0	99.9	6.66	66.66	99.9	99.9	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5
	Score	1240	1239	1239	1239	1239	1239	1135	1135	1135	1135	1135	1135	1135	1135	1135	1135	1135	1135	1135
	Result No.	1	8	٣	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19

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source

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Location/Qualifiers
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Location/Qualifiers

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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 BD26821 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT

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other sequences; artificial sequences.

Is (bases 1 to 7231)

S Nemerow, G.R., Seggern, D.J.V., Hallenbeck, P.L., Stevenson, S.C. and Skripchenko, Y.
Adenovirus vector, packaging cell line, composition and method for production and use

Droduction and use

NOVARIS AG, THE SCRIPPS RESEARCH INSTITUTE

OS Artificial Sequence

PN JP 2002534130-A/56

PP 14-JAN-2000 JP 200593765

PR 14-JAN-1999 US 60/11520

PI GLEN ROBERT NEMEROW, DANIEL, J VON SEGGERN, PAUL L HALLENBECK, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DN JP 2002534130-A/56
PN JP 2002534130-A/56
PD 15-OCT-2002
PP 14-JAN-1909 US 60/115920
PI 4-JAN-1999 US 60/115920
PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO
PC C12N15/09, A61K35/76, A61K48/00, A61P43/00, A61P43/00, PC C12N5/10, PC C12N5/10, A61K35/76, A61K48/00, A61P3/35, G01N33/566, C12N15/00, C12N5/00 CC Description of Artificial Sequence: plasmid FH Key Location/Qualifiers
FT Source //organism-/artificial/
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CTGAAAAGGCGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGGATTT
                                                                                                       GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG
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                                                                           GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG
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Adenovirus vector, packaging cell line, composition and method for production and use production and use Patent: JP 200534130-A 37 15-OCT-2002; NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
OS Artificial Sequence
PN JP 2002534130-A/37
PD 15-OCT-2002
PF 14-JAN-2000 JP 200593765
PR 14-JAN-1999 US 60/115920
PT GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO
PC CLINIS/09, A61K35/76, A61K48/00, A61P35/00, A61P3/00, PC CLINIS/00, CLINIS/100, CLINI
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(bases 1 to 7960)
Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C.
Skripchenko,Y.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="teaxon:32630"
  7960 bp DNA packaging cell line,
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JP 2002534130-A/37.
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production and use.
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PC C12N15/09, A61K35/76, A61K48/00, A61P35/00, A61P43/00, PC C12N5/10,
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                                                                                                                                                                                                                             TCTCGAGAAAGGCGTCTAACCAGTCACAGTCGCAAGATC 1239
                                                                                                                                                                                                                                              Score 1239; DB 6; I
Pred. No. 1.4e-237;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="teaxon:32630"
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 1239; Conservative
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PAT 27-AUG-2002
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                                                                                                                           5428 GCAGCTTGTTTGACCTCGCGCGCGTCACCTGCACGTCTAGGGCGCAGTAGTCCAGGGTTT
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TTCCAAGATATGTAGGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACGTAATCGTATA
                5188 TTCCAAGATATGTAGGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACGTAATCGTATA
                                                                               CCTTGATGATGTCATACTTATCCTGTCCCTTTTTTTTCCACAGCTCGCGGTTGAGGACAA
                                                        GCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCAGTAGTCCAGGGTTT
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Quax, P.H.A. and Verheijen, J.H.
Method and construct for inhibition of cell migration
Patent: JP 2001525669-A 13 11-DEC-2001;
WEDERLANDSE ORGANISATIE VOOR TOEGEPAST NATUURWETENSCHAPPELIJK
ONDERZOEK TNO
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PD 11-DEC-2001
PP 11-MAY-1998 D1 1998549077
PR 12-MAY-1997 EP 97201423.7
PI PAULUS HUBERTUS ANDREAS QUAX, JOHAN HENDRIKUS VERHEIJEN C12N9/72, C12N15/62, C07K14/81//C07K19/00
CC Strandedness: Unknown;
CC Topology: Unknown;
PH Key
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Pred. No. 8.6e-217;
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0; Mismatches
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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unclassified.

l (bases 1 to 10332)

Verheijen, J. H. and Quax, P. H.

WETHOD AND CONSTRUCT FOR INHIBITION OF CELL MIC

PACENT: WO 9851788-A 13 19-NOV-1998;

VERHEIJEN JOHAN HENDRIKUS (NL); TNO (NL)

Location/Qualifiers
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100.0%; Pred. No. 8.6e-217;
ive 0; Mismatches 0;
              DNA
                                                                                                                                                                                                                           /organism="unidentified"
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/db_xref="taxon:32644"
           A83180
Sequence 13 from Patent A83180
                                                     A83180.1 GI:6732627
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ACCESSION	KEYWORDS	ORGANISM	TITLE JOURNAL MEDLINE	REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUBMED	AUTHORS TITLE	JOURNAL MEDLINE PUBMED	AUTHORS TITLE	MEDLINE PUBMED REFERENCE	TITLE JOURNAL	MEDELINE PUBMED REFERENCE AUTHORS	JOURNAL	REFERENCE AUTHORS	JOURNAL	MEDLINE PUBMED REFERENCE AUTHORS	JIILE JOURNAL MEDLINE PUBMED REFERENCE	AUTHORS
TCACCTGGCCCGCGGTGATGCCTTTGAGGGTGGCCGCATCCATC	186 TCTTTTTGTTGTCAAGCTTGGTGGCAAACGACCCGTAGGGGGGGTTGGACGAACTTGG 245	246 CGATGGAGCGCAGGGTTTGGTCGCGATCGCGCGCTCCTTGGCCGCATGTTTA 305 	306 GCTGCACGTATTCGCGCCACACGCCCTTCGGGAAAGACGGTGCGCTCGTCGG 365	366 GCACCAGGTGCACGCGCCAACCGCGGTTGTGCAGGTCAACGCTCAACGCTGGTGGCTA 425	426 CCTCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGCGGCCGCCCTTGCGCGAGAGAATG 485	486 GCGGTAGGGGGTCTAGCTGCCTCGTCCGGGGGGTCTGCGTCCACGGTAAAGACCCCGG 545	546 GCAGCAGGCGCGCGCGTCGAAGTACTATCTTGCATCCTTGCAAGTCTAGCGCCTGCTGCC 605 	606 ATGCGCGGCGGCAAGCGCGCGCTCGTATGGGTTGAGTCGGGAACCCCATGGCATGGGGT 665	666 GGGTGAGCGCGGAGGCGTACATGCCGCAAATGTCGTAAACGTAGAGGGGCTCTCTGAGTA 725 	726 TTCCAAGATATGTAGGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACGTAATCGTATA 785	786 GTTCGTGCGAGGAGCGAGGACCCGAGGTTGCTACGGGCGGG	846 GGAAGACTATCTGCCTGAAGATGGCATGTGGAGTTGGATGATATGGTTGGACGCTGGAAGA 905	906 CGTTGAAGCTGGCGTCTGTGAGACCTACCGCGTCACGACGAGGAGGGGTAGGAGTCGC 965	966 GCAGCTTGTTGACCAGCTCGGCGGTGACTCTAGGGCCCAGTAGTCCAGGGTTT 1025	1026 CCTTGATGATGTCATACTTATCCTGTCCCTTTTTTTCCACAGGTCGCGGTTGAGGACAA 1085 	1086 ACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGAACG 1140 	
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AD5001 11570 bp DNA linear VRL 09-SEP-2004 Adenovirus type 5 left 32% of the genome (coordinates 0% to 32.39%

RESULT 9
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P.H., Maat, J., van Ormondt, H. and Sussenbach, J.S.

tide sequence at the termini of adenovirus type 5 DNA

ids Res. 4 (12), 4371-4389 (1977)
                                                                                                    plicing, DNA polymerase, overlapping genes; polymerase; ase III; terminal protein; terminal repeat; transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Van Ormondt, H.

1 Van Ormondt, H.

1 ide sequence of the transforming HindIII-G fragment of type 5 DNA. The region between map positions 4.5 (HpaI 75-90 (1979)
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In Beveren,C.P. and van Ormondt,H.
inde sequence of adenovirus type 5 early region E1: the reen map positions 8.0 (HindIII site) and 11.8 (Smal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleotide sequences, transcription and translation and restriction endonuclease cleavage maps of group-c
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van Ormondt, H., Maat, J. and van Beveren, C.P.
The nucleotide sequence of the transforming early region El of adenovirus type 5 DNA
Gene 11 (3-4), 299-309 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                          . to 1574)
.,H., Maat,J., De Waard,A. and Van der Eb,A.J.
de sequence of the transforming Hpal-E fragment of
type 5 DNA
309-328 (1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,M., Akusjarvi,G., Virtanen,A. and Pettersson,U.
of two spliced mRNAs from the transforming region of
coup C adenoviruses
(5733), 694-696 (1979)
. by <ad2>).
67 J01968 J01970 J01971 J01972 J01974 J01976 J01977
79 K00515 V00025 V00026 V00027 V00029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mylch alters initiation of transcription by RNA III on the Ad5 chromosome , 947-954 (1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ',M., Le Moullec,J.M. and Pettersson,U.
tructure of two adenovirus tumor antigens
Acad. Sci. U.S.A. 77 (7), 3778-3782 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. (Ed.);
IRUSES: 937-1002;
Harbor Laboratory (1980)
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This sequence corresponds to bases 1 to 11560 of <ad2>, which serve as some basis for the annotation of sites. the differences between <ad2> and <ad5> are too many to report herein, however a printout of those is available upon request from genbank. the map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 (bases 325 to 604)
Hearing, P. and Shenk, T.
Functional analysis of the nucleotide sequence surrounding the cap
site for adenovirus type 5 region BIA messenger RNAs
J. Mol. Biol. 167 (4), 809-822 (1983)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 (bases 6242 to 11570)
Dekker,B.M. and van Ormondt,H.
The nucleotide sequence of fragment HindIII-C of human adenovirus
type 5 DNA (map posttions 17.1-31.7)
Gene 27 (1), 115-120 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Here Adeno virus sequences are always given in 5' to 3' direction and the sequence of the 1-strand is displayed irrespective of the direction the viral transcription takes.
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J. Virol. 50 (1), 30-37 (1984)
                                                                                                                                                                                                                                                                                                                                       12 (bases 4001 to 6246)
van Beveren, C.P., Maat, J., Dekker, B.M. and van Ormondt, H.
The nucleotide sequence of the gene for protein IVa2 and of the leader segment of the major late mRNAs of adenovirus type 5
Gene 16 (1-3), 179-189 (1981)
10 (bases 10555 to 10733)
Fowlks,D.w. and Shenk,T.
Transcriptional control regions of the adenovirus VAI RNA gene Cell 22 (2 Pt 2), 405-413 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deletion mutants
14 (bases I to 66)
Nagata,K., Guggenheimer,R.A. and Hurwitz,J.
Specific binding of a cellular DNA replication protein to the origin of replication of adenovirus DNA proc. Natl. Acad. Sci. U.S.A. 80 (20), 6177-6181 (1983)
                                                                                                                                                                Bos, J.L., Polder, L.J., Bernards, R., Schrier, P.I., van den
Elsen, P.J., van der Bb, A.J. and van Ormondt, H.
The 2.2 kb Elb mRNA of human Ad12 and Ad5 codes for two tumor
antigens starting at different AUG triplets
Cell 27 (1 Pt 2), 121-131 (1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This often causes confusion because the generally accepted
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with ad2, not all the transcripts from this region have been characterized at the sequence level. the nine proteins given in features table below are not the only possible gene products (see the main adenovirus 2 entry).

large amounts of small rnas are produced from the vai and vail genes late in development for unknown reasons. [5] and [6] demonstrate that vai gene activity influences vali expression; that the 5' flank affects the start site of the rna but that an intragenic promoter (bases 10626 to 10690 below) determines whether the rna is actually produced; and that there is striking similarity between this rna and trans.
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/translation="MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFEPPTLH
ELYDLDVTAPEDPNEEAVSQIFPDSVMLAVQEGIDLLTFPPAPGSPEPPHLSRQPEQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQRALGPVSMPNLVPEVIDLTCHEAGFPPSDDEDEEGEEFVLDYVEHPGHGCRSCHYH
RRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPEPEPEPEPEPARPTRRPKMAPAILRRPT
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                                                                                           the sequence represents the early mrna transcripts ela and elb and the intermediate mrna transcript ix, all of which are transcribed rightwardly off the r-strand; the iva2 and e2b mrnas which are transcribed leftwardly off the l-strand ((indicated by 'ic)' and 'comp strand' below)); and the 5' end of the 28 kb major late mrna the cap sites and possible promoter sequences for these are summarized in the following table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125
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coordinates in the sites presume 360 bases per map unit. although there are approximately 115 sequence differences between the two strains over this region, no site difference exceeds 0.02% by this
                                                                                                                                                                                                                                                                                                                                                                                                                                             tataaaa at bases 6018-6024 [10] as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(560. .1112,1229. .1545)
/note="unnamed protein product; Bla protein from 13s mrna
(32k,regulation and transformation)"
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/mol_type="genomic DNA"
/db_xref="taxon:28285"
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/note="mRNA 1 (part 1)"
join(699. .974,1229. .1632)
/note="mRNA 2 (part 1)"
join(560. .1112,1229. .1545)
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/db_xref="GI:4584382"
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PAT 23-AUG-2004

linear

31976 bp DNA Sequence 1 from Patent WO2004066947. CQ854904.1 GI:51510464

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 10 CQ854904 LOCUS

. unidentified adenovirus unidentified adenovirus Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

1 Hu, F. and Wu, B.

REFERENCE AUTHORS

	Db   5882 GGGTGAGCGCAGAGCTACATGCCGCAATGTCGTAAACGTAGAGGGGCTCTCGAGTA 5941	Oy 1086 ACTCTTGGGGTCTTTCCAGTACTCTTGGATCGGAACCCGTCGGCTCCGAACG 1140
Oy         906         CGTTGAAGCTGGCGTCTGTGAAACCTACCGCGTCACGAAGGAGGCGTAGGAGTCGC         965           bb         6122         CGTTGAAGCTGGCGTCTGTGAACCTACCGCGTCACGCACG	RESULT 11  CQ854905  LOCUS  LOCUS  Sequence 2 from Patent W02004066947.  ACCESSION  CQ854905  VERSION  VERSION  VERSION  VIRUSES  VIRUS	CCCCATCGCTGCTGCGGGGCGCCACTTGGGGTGATACTCCTTGAA  CCCCATCGCTGTTGCGGGGGCCACTTGTGGGGTGATACTCCTTTGAA  CCCCATCGCTTGTGTGGGGGGGCCACTTTGGGGTGATTTGATAT  TGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGATTTGATAT  TGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGGATTTGATAT  TGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGGATTTGATAT  TGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGGATTTGATAT  TGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGGATTTGATAT  TGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGAAAAGACAA  TGACGGGTAATGGTTTGAGGGTGGCCGCATCCATCTGGTCAGAAAAGACAA  TGTCAAGGTTTGGTTT

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PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,PC 212N5/10.
PC C12N5/10.
PC C12N5/10.
Adenovirus vector, packaging cell line,
CC composition and method
CC production and use
FH Key Location/Qualifiers
FT source | 1.3480
FT source | 20 proganism='Adenovirus'.
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Pred. No. 7.9e-217;
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Brough, D.E., King, C.R., Kovesdi, I. and Schaible, J.J.
Replication deficient adenoviral TNF vector
Patent: us 6579522-A 1 17-JUN-2003;
Location/Qualifiers
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ORIGIN  Query Match  Query Match  Best Local Similarity 100.0%; Pred. No. 7.9e-217;  Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 6 CACTCTTCCGCATGGTGTTTCGGAGGGCCAGTTTGGGGTGAGTACTCCTTGAA 65		246 CGATGCAGGCAGGGTTTGTTGTTGTGGGGGCGTTGGGGGGGTTGGAACTTGG 246 CGATGGAGGCAGGGTTTGTTGTGGGGGATCGGGGGGCGTTGGCGGAACTTTG 2525 CGATGGAGGGAGGGTTGGTTTTTGTCGCGATCGGCGGCTCCTTGGCCGCATGTTTA 5295 CGATGGAGGGAGGGTTGGTTTTTTGTCGCGCATCGGCGCCTCCTTGGCCGCGATGTTTA 306 GCTGCACGTATTCGCGCAACGCACCGAACGCAACGGAAAAAACGCGCGCTCGTCGG				DD   5715 GGGTGAGGGGGGGGGCTACATGCGCAAATGTCGTAAACGTAGAGGGGCTCTCTCAGGTA 5774
Qy         366 GCACCAGGTGCAACCGCGGTTGTGCAGGGTCAACGCTGGTGGTTG 425           Db         5415 GCACCAGGTGCACCGCGGTTGTGCAGGGTGACAACGCTGGTGGTTA         425           Qy         426 CCTCTCCGCGTAACGCTCGTTGTCCAGCAGGTGCCGAGCAGATG         485           Db         5475 CCTCTCCGCGTAAGGCTCGTTGGTCCAGCAGAGGCGCCCCTTTCGCGCAGCAGATG         485           CTCTCCCGCGTAAGGCGCTCGTTGGTCCAGCAGAGGCGCCCCCTTCGCGAGCAGATG         534           Qy         486 GCGTAAGGGGTCTAGCTCGTCGCTCGCGGGGGTCTGCGCTCACGGTAAACACCCCGG         545           CD         5535 GCGGTAGGGGTCTAGCTCCGCGGGGGTCTGCCCCCGGTAAACACCCCGG         5594		666 GGGTGAGCGCGGAGCGTACATGCCGCAAATGTCGTAAACGTAGAGGGCCTCTCTGGTAA	Qy         786 GTTCGTGCGAGGAGGAGGAGGACCGAGGTTGCTACGGGCGGG	Qy         906         CGTTGAAGCTGGCGTCTGTGAGACCTACCGCGTCACGCACG	Qy         1026         CCTTGATGATGATGATTACTTATCCTGTCCCTTTTTTTTCCACAGCTCGCGGTTGAGGACAA         1085           Db         6075         CCTTGATGATGATGATCTTATCCTGTCCCTTTTTTTTTCCACAGCTCGCGGTTGAGGACAA         6134           Qy         1086         ACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG         1140           Db         6135         ACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG         6189	AX382187 AX382187 AX382187 DEFINITION Sequence 1 from Patent W00200906. ACCESSION AX382187 AX

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/mol_type="unassigned DNA"
/db_xref="taxon:10535"
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                                                                                                                                                                                                                  Hu,F. and Wu,B.
Therapy for primary and metastatic cancers
Patent: WO 20040666947-A 3 12-AUG-2004;
Shanghai Sunway Biotech Co Ltd (CN)
Location/Qualifiers
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                                                                                                                   CQ854906 32802 bp DN
Sequence 3 from Patent WO2004066947.
CQ854906.1 GI:51510466
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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

July 14, 2005, 04:35:42; Search time 1748.26 Seconds (without alignments) 4198.742 Million cell updates/sec Run on:

US-09-482-682-32 1240 Title: Perfect score:

1 ggatccactctcttccgcat......cagtcacagtcgcaagatct 1240 Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04:\* Database :

geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\*

geneseqn2003ds:\*geneseqn2004as:\*geneseqn2004bs:\* geneseqn2001as:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Aaa59060 Nucleotid	Aba94272 Adenoviru	Adb75118 Adenoviru	Adf48742 Ad5 tripa	Aaa59090 Nucleotid	Aba94286 Nucleotid	Adb75132 Plasmid p	Adf48774 Adenoviru	Aaa59072 Nucleotid	Aba94274 Nucleotid	Adb75120 Plasmid p	Adf48754 Fibre exp	Aaa59075 Nucleotid	Aba94277 Nucleotid	Adb75123 Plasmid p	Adf48757 Fibre exp	Aaa59071 Nucleotid	Aba94273 Nucleotid	Adb75119 Plasmid p	Adf48753 Fibre exp
	ID	AAA59060	ABA94272	ADB75118	ADF48742	AAA59090	ABA94286	ADB75132	ADF48774	AAA59072	ABA94274	ADB75120	ADF48754	AAA59075	ABA94277	ADB75123	ADF48757	AAA59071	ABA94273	ADB75119	ADF48753
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æ	Query Match	100.0	100.0	100.0	100.0	6.66	99.9	99.9	6.66	99.9	6.66	6.66	99.9	6.66	99.9	99.9	99.9	99.9	99.9	99.9	99.9
	Score	1240	1240	1240	1240	1239	1239	1239	1239	1239	1239	1239	1239	1239	1239	1239	1239	1239	1239	1239	1239
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Aaa59091 Nucleotid	Adrae//5 libre exp Aav33921 Nucleotid	Aad03963 Adenoviru	Aaa09088 AdPB-beta	Ado09305 WT1-F-ade	Adr41670 Oncolytic	Adr41669 Oncolytic	Aat60559 Recombina	Aaa09092 AdMMTV-be	Aaa14723 Nucleotid	Aaa09090 AdPSA-bet	Aac89170 AdRSVpHYD	Aaa14803 Nucleotid	Aaz93332 Partial s	Ado36637 Adenovira	Aaa59055 Nucleotid	Aba94267 Adenoviru	Adb75113 Adenovira	Adf48737 Adenoviru	Ado36636 Adenovira	Aba97684 Replicati	Adr41671 S98-100 (	Aaa09086 AdRSV-bet	Adp79484 Adenoviru
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## ALIGNMENTS

Adenovirus; tripartite leader; adenovirus vector particle; gene delivery; Nucleotide sequence of a tripartite leader sequence. (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH. (§CRI ) SCRIPPS RES INST. AAA59060 standard; DNA; 1240 BP 14-JAN-2000; 2000WO-EP000265. 99US-0115920P. (revised)
(first entry) 'n, Human adenovirus type WO200042208-A1. 14-JAN-1999; 15-SEP-2003 07-NOV-2000 20-JUL-2000. AAA59060; 

Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC; Skripchenko  $Y_i$ 

WPI; 2000-476068/41.

Claim 5; Page 180; 212pp; English.

New nucleic acid comprising an adenovirus tripartite leader nucleotide for producing high-capacity and targeted vectors for adenovirus-based gene therapy.

The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL exons. The nucleic acid is used to produce an adenovirus vector particle,

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WO200183729-A2.
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                                                                                                                                   Gaps
          vectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a gutless adenoviral vector particle. The present sequence represents sequence, which is used to construct nucleic acid molecules of the invention. (Updated on 15-SEP-2003 to standardise OS field)
  pseudotype recombinant
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                                                                                                           DB 3; Length 1240;
                                                                                   Sequence 1240 BP; 231 A; 327 C; 411 G; 271 T; 0 U; 0 Other;
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  deliver an exogenous gene to a target cell,
                                                                                                        Query Match 100.0%; Score 1240; Best Local Similarity 100.0%; Pred. No. 0; Matches 1240; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides an isolated polynucleotide comprising adenovirus (AV) inverter terminal repeat sequences (ITRS), AV packaging signal operatively linked to ITRS and a photoreceptor-specific promoter. A recombinant AV vector (AVV) comprising the polynucleotide is useful for targeted delivery of a gene product to the eye (especially to the vitreous cavity), for treating an ocular disease, e.g., retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adenovirus; inverter terminal repeat sequence; ITRS; ocular disease; fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STDG1; opthalmological; antiinflammatory; antidiabetic; cytostatic; enequese therapy; tripartite leader; TPL; ds.
                                                                               GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCAGTAGTCCAG
                                                                                                                                             GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCAGTAGTCCAG
                                                                                                                             GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG
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GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tripartite leader (TPL) nucleotide sequence
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(first entry)
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FRIEDLANDER
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA94272 standard;
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degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic retinopathies, retinal vascularizations, and retinoblastoma of a mammal preferably human. The AAV comprises a fiber protein that specifically or selectively binds to receptors that are expressed on cells (preferably photoreceptors in the eye). Preferably, the recombinant virus comprise a chiber protein from an adenovirus type D subgroup or is a chimmeric protein containing a portion of the Nterminus of an adenovirus type 2 or type 5 penton, and the therapeutic product is a trophic factor, an anti-containing a portion of the Nterminus of an adenovirus type 2 or type 5 penton, and the therapeutic product is a trophic factor, an anti-corpusate disease gene (STDGI) an anti-cancer agent and a protein that regulates expression of a photoreceptor specific gene product. The viral nucleic acid of AAV comprises ITRS and packaging signal derived from AAV subgroup B or C, especially an AV type 2 or type 5. AAV is also useful for targeted gene therapy, where the vector comprises an AV type 37 fiber protein or its portion, and selectively transduces photoreceptors and delivers a gene product encoded by AAV. The present sequence represents a deenovius 5 tripartite lander (TPL) nucleotide sequence. (Updated on 07-AUG-2003 to correct OS field.)
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100.0%; Score 1240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1240; Conservative 0; Mismatches
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1140 1200 1080 GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGCGCACTTGTAGTCCAG 1020 1141 AGATCCGTACTCCGCCGCGCGGACCTGAGCGAGTCCGCATCGACCGGATCGGAAAACC 1200 1020 780 780 840 840 900 900 960 960 ophthalmological; antiinflammatory; antidiabetic; gene therapy; adenovirus inverted terminal repeat sequence; adenovirus packegding signal; photoreceptor-specific promoter; adenovirus type 37; adenovirus type D serotype; adenovirus type 2; adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor; rhodopsin; wild-type Stargardt disease gene; STDG1; anti-cancer agent; retinal degenerative disease; retinitis pigmentosa; Stargardt's disease; diabetic retinopathy; retinal vascularisation; choroideraemia; gyrate atrophy; macular dystrophy; retinoblastoma; photoreceptor-restricted transgene expression; TGCTCGGAAGACTATCTGCCTGAAGATGGCATGTGAGTTGGATATGGTTGGACGCTG GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCAGTAGTCCAG GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG 1081 GACAAACTCTTGGGGGTCTTTCCAGTACTCTTGGATCGGAAACCGTCGGCCTCCGAACG GAGTATTCCAAGATATGTAGGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACGTAATC GAGTATTCCAAGATATGTAGGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACGTAATC TCTCGAGAAAGGCGTCTAACCAGTCACAGTCGCAAGATCT 1240 TCTCGAGAAAGGCGTCTAACCAGTCACAGTCGCAAGATCT 1240 recombinant adenovirus vector; adenovirus type 5; Ad5, tripartite leader sequence; TPL; ds. #2. Adenovirus type 5 tripartite leader sequence Σ̈́ Nemerow GR, Von Seggern DJ, Friedlander BP. ADB75118 standard; DNA; 1240 01-MAY-2000; 2000US-00562934. 01-MAY-2001; 2001US-00847101 04-DEC-2003 (first entry) (SCRI ) SCRIPPS RES INST 'n. Human adenovirus type US2002193327-A1. 19-DEC-2002 106 1081 1141 781 841 1021 1201 1201 781 841 901 961 961 721 721 g g ò g 원 ò 셤 g ò g à a ò g ઠે ò ò

us-09-482-682-32.rng

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The invention describes an isolated nucleic acid (I) comprising
adenovirus inverted terminal repeat sequence, an adenovirus packaging
conder. A Recombinant adenovirus vector (II) comprising (I) is useful
convoicer. A Recombinant adenovirus vector (II) comprising (I) is useful
for targeted delivery of a gene product to the eye of a mammal which
convoices administering (II) that comprises heterologous DNA encoding the
gene product or resulting in expression of the gene product, where the
recombinant virus comprises a fibre protein that specifically or
recombinant virus comprises a fibre protein that specifically or
convoiced to the eye. The recombinant virus comprises a fibre
protein which is an adenovirus type 37, from an adenovirus type D
convoiced to a nadenovirus type 2 or type 5 penton, and a sufficient
cof the N-termins of an adenovirus type 2 or type 5 penton, and a sufficient
cof the N-termins of an adenovirus type 2 or type 5 penton, and a sufficient
cof the N-termins of an adenovirus type 2 or type 5 penton, and a sufficient
contain which is an adenovirus type 2 or type 5 penton, and a sufficient
contain which is chosen from trophic factor, anti-apoptotic factor, gene encoding
a rhodopsin protein, wild-type Stargardt disease gene (STGGI), an anti-
concer agent and a protein that regulates expression of a photoreceptor-
concer agent and a protein that regulates expression of a photoreceptor-
conlar disease such as retinal degenerative disease e.g., retinial
conlar disease such as retinal degenerative disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inverted terminal repeat (ITR) sequences, and an adenovirus packaging signal operatively linked to the sequence. The ITRs and packaging signal are derived from an adenovirus serotype B or C, or adenovirus type 2 or 5. The viral nucleic acid further comprises a photoreceptor-specific promoter. (II) includes photoreceptor promoters providing a means not only for specific targeting of expression in these cells, but also for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . (tripartite leader sequence) from the adenovirus type 5 genome, used enhance the expression of complementing adenoviral proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              photoreceptor-restricted transgene expression. This sequence represents 
TPL (tripartite leader sequence) from the adenovirus type 5 genome, used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pigmentosa, Stargardt's disease, diabetic retinopathies, retinal vascularisation, choroideraemia, gyrate atrophy or macular dystrophy or retinoblastoma inherited and acquired retinal and neovascular degenerative diseases. The viral nucleic acid comprises an adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACAATCTTTTTGTTGTCAAGCTTGGTGGCAAACGACCCGTAGAGGGCGTTGGAAA
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                                                                                                sequences, adenovirus packaging signals operatively linked to the sequences and photoreceptor-specific promoters, useful for treating
                                                                         nucleic acids comprising adenovirus inverted terminal repeat
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                             Example 3; Page 78; 106pp; English
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Matches 1240; Conservative
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ADF48742 standard; DNA; 1240

RESULT 4

(first entry)

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CTTGGCGATGGAGCCCAGGGTTTTGTTTGTCGCGATCGGCGCGCCTTGGCCGCGCGTT

ADF48742

ADF48742 ID ADF4 XX AC ADF4 XX DT 12-F GGATCCACTCTCTTCCGCATCGCTGTCTGCGAGGCCCAGCTGTTGGGGTGAGTACTCCCT

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tripartite leader sequence. 14-JAN-1999; 26-JUN-2000; 21-AUG-2003 (NEME/) (HALL/) (STEV/) SKRI/) 

packaging cell line; pseudotyping; adenovirus vector; gene therapy; hereditary disorder; tumour; HIV infection; tripartite leader sequence; cytostatic; anti-HIV; gene therapy; HIV gene expression inhibitor; HIV gene expression activation; adenovirus tripartite leader; TPL; gutless adenoviral vector particle; helper-independent fiberless recombinant adenovirus vector; ŝ Stevenson Hallenbeck P, GR, 99US-0115920P 2000US-00423783 14-JAN-2000; 2000US-00482682 Von Seggern DJ, Nemerow Skripchenko Y; Human adenovirus type 5. (VSEG/) VON SEGGERN D J STEVENSON S. SKRIPCHENKO Y. NEMEROW G R. HALLENBECK P. WPI; 2003-843463/78. US2003157688-A1

Novel isolated nucleic acid molecule useful for delivering heterologous gene to human or any animal, or for producing gutless adenoviral vector particle.

Claim 14; SEQ ID NO 32; 157pp; English.

The invention describes an isolated nucleic acid molecule (I) comprising an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide comprising a first and second different TPL exons chosen from second and third same or different TPL exons, the TPL exons chosen from complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon 3. (I) is useful for delivering a patterologous gene to a human or any animal, or for producing a gutless adenoviral vector particle. A recombinant adenovirus particle (II) is useful for delivery of an amount of (II) sufficient to infect the cell. A helper-independent of the second in an adenovirus vector genome (III) is useful for producing an adenovirus vector particle containing (III) which involves containing particles and harvesting the particle produced by the cell of packaging of the genome and (III) which is deficient in expressing sufficient functional fiber protein to support assembly of fiber containing particles and harvesting the particle produced by the cell involves complementing a missing fiber gene of (III) or helper-dependent complements recombinant adenovirus vector genome by expressing in packaging colls a fiber gene from a different adenoviral serotype than the recombinant adenovirus vector to a cell of choice. (I) is useful for reducing proliferation of tumour cells in a subject, or disorder, and for reducing proliferation of tumour cells in a subject, or adenovirus to the particle of tumour cells in a subject, or adenovirus to the particle of tumour cells in a subject, or adenovirus to the particle of tumour cells in a subject, or adenovirus to the particle of tumour cells in a subject, or adenovirus to the particle of tumour cells in a subject, or adenovirus to the particle of tumour cells in a subject, or adenovirus to the particle of tumour cells in a subject, or adenovirus to the particle of tumour cells in a subject, or adenovirus to the particle of tumour cells in a subje to disrupt HIV infection. This sequenc Adenovirus tripartite leader sequence.

Sequence 1240 BP; 231 A; 327 C; 411 G; 271 T; 0 U; 0 Other;

DB 10;

ö GGATCCACTCTTTCCGCATCGCTGTCTGCGAGGGCCCAGCTGTTGGGGTGAGTACTCCCT ö Indels ; 0 Score 1240; I Pred. No. 0; ); Mismatches .; 0 Query Match
Best Local Similarity 100.0%;
Matches 1240; Conservative 0

1020 GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG 1140 GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCGCAGTAGTCCAG 1020 480 540 780 240 240 300 360 360 420 420 900 CCCGGGCAGCAGCAGCGCGCGTCGAAGTAGTCTATCTTGCATCCTTGCAAGTCTAGCGCCTG 600 999 99 720 720 780 840 840 GGCTACCTCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGGCGGCCGCCCTTGCGCGCAAA0 900 960 GTATAGTTCGTGCGAGGGGGGGGGGGGGTCGGGACCTGCTACGGGCGGCGCTCCTC GTTTAGCTGCACGTATTCGCGCGCAACGCACCGCCATTCGGGAAAGACGGTGGTGCTC GTTTAGCTGCACGTATTCGCGCGCACGCACCGCATTCGGGAAAGACGGTGGTGGTGCCTC GAATGGCGGTAGGGGGTCTAGCTGCGTCTCGTCCGGGGGGTCTGCGTCCACGGTAAAGAC GGGGTGAGCGCGGAGGCGTACATGCCGCAAATGTCGTAAACGTAGAGGGGCTCTCT GAGTATTCCAAGATATGTAGGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACGTAATC TGCTCGGAAGACTATCTGCCTGAAGATGGCATGTGAGTTGGATGATATGGTTGGACGCTG TGCTCGGAAGACTATCTGCCTGAAGATGGCATGTGAGTTGGATGATATGGTTGGACGCTG GACAATCTTTTTGTTGTCAAGCTTGGTGGCAAACGACCCGTAGAGGGCGTTGGACAGCAA GACAATCTTTTTGTTGTAGAGCTTGGGCAAACGACCCGTAGAGGGCGTTGGAAA GAATGGCGGTAGGGGGTCTAGCTGCGTCTCGTCCGGGGGTCTGCGTCCACGGTAAAGAC CTGCCATGCGCGGCGGCGCGCGCGCTCGTATGGGTTGAGTGGGGACCCCATGGCAT CTTGGCGATGGAGCGCAGGGTTTTGGTCGCGATCGGCGCGCTCCTTGGCCGCGAT GTCGGGCACCAGGTGCACGCGCCAACCGCGGTTGTGCAGGGTGACAAAGGTCAACGCTGGT GTCGGGCACCAGGTGCACGCGCCAACCGCGGTTGTGCAGGGTGACAAGGTCAACGCTGGT GGCTACCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGGCGGCCGCCCTTGCGCGAGCA CCCGGGCCAGCAGCGCGCGCGCGCGAGTAGTCTATCTTGCATCCTTGCAAGTCTAGCGCCTG CTGCCATGCGCGGGCGCGCAAGCGCGCGCTCGTATGGGTTGAGTGGGGGACCCCATGGCAT GGGGTGGGTGGCGCGGAGGCGTACATGCCGCAAATGTCGTAAAACGTAGAGGGGCTCTCT GTCGCGCAGCTTGTTGACCAGCTCGCCGGTGACCTGCACGTCTAGGGCGCCAGTAGTCCAG GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGGTCGGCCTCCGAACG 1021 1021 1081 1081 61 121 121 241 361 421 421 481 541 601 661 781 781 841 901 901 61 181 181 241 301 301 361 481 541 601 661 721 721 841 961 196 ð 요 ઠ 셤 ò 셤 ò g ò 셤 ઠે 셤 Š 셤 Š 셤 ò g ઠે 셤 ò ద 8 염 8 g δ g δ g 8 a Š 9 ò 원 ø

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL exons. The nucleic acid is used to produce an adenovirus vector particle, deliver an exogenous gene to a target cell, pseudotype recombinant viral vectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a guiless adenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid comprising an adenovirus tripartite leader nucleotide producing high-capacity and targeted vectors for adenovirus-based
                                 CTGAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGGATTT
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NOVARTIS-ERFINDUNGEN VERW GES MBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 200-201; 212pp; English
                                                                                                                                                                                                                                    Nucleotide sequence of plasmid pDV80.
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Skripchenko
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Matches 1239;
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The invention provides an isolated polynucleotide comprising adenovirus (AV) inverter terminal repeat sequences (ITRS), AV packaging signal coperatively linked to ITRS and a photoreceptor-specific promoter. A recombinant AV vector (AVV) comprising the polynucleotide is useful for targeted delivery of a gene product to the eye (especially to the vitreous cavity), for treating an ocular disease, e.g., retinal degenerative disease, retinal specularizations, and retinoblastoma, of a mammal preferably human. The AAV comprises a fiber protein that specifically or selectively binds to receptors that are expressed on cells (preferably photoreceptors in the eye). Preferably, the recombinant virus comprise a fiber protein from an adenovirus type D subgroup or is a chimeric protein containing a portion of the N-terminus of an adenovirus type 2 or type 5 penton, and the therapeutic product is a trophic factor, an anticappated disease gene (GTDG1), an anticancer agent and a protein that regulates expression of a photoreceptor specific gene product. The viral cublic caid of AAV comprises ITRS and packaging signal derived from AAV subgroup B or C, especially an AV type 2 or type 5. AAV is also useful contained sequence represents contained sequence represents contained sequence of plasmid pbV80, an expression plasmid for administration of the nucleotide sequence of plasmid pbV80, an expression plasmid for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat sequences, packaging signal and photoreceptor-specific promoter.
                                                                                                                                                                                                                                                        Adenovirus; inverter terminal repeat sequence; ITRS; ocular disease; fiber protein; photoceceptor; rhodopsin; stargardt disease gene; STDG1; opthalmological; antiinflammatory; antidiabetic; cytostatic; gene therapy; fiber protein; ss.
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  2049 TCTCGAGAAAGGCGTCTAACCAGTCACAGTCGCAAGATC 2087
                                                                                                                                                                                                                     Nucleotide sequence of expression plasmid pDV80
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                                                                                            ABA94286 standard; DNA; 7231
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(SCRI ) SCRIPPS RES INST.
(NEME/) NEMEROW G R.
(VSEG/) VON SEGGERN D J.
(FRIE/) FRIEDLANDER M.
                                                                                                                                                                            (first entry)
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Pred. No. 0; Score 1239;

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Query Match Best Local Similarity

1028 1148 1268 1508 1568 1628 1269 GGCTACCTCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGGCGGCCGCCCTTGCGCGAGCA 1328 1329 GAATGGCGGTAGGGGGTCTAGCTGCGTCTCGTCCGGGGGGTCTGCGTCCACGGTAAAGAC 1388 CCCGGGCCAGCAGGCGCGCGTCGAAGTAGTCTATCTTGCATCCTTGCAAGTCTAGCGCCTG 1448 1808 1020 1080 1928 240 360 540 99 908 120 968 180 420 480 780 840 900 960 9 CTGAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGGATTT 1149 GITTAGCTGCACGTATTCGCGCGCAACGCACCGCCATTCGGGAAAGACGGTGGTGCGCTC 1449 CTGCCATGCGCGGCGGCAAGCGCGCGCTCGTATGGGTTGAGTGGGGGCCCCCATGGCAT GGTTTCCTTGATGATGATACTTATCCTGTCCCTTTTTTTCCACAGCTCGCGGTTGAG GACAATCTTTTTGTTGTAAGCTTGGTGGCAAACGACCCGTAGAGGGCGTTGGACAAA CTTGGCGATGGAGCGCAGGGTTTGGTTTTTGTCGCGATCGGCGCGCCTTCGCCGCGAT GTTTAGCTGCACGTATTCGCGCGCAACGCACCCCCATTCGGGAAAGACGGTGGTGCGCTC CTGCCATGCGCGGCGGCAAGCGCGCGCTCGTATGGGTTGAGTGGGGAACCCCATGGCAT GAGTATTCCAAGATATGTAGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACGTAATC GTATAGTTCGTGCGAGGAGCGAGGAGGTCGGAACCCGAGGTTGCTACGGCGGGCTGCTC 849 GGATCCACTCTTCCGCATCGCTGTCTGCGAGGGCCAGCTGTTGGGGTGAGTACTCCCT CTGAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGGATTT GTCGGGCACCAGGTGCACGCGCCAACCGCGGTTGTGCAGGGTGACAAGGTCAACGCTGGT GGCTACCTCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGGCGGCCGCCCTTGCGCGAGCA GAATGGCGGTAGGGGGTCTAGCTGCTCTCGTCCGGGGGGTCTGCGTCCACGGTAAAGAC CCCGGGCAGCAGCGCGCGCGTCGAAGTAGTCTTGCATCTTGCAAGTCTAGCGCCTG GGGGTGGGTGAGCGCGGAGGCGTACATGCCGCAAATGTCGTAAACGTAGAGGGGCTCTCT 721 GAGTATTCCAAGATATGTAGGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACGTAATC TGCTCGGAAGACTATCTGCCTGAAGATGGCATGTGAGTTGGATGATATGGTTGGACGCTG recressas de la recerca de la recencia del recencia de la recencia della della recencia de la recencia della rec GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCAGTAGTCCAG Greececacerrerreaceaceresecesecreececererrassecececaracides GGATCCACTCTCTCCGCATCGCTGTCTGCGAGGGCCAGCTGTTGGGGTGAGTACTCCCT Gaps ö Indels ö Mismatches ; 0 Matches 1239; Conservative 181 1389 1629 ( 841 1689 1809 ( 696 301 361 1569 781 Н 606 121 241 481 61 421 1021 541 601 199 901 961 g g q g qq 셤 셤 g g g g 8 à ò g ò 8 셤 ò ò ò ð à ò ð ò 셤 à 셤 셤 Š 유 8 8 à ocular diseases DB 6; Length 7231;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ophthalmological; antiinflammatory; antidiabetic; gene therapy; ademovirus inverted terminal repeat sequence; adenovirus packaging signal; photoreceptor-specific promoter; adenovirus type 37; adenovirus type 9 serotype; adenovirus type 2; adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor; rhodopini, wild-type Stargardt disease gene; STDG1; anti-cancer agent; retinal degenerative disease; retinitis pigmentosa; Stargardt's disease; diabetic retinopathy; retinal vascularisation; choroideraemia; photoreceptor-restricted transgene expression; photoreceptor-restricted transgene expression; recombinant adenovirus vector; adenovirus type 5; plasmid; cyclic;
GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG
                     GACAAACTCTTGGGGGTCTTTCCAGTACTCTTGGATGGGAAACCCGTCGGCCTCCGAAAG
                                                                                                   AGATCCGTACTCCGCCGCCGAGGGACCTGAGCGAGTCCGCATCGACCGGATCGGAAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences, adenovirus packaging signals operatively linked to the sequences and photoreceptor-specific promoters, useful for treating
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                                                                                                                                                                                                                                                                                                     ADB75132 standard; DNA; 7231 BP
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interaction, with an adenovirus expression to the percent theory of a mammal. The encapsulated mucleic acid comprises a photoreceptor-specific promoter concapsulated mucleic acid comprises a photoreceptor-specific promoter operatively linked to a nucleic acid comprising the therapeutic product which is chosen from trophic factor, anti-apoptotic factor, gene encoding a rhodopsin protein, wild-type Stargard disease gene (STDGI), an anti-cancer agent and a protein that requiates expression of a photoreceptor-specific gene product. The delivery is effected for treatment of an coular disease such as retinal degenerative disease e.g., retinal coular disease such as retinal degenerative disease. Coular disease inherited and acquired retinal and neovascular certinoblastoma inherited and acquired retinal and neovascular degenerative diseases. The viral nucleic acid comprises an adenovirus packaging inverted terminal repeat (ITR) sequences, and an adenovirus packaging configuratively linked to the sequence. The ITRs and packaging signal care derived from an adenovirus serctype B or C, or adenovirus type 2 or configuratively linked to the sequence The ITRs and packaging signal care derived from an adenovirus serctype B or C, or adenovirus type 2 or configuration are derived from an adenovirus serctype B or C, or adenovirus type 2 or configuration of sphotoreceptor promoters providing a means not conly for specific targeting of expression in these cells, but also for photoreceptor-restricted transgene expression in the preparation of adamoniral care distances and an adenovirus provession of a adenovirus contraction of the sequence of the preparation of the adamoniral care distances and an adenovirus and adamonical care distances and an adenovirus and adamonical care distances and an adenovirus provession of the sequence of the preparation of the adamonical care distances and an adenovirus and adamonical care distances and an adenovirus provession of the adamonical care distances and an adenovirus provession of the adamonic
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The invention describes an isolated nucleic acid molecule (I) comprising an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide comprising a first and second different TPL exons chosen first, second and third same or different TPL exons, the TPL exons chosen from complete or partial TPL exon 1, complete TPL exons chosen from complete or partial TPL exon 2 and complete TPL exon 3. (I) is useful for delivering a peterologous gene to a human or any animal, or for producing a gutless adenoviral vector particle. A recombinant adenovirus particle (II) is useful for delivery of an exogenous gene to a target cell which involves contacting the cell with an adenovirus vector particle containing (III) is useful for producing an adenovirus vector particle containing (III) which involves containing particles and harvesting the particles and harvesting the particles and harvesting the particles produced by the cell containing particles and harvesting recombinant adenovirus vector genome by expressing containing particles and harvesting recombinant viral vectors which involves complementing a missing fiber gene of (III) or helper-dependent cells a fiber gene from a different adenoviral serotype than the recombinant adenovirus vector genome by expressing in packaging cells a fiber gene from a different adenoviral serotype than the recombinant adenovirus vector (III) is abequit for specifically targeting an adenovirus vector to a cell of choice. (I) is useful for cecombinant adenovirus vector to a cell of choice. (I) is useful for treating diseases such as such as subject, or disorder, and for reducing proliferation of tumour cells in a subject, the disorder, and for reducing proliferation of tumour cells in a subject, or the contains the particle of the pace of the pac
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                                    STEVENSON S.
SKRIPCHENKO
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                                             GGCTACCTCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGGCGCCGCCCCTTGCGCGCGAGCA
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The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL or the nucleic acid is used to produce an adenovirus vector particle, deliver an exogenous gene to a target cell, pseudotype recombinant vectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a gutless adenovirus retor particle. The present sequence represents

plasmid pDV67, which contains a TPL

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GTTTAGCTGCACGTATTCGCGCGCAACGCACCGCCATTCGGGAAAGACGCGTGCTGCGCTC
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1348

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07-NOV-2000

AAA59072;

AAA59072 standard;

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s tripartite leader nucleotide vectors for adenovirus-based

nucleic acid comprising an adenovirus producing high-capacity and targeted v

therapy

gene New

WPI; 2000-476068/41

Skripchenko Y;

GR,

Nemerow

Claim 10; Page 184-186; 212pp; English

SC;

Stevenson

PL,

Hallenbeck

Von Seggern DJ,

VERW GES MBH

(NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN (SCRI ) SCRIPPS RES INST.

14-JAN-2000; 2000WO-EP000265

WO200042208-A1

Synthetic

20-JUL-2000

99US-0115920P

14-JAN-1999;

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Friedlander

Nemerow GR, Von Seggern DJ,

WPI; 2002-082846/11

30-APR-2001; 2001WO-EP004863 01-MAY-2000; 2000US-00562934

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99.9%; Score 1239; D 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 1239; Conservative 1109 1169 н 929 61 121 181 241 Query Match à đ ò a ò g g ò 셤 8 Adenovirus; inverter terminal repeat sequence; ITRS; ocular disease; fiber protein; photoraceptor; thodopsin; stargardt disease gene; STDG1; opthalmological; antidiammatory; antidiabetic; cytostatic; gene therapy; tripartite leader; TPL; ss. Nucleotide sequence of adenoviral plasmid pDV67. BP ABA94274 standard; DNA; 7960 (first

13-MAR-2002

ABA94274;

RESULT 10 **ABA9427** 

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The invention provides an isolated polynucleotide comprising adenovirus (AV) inverter terminal repeat sequences (ITRS), AV packaging signal coperatively linked to ITRS and a photoreeptor-specific promoter. A recombinant AV vector (AVV) comprising the polynucleotide is useful for recombinant AV vector (AVV) comprising the polynucleotide is useful for targeted delivery of a gene product to the eye (especially to the confine to the sease, retinal and coular disease, e.g., retinal confines, retinal vascularizations, and retinoblastoma, of a mammal degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic retinopathies, retinal vascularizations, and retinoblastoma, of a mammal confirmation to receptors that are expressed on cells (preferably vector from an adenovirus type D subgroup or is a chimeric protein containing a portion of the N-terminus of an adenovirus type 2 or type 5 penton, and the therapeutic product is a trophic factor, an anti-cancer agent edisease gene (STDGI) an anti-cancer agent and a protein that regulates expression of a photoreceptor specific gene product. The viral concludes expression of a photoreceptor agent and a protein that comprises of the regulates expression of a photoreceptor specific gene product. The viral concludes agene therapy, where the vector comprises and the rageled gene therapy, where the vector comprises and the nucleotide sequence of plasmid pDV67, a plasmid containing adenoviral
                                                                                                                                                                                                                                                                                                                                          Polynucleotide for making vectors, useful for treating ocular diseases, e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat sequences, packaging signal and photoreceptor-specific promoter.
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Length 7960;

DB 6;

301 GITTAGCTGCACGTATTCGCGCGCAACGCACCGCCATTCGGGAAAGACGGTGGTGCGCTC 360

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WO200183729-A2

08-NOV-2001

adenovirus type 37; adenovirus type D serotype; adenovirus type 2; adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor; hodopsin; wild-type Stargardt disease gene; STDG1; anti-cancer agent; retinal degenerative disease; retinitis pigmentosa; Stargardt's disease; diabetic retinopathy; retinal vascularisation; choroideraemia; gyrate atrophy; macular dystrophy; retinoblastoma; photoreceptor-restricted transgene expression;

ophthalmological; antiinflammatory; antidiabetic; gene therapy; adenovirus inverted terminal repeat sequence; adenovirus packaging signal; photoreceptor-specific promoter;

adenovirus vector; adenovirus type 5; plasmid; cyclic;

circular; ds; pDV67; tripartite leader sequence; TPL.

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sequences, adenovirus packaging signals operatively linked to the sequences and photoreceptor-specific promoters, useful for treating

nucleic acids comprising adenovirus

Novel

Friedlander M;

DJ,

Von Seggern

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Nemerow

WPI; 2003-657234/62.

(SCRI ) SCRIPPS RES INST

01-MAY-2001; 2001US-00847101 01-MAY-2000; 2000US-00562934

US2002193327-A1 19-DEC-2002

Synthetic.

The invention describes an isolated nucleic acid (I) comprising
adenovirus inverted terminal repeat sequence, an adenovirus packaging
conduct. A Recombinant adenovirus vector (II) comprising (I) is useful
conformatively linked to the sequence, and a photoreceptor-specific
promoter. A Recombinant adenovirus vector (II) comprising (I) is useful
conversed administering (II) that comprises heterologous DNA encoding the
conversed administering (II) that comprises heterologous DNA encoding the
compinant virus comprises a fibre protein that specifically or
conversed to receptors that are expressed on cells which are
protein which is an adenovirus type 37, from an adenovirus type D
conversed to a denovirus type 37, from an adenovirus type D
conversed to a nadenovirus type 2 or type 5 fibre protein for
interaction with an adenovirus type 2 or type 5 fibre protein for
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conteraction with an adenovirus type 2 or type 5 fibre protein for
conteraction with an adenovirus serotype D knob portion of an adenovirus serotype D knob portion of the fiber for
concernative binding to photoreceptors in the eye of a mammal. The
concernatively linked to a nucleic acid comprising the therapeutic product
which is chosen from trophic factor, anti-isapprotic factor, gene encoding
concernatively linked to a nucleic acid comprising the therapeutic product
which is chosen from trophic factor, anti-isapprotic factor, gene encoding
cancer agent and a protein that requiates expression of a photoreceptorconcernative disease such as retinal degenerative disease e.g., retinal
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conlar disease such and aden promoter. (II) includes photogeoceptor promoters providing a means not only for specific targeting of expression in these cells, but also for photoreoceptor-restricted transgene expression. This sequence represents an adenovirus fibre-expressing plasmid for complementation of fibre-genedeleted adenoviruses that also comprises the adenovirus tripartite leader inverted terminal repeat (ITR) sequences, and an adenovirus packaging signal signal operatively linked to the sequence. The ITRs and packaging signal are derived from an adenovirus serotype B or C, or adenovirus type 2 or 5. The viral nucleic acid further comprises a photoreceptor-specific Example 5; Page 82-86; 106pp; English. retinitis pigmentosa.

BP

ADB75120 standard; DNA; 7960

Plasmid pDV67 DNA sequence

(first entry)

04-DEC-2003

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sequence for enhancing the expression of complementing adenoviral
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                                    Sequence 7960 BP; 1934 A; 2070 C; 1993 G; 1963 T; 0 U; 0 Other;
                                                           Length 7960;
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                                                         Query Match 99.9%; Score 1239; DB 10; Best Local Similarity 100.0%; Pred. No. 0; Matches 1239; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule useful for delivering heterologous gene to human or any animal, or for producing gutless adenoviral vector particle.
GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCAGTAGTCCAG
                  GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCAGTAGTCCAG
                                                                        AGATCCGTACTCCGCCGCCGAGGGACCTGAGCGAGTCCGCATCGACCGGATCGGAAAACC
                                                         GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG
                                                                                                                                             GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression inhibitor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; anti-HIV; gene therapy; HIV gene expression inhibit HIV gene expression activation; adenovirus tripartite leader; gutless adenoviral vector particle; helper-independent fiberless recombinant adenovirus vector; packaging cell line; pseudotyping; adenovirus vector; gene the heraditary disorder; tumnour; HIV infection; fibre; fibre; tibere-gene-deleted adenoviruses; hygromycin resistance; tripartite leader sequence; ds; pCLF; pCDN3/fibre.
                                                                                                                                                                                                                                                                                                                                                                                                                          Fibre expressing/tripartite leader sequence plasmid pDV67.
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                                                                                                                                                                                                                                                 TCTCGAGAAAGGCGTCTAACCAGTCACAGTCGCAAGATC 2167
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                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                                                     ADF48754 standard; DNA; 7960
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26-JUN-2000; 2000US-00423783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
Human adenovirus type 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VSEG/) VON SEGGERN D J.
(NEME/) NEMEROW G R.
(HALL/) HALLENBECK P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEVENSON S.
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Skripchenko Y;
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complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon 3. (I) is useful for delivering a heterologous gene to a human or any animal, or for producing a gutless adenoviral vector particle. A recombinant adenovirus particle (II) is useful for delivery of an exogenous gene to a target cell which involves contacting the cell with an amount of (II) sufficient to infect the cell. A helper-independent fiberpersory sector particle containing (III) which involves producing an adenovirus vector particle containing (III) which involves producing a packaging of the genome and (III) which is deficient in expressing containing particles and harvesting the particle produced by the cell containing particles and harvesting the particle produced by the cell containing particles and harvesting the particle produced by the cell containing particles and harvesting the particle produced by the cell containing particles and harvesting the particle produced by the cell involves complementing a missing fiber gene of (III) or helper-dependent fiber secombinant adenovirus vector. (III) is also useful for repeating to a denovirus vector to a cell of choice. (I) is useful for reducing proliferation of tumour cells in a subject, or confiscutt the leader sequence added to plasmid pCDN3/fibre to create plasmid confiscution. This sequence represents an adenovirus sequence represents an adenovirus of the complementation of E4-
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Polynucleotide for making vectors, useful for treating ocular diseases, e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat
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GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCACGTAGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2069 AGATCGTACTCCGCCGCCGAGGACCTGAGCGAGTCCGCATCGACCGGATCGAAAACC
                                                                                                                         TGCTCGGAAGACTATCTGCCTGAAGATGGCATGTGAGTTGGATGATATGGTTGGACGCTG
                                                                                                                                             TGCTCGGAAGACTATCTGCCTGAAGATGGATGTGAGTTGGATGATGATGATGGTTTGGACGTG
                                                                                                                                                                                                                        GAAGACGTTGAAGCTGGCGTCTGTGAGACCTACCGCGTCACGCGCGCAGGAGGAGGCCGTAGGA
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                                                     GTCGCGCAGCTTGTTGACCAGCTCGGCGGTGACCTGCACGTCTAGGGCGCAAGTAGTCCAG
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SCRIPPS RES INST.
NEMEROW G R.
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                                                                                                                                    The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL exons. The nucleic acid is used to produce an adenovirus vector particle, deliver an exogenous gene to a target cell, pseudotype recombinant viral vectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a gutless adenoviral vector particle. The present sequence represents
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                                  nucleic acid comprising an adenovirus tripartite leader nucleotide producing high-capacity and targeted vectors for adenovirus-based
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The invention provides an isolated polynucleotide comprising adenovirus (AV) inverter terminal repeat sequences (ITRS), AV packaging signal coperatively linked to TRS and a photoreceptor-specific promoter. A recombinant AV vector (AVV) comprising the polynucleotide is useful for recombinant AV vector (AVV) comprising the polynucleotide is useful for transparent and sease, e.g., retinal confidence of degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic retinopathies, retinal vacularizations, and retinoblastoma, of a mammal preferably human. The AAV comprises a fiber protein that specifically or selectively binds to receptors that are expressed on cells (preferably photoreceptors in the eye). Preferably, the recombinant virus comprise a fiber protein from an adenovirus type D subgroup or is a chimeric protein containing a portion of the Nterminus of an adenovirus type 2 or type 5 penton, and the therapeutic product is a trophic factor, an anticapport according a trophic factor, an anticapport according a trophic factor, an anticapport of a photoreceptor specific gene product. The viral capport according a from packaging signal derived from AAV cubering and according a protein from AAV cubering and product sease gene fargeted gene the vector comprises an AV type 37 fiber of the nucleotide sequence of plasmid pDV69, a plasmid containing a modified adamnial plantice of plasmid pDV69, a plasmid containing a modified
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                                       Example 5; Page 137-139; 149pp; English
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adenovirus packaging signal; photoreceptor-specific promoter;
adenovirus type 37; adenovirus type D serotype; adenovirus type 2;
adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor;
rhodopsin; wild-type Stargardt disease gene; STDG1; anti-cancer agent;
retinal degenerative disease, retinitis pigmentosa; Stargardt's disease;
diabetic retinopathy; retinal vascularisation; choroideraemia;
gyrate atrophy; macular dystrophy; retinoblastoma;
photoreceptor-restricted transgene expression;
true for the star of the star
                                                                                                                                                                                                                                                                                                              1649 GAGTATTCCAAGATATGTAGGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACAATC
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circular; ds; pDV69; tripartite leader sequence; TPL.
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Von Seggern DJ, 01-MAY-2001; 2001US-00847101. 2000US-00562934 (SCRI ) SCRIPPS RES INST WPI; 2003-657234/62. 01-MAY-2000; Nemerow GR, 

Friedlander M;

sequences, adenovirus packaging signals operatively linked to the sequences and photoreceptor-specific promoters, useful for treating retinitis pigmentosa. Novel nucleic acids comprising adenovirus inverted terminal repeat

Example 5; Page 86-90; 106pp; English.

The invention describes an isolated nucleic acid (I) comprising adenovirus inverted terminal repeat sequence, an adenovirus packaging signal operatively linked to the sequence, an adenovirus packaging signal operatively linked to the sequence, and a photoreceptor-specific promoter. A Recombinant adenovirus vector (II) comprising (I) is useful for targeted delivery of a gene product to the eye of a mammal which involves administering (II) that comprises heterologous DNA encoding the gene product or resulting in expression of the gene product, where the gene product or receptors that are expressed on cells which are photoreceptors, in the eye. The recombinant virus comprises a fibre protein which is an adenovirus type 37, from an adenovirus type D serotype. The fibre is a chimeric protein containing a sufficient portion of the N-terminus of an adenovirus type 2 or type 5 fibre protein for interaction with an adenovirus type 2 or type 5 pencon, and a sufficient portion of an adenovirus serotype D knob portion of the fiber for selective binding to photoreceptors in the eye of a mammal. The operatively linked to a nucleic acid comprising the therapeutic product which is chosen from trophic factor, anti-apoptotic factor, gene encoding a rhodopsin protein, wild-type Stargardt disease gene (STDG1), an antiphotoreceptor-restricted transgene expression. This sequence represents an adenovirus fibre-expressing plasmid for complementation of fibre-genedeleted adenoviruses that also comprises the adenovirus tripartite leader cancer agent and a protein that regulates expression of a photoreceptorspecific gene product. The delivery is effected for treatment of an
ocular disease such as retinal degenerative disease e.g., retinitis
pigmentosa, Stargardt's disease, diabetic retinopathies, retinal
vascularisation, choroideraemia, gyrate atrophy or macular dystrophy or
retinoblastoma inherited and acquired retinal and neovascular
degenerative diseases. The viral nucleic acid comprises an adenovirus inverted terminal repeat (ITR) sequences, and an adenovirus packaging signal signal operatively linked to the sequence. The ITRs and packaging signal are derived from an adenovirus service B or C, or adenovirus type 2 or 5. The viral nucleic acid further comprises a photoreceptor-specific only for specific targeting of expression in these cells, but also for includes photoreceptor promoters providing a means not sequence for enhancing the expression of complementing adenoviral promoter. (II) proteins.

Sequence 7989 BP; 1934 A; 2072 C; 1997 G; 1983 T; 0 U; 3 Other;

Length 7989;

DB 10;

Local Similarity

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Query Match

1048 9 CTGAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAACGAGGAGGATTT GGATCCACTCTTTCCGCATCGCTGTCTGCGAGGGCCAGCTGTTGGGGTGAGTACTCCCT GGATCCACTCTTCCGCATGCCTGTCTGCGAGGGCCAGCTGTTGGGGTGAGTACTCCCT CTGAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCCAAAAACGAGGAGGATTT Gaps ö Indels .; 0 99.9%; Scc. 100.0%; Pred. No. v. 0; Mismatches Best Local Similarity 100. Matches 1239; Conservative Н 929 61

1168 1348 1408 1708 1828 1948 2068 2128 360 480 540 900 720 840 900 GACAATCTTTTTGTTGTTGTAAGCTTGGTGGCAAACGACCCGTAGAGGGCGTTGGAACAA GTCGGGCACCAGGTGCACGCGCCAACGCGGTTGTGCACAAGGTCAACGCTGGT 1409 GAATGGCGGTAGGGGGTCTAGCTGCGTCTCGTCCGGGGGGGTCTGCGTCACGGTAAAGAC CTGCCATGCGCGGGGGAAGCGCGCGCTCGTATGGGTTGAGTGGGGGGGACCCCATGGCAT 1649 GAGTATTCCAAGATATGTAGGGTAGCATCTTCCACCGCGGATGCTGGCGCGCACGTAATC 2069 AGATCCGTACTCCGCCGCCGAGGGACCTGAGCGAGTCCGCATCGACCGGATCGAAAACC CTTGGCGATGGAGCGCAGGGTTTGGTTTTTGTCGCGATCGGCGCGCTCCTTGGCCGCGAT 1229 GTTTAGCTGCACGTATTCGCGCGCAACGCACCGCCATTCGGGAAAGACGGTGGTGCGCTC 1349 GGCTACCTCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGGCGGCCGCCCTTGCGCGGAGCA CCCGGGCACCAGGCGCGCGTCGAAGTAGTCTATCTTGCATCCTTGCAAGTCTAGCGCCTG CCCGGGCCAGCAGCGCGCGTCGAAGTAGTCTATCTTGCATCCTTGCAAGTCTAGCGCCTG CTGCCATGCGCGGGCGCGCGCGCGCTCGTATGGGTTGAGTGGGGGACCCCATGGCAT 1769 TGCTCGGAAGACTATCTGCCTGAAGATGGCATGTGAGTTGGATGATATGGTTGGACGCTG 1889 Greececagerrerreaceacerececegreacerececereragesececaging gerrrectrigargargrearactrarecterecertrirrrrecaeaecreecegrigae GACAATCTTTTTGTTGTCAAGCTTGGTGGCAAACGACCCGTAGAGGGCGTTGGACAGCAA GTTTAGCTGCACGTATTCGCGCGCAACGCACCCCCATTCGGGAAAGACGGTGCGCTC GTCGGGCACCAGGTGCACGCGCCAACCGCGGTTGTGCAGGGTGACAAGGTCAACGCTGGT GGCTACCTCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGGCGGCCGCCCTTGCGCGAGCA GAATGGCGGTAGGGGGTCTAGCTGCGTCTCGTCCGGGGGGTCTGCGTCCACGGTAAAGAC GGGGTGGGTGAGCGCGGAGGCGTACATGCCGCAAATGTCGTAAAACGTAGAGGGGCTCTCT 1589 GGGGTGGGTGAGCGCGGAGGCGTACATGCCGCAAATGTCGTAAACGTAGAGGGGCTCTCT TGCT/CGGAAGACTATCTGCCTGAAGATGGCATGTGAGTTGGATGATATGGTTGGACGCTG GTCGCGCAGCTTGTTGACCAGCTCGCGGGGACCTGCACGTCTAGGGCGGCAGTAGTCCAG GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG GACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAACCCGTCGGCCTCCGAACG AGATCCGTACTCCGCCGCCGAGGGACCTGAGCGAGTCCGCATCGACCGGATCGGAAAACC 1201 TCTCGAGAAAGGCGTCTAACCAGTCACAGTCGCAAGATC 1239 1109 ( 1169 1289 ( 541 781 ( 1469 121 1529 1141 181 241 601 841 1949 2009 301 361 421 481 661 721 901 1021 셤 g d à g ò 셤 셤 ò 유 g 유 ઠે 엄 유 셤 g 셤 셤 셤 g 요 Š ò ò ò ò ò 8 ò ð ð ò ò ò à

2129 TCTCGAGAAAGGCGTCTAACCAGTCACAGTCGCAAGATC 2167

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PUFVQ60TD PUFVQ60TB SCEZFL403

46.8 46.8 46.8

CG344984 OGYCK40TV AY103647 Zea maye CK122370 BES182410 B1776330 EBEM04 SG CV057862 BNEL13174 CV054175 BNEL13174 CV054175 BNEL13174 EX3344097 BX384097 BE14157 HV CED000 B1157458 602920372 CA086410 SCMCAM208 AG114606 Pan LYGQ1 CG433993 OCYGR76TV AL065629 Drosophil AL103945 Drosophil AL103945 CROSOPHIL CK209664 FGAS02143 BM915656 AGENCOURT CK209664 FGAS02143 BM915656 AGENCOURT CCD931334 GR45.114C	STN	617 bp mRNA linear GSS 26-JUL-2004 K-GTA Mus musculus cDNA clone FHCRC-GT-S22-5F 5', 93553 e mouse) ; Chordata; Craniata; Vertebrata; Euteleostomi; ; Rodentia; Sciurognathi; Muridae; Musn. /soriano/ soriano/ Sciences, A2-025 ncer Research Center N., Seattle, WA 98109, USA crc.org insertiand cDNA flanking sequence. Additional ing this ES cell line and the insertion mutation request at org/labs/soriano/GTdb/ Qualifiers ="Mus musculus" ="mRNA" HCRC-GT-S22-5F" HCRC-GT-S22-5F" e="Embryonic stem cell" b="ZS4" "taxon:10090" HCRC-GT-S22-5F" e="Embryonic stem cell" b="ZK-GTA"	.2; DB 9; Length 617; 1.2e-20; ches 24; Indels 0; Gaps 0;
CG344984 AX103647 CK122370 EK122370 CV057862 CV0535513 CV0541157 BK134107 BK1157458 CA086410 AG114606 CG413993 CK05060N CK05060N CK050664 CK1970584 AG363333 CK0531334 CK0531334	ALIGNMENTS	HCRC-GT-S22-5F1 ZK-GTA Mus musculus CDRANA sequence. L1706515.1 GI:S059353 L2706515.1 GI:S059353 SS. L2706515.1 GI:S059353 SS. Us musculus (house mouse) Us musculus (bases 1 to 617) Us soriano P Us soriano Esperimente (ag is governed to be soriano Especial (ad Especial Conterned Unit (ad Especi	Score 116.2; Pred. No. 1.2 0; Mismatches
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637 bp DNA linear GSS 10-FEB-2004
FHCRC-GT-S9-7G1 2K-GTA Mus musculus genomic clone FHCRC-GT-S9-7G1
S', genomic survey sequence.
CG899744
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FHCRC-GT-S12-1B1 2K-GTA Mus musculus genomic clone FHCRC-GT-S12-1B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: psoriano@fhcrc.org
ROSAFARY gene trap. The sequence tag is generated by 3'RACE and
represents the 3' insertional cDNA flanking sequence. Additional
information regarding this ES cell line and the insertion mutation
is available upon request at
https://www.fhcrc.org/labs/soriano/GTdb/
Class: Gene Trap.
Location/Qualifiers
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 404)
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Soriano,P.
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Unpublished (2003)
Contact: Soriano P
Duriston of Basic Sciences, A2-025
Pred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Seattle, WA 98109, USA
Fax: 206 667 6522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
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/cell_line="AK7.1"
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FHCRC-GT-S17-4D1 2K-GTA Mus musculus cDNA clone FHCRC-GT-S17-4D 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: psorianoefhorc.org

ROSAPARY gene trap. The sequence tag is generated by 3'RACE and represents the 3' insertional cDNA flanking sequence. Additional information regarding this ES cell line and the insertion mutation is available upon request at https://www.fhorc.org/labs/soriano/GTdb/

Class: Gene Trap.

Location/Qualifiers
                                                                                                             48 GTGAGTACTCCCTCTGAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCAAAA 107
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    GTGAGTACTCCCTCTGAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCAAAA 107
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 581)
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www.fhrc.org/labs/soriano/
contact: Soriano P
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Fred Hutchinson Cancer Research Center
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Fax: 206 667 6522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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84.4%; Pred. No. 1.8e-20;
tive 0; Mismatches 24
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Best Local Similarity 84.4
Matches 130; Conservative
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FHCRC-GT-S10-8A1 2K-GTA Mus musculus genomic clone FHCRC-GT-S10-BA1
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Class:Gene Trap.
Location/Qualifiers
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 728)
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Unpublished (2003)
Contact: Soriano P
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Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                          DB 9;
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                                                                                                                                                                                                                                         /cell_type="Embryonic stem cell"
/cell_line="AK7.1"
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/cell_type="Embryonic stem cell"
/cell_line="AK7.1"
  is available upon request at https://www.fhcrc.org/labs/soriano/GTdb/Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                          8.8%; Score 108.6; DB 9
83.7%; Pred. No. 1.6e-18;
iive 0; Mismatches 24
                                                                                                        /organism="Mus musculus"
/mol type="genomic DNA"
/strain="12954"
/db_xref="texon:10090"
/clone="FHCRC-GT-S10-8F1"
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/clone="FHCRC-GT-S10-8A1"
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/note="Vector: ROSAFARY"
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/strain="12984"
                                                                 Location/Qualifiers
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Fax: 206 667 6522
Email: psoriano@fhcrc.org
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                                                                                                                                                                                                                         /sex="Male"
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Best Local Similarity 83.7
Matches 123; Conservative
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FHCRC-GT-S10-8F1 2K-GTA Mus musculus genomic clone FHCRC-GT-S10-8F1
                                                                                                                                                                                            Email: psoriano@fhcrc.org
ROSAFARY gene trap. The sequence tag is generated by 3'RACE and
represents the 3' insertional cDNA flanking sequence. Additional
information regarding this ES cell line and the insertion mutation
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ROSAFARY gene trap. The sequence tag is generated by 3'RACE and
represents the 3' insertional cDNA flanking sequence. Additional
information regarding this ES cell line and the insertion mutation
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 TGAGTACTCCCTCTGAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCAAAAA
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                                                 Contact: Soriano P
Division of Basic Sciences, A2-025
Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Seattle, WA 98109, USA
Tel: 206 667 6825
Exa: 206 667 6522
Email: psoriano@fhcrc.org
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Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Seattle, WA 98109, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Embryonic stem cell"
/cell_line="AK7.1"
/clone_lib="ZK-GTA"
/note="Vector: ROSAFARY"
                                                                                                                                                                                                                                                                                  is available upon request at
https://www.fhcrc.org/labs/soriano/GTdb/
Class: Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="FHCRC-GT-S12-1B1"
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/mol_type="genomic DNA"
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                    www.fhcrc.org/labs/soriano/
Unpublished (2003)
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Contact: Soriano P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 206 667 6825
Fax: 206 667 6522
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CNS0091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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ROSAFARY gene trap. The sequence tag is generated by 3'RACE and represents the 3' insertional cDNA flanking sequence. Additional information regarding this Es cell line and the insertion mutation is available upon request at https://www.fhorc.org/labs/soriano/GTdb/
Class: Gene Trap.
74 ATGACTICTGCGCTAAGATIGTCAGTITCCAAAAACGAGGAGGATTTGATATTCACCTGG 133
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 579)
Soriano, P.
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100.0%; Pred. No. 6.9e-13;
ative 0; Mismatches 0; Indels
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Unpublished (2003)
Contact: Soriano P
Ovision of Basic Sciences, A2-025
Fred Hutchinson Cancer Research Center
1100 Pairview Ave. N., Seattle, WA 98109, USA
Pax: 206 667 6522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="AK7.1"
/clone_lib="2K-GTA"
/note="Vector: ROSAFARY"
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/strain="12984"
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AL053013
AL053013.1 GI:4934461
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Mus musculus
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                                                                 185 ATCTTTTTGTTGTCAAG 201
                                                                                                         136 AAGTICCIAITCICTÁG 152
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Best Local Similarity 100.C
Matches 88; Conservative
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CG691637
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Contact: Soriano P
Division of Basic Sciences, A2-025
Division of Basic Sciences, A2-025
Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., Scattle, WA 98109, USA
Tel: 206 667 6825
Fax: 206 667 6522
Email: psoriano@fhorc.org
ROSMFARY gene trap. The sequence tag is generated by 3'RACE and represents the 3' insertional Charles and requesting this ES cell line and the insertion mutation is available upon request at https://www.fhorc.org/labs/soriano/GTdb/
Class: Gene Trap.
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FHCRC-GT-S20-7B1 2K-GTA Mus musculus cDNA clone FHCRC-GT-S20-7B 5',
                                                                                                                                                                        107
                                                                                                                                                                                                                                                     108 ACGAGGAGTTTGATATTCACCTGGCCCGCGGTGATGCCTTTGAGGCTGCCGCATCCA 167
                                                                                                                                                                                                                                                                             60 ACGAGGAGGATTTGATATTCACCTGGCCCGCGGTATGCTTTGAGGCTGGCCGCCGCA 119
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 640)
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                                                                                                                                                                      48 GIGAGTACTCCCTCTGAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCCAAAA
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                                                                                       DB 9; Length 728;
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/cell_line="AK7.1"
/clone_lib="ZK-GTA"
/note="Vector: ROSAFARY"
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                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/strain="12984"
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/clone="FHCRC-GT-S20-7B"
  /clone_lib="2K-GTA"
/note="Vector: ROSAFARY"
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www.fhcrc.org/labs/soriano/
Unpublished (2003)
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ORGANISM

SOURCE

TITLE AUTHORS

COMMENT

REFERENCE

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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPACR Resource Center can be
                                                                                                                                                                                                                                                               BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCGCCATTCGGGAAAGACGGTGGTGCGCTCGTCGGGCACCAGGTGCACGCGCCAACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 865 SSGTSSACVKCNASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
1. (bases 1 to 925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           689 CCGCAAATGTCGTAAACGTAGAGGGGCTCTCTGAGTATTCCAAGATATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.7%; Score 58.2; DB 9;
14.1%; Pred. No. 0.00012;
vative 177; Mismatches 175;
                           Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 177;
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                                                                                                                                                                                    Genoscope
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Best Local Simi
Matches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329
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                                                    ORGANISM
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TITLE
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  KEYWORDS
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                                                                                                                                                                                                                                                      - Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googawa and Aaron Mammoser in Pieter d Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467
                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGTGGTGCGCTCGTCGGGCACCAGGTGCACGCCCCAACCGCGGTTGTGCAGGGTGACAA 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        762 TCCCSYSYSSSTSSSSSTSWGSTSGSSSSVGTSSSSDSTSTCCSCCYMCTCCSTYBMB 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 GGTCAACGCTGGTGGCTACCTCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGGCGGCCGC
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                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Drosophila melanogaster"
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larity 13.8%; Pred. No. 9.5e-06;
Conservative 161; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACCCCATGGCATGGGGTGGGTGAGCGCGGAGG 680
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/db_xref="taxon:7227"
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                                                                                                   Ephydroidea; Drosog
1 (bases 1 to 925)
                                                                                                                                                                                    Submission
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                        Senoscope
                                                                                                                                                                                    rect
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GSS 19-JUN-2003

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DNA

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RESULT 10 CNS0091P/c LOCUS DEFINITION

ACCESSION

VERSION

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/mol_type="mRNA"
/cultivar="Puma (winter rye)"
/db_xref="taxon:4550"
/clone="Sc01_01d12"
/tissue_type="leaf, crown"
/dev_stage="seedling three-leaf stage"
/clone_lib="Sc01_AAFC_ECORC_cold_stressed_winter_rye_seedl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS01213 645 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN08C07 of DrosBAC library from Drosophila melanogaster (fruit
                                                      Secale cereale
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Dooideae; Triticaes; Secale.
1 (bases 1 to 728)
Singh, J. M., Piche, C., Couroux, P., De Moors, A., Harris, L.J.,
Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 GGTGGCTACCTCTCCGCGTAGGCGCTCGTTGGTCCAGCAGAGGCGGCCGCCCTTGCGCGA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478 GCAGAATGGCGGTAGGGGGTCTAGCTGCGTCTCGGGGGGGTCTGCGTCACGGTAAA 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI
Site_2: Xho I; Sampled three-leaf seedlings treated for
one week at 2oC, 12 hrs light/day. Library made with
Stratagene UNIZAP XR Kit/Gigapack III Gold Kit. Lambda
library is amplified, then mass excised in SOLR cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 CTCGTCGGGCACCAGGTGCACGCCCAACCGCGGTTGTGCAGGGTGACAAGGTCAACGCT
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.3%; Score 52.8; DB 2; Length 728; Best Local Similarity 53.6%; Pred. No. 0.0035; Matches 105; Conservative 1; Mismatches 90; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS.
Drosophila melanogaster (fruit fly)
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/organism="Secale cereale"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@agr.gc.ca.
Location/Qualifiers
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Clack, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)
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                                                                                     Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
drosophila was prepared from embryos by Alain Bucheton
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
   Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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1 (bases 1 to 525)
1 (bases to 525)
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W.,
Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
The analysis of 100 genes supports the grouping of three highly
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|organism="Drosophila melanogaster"
|/mol type="genomic DNA"
|db_xref="taxon:7227"
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Best Local Similarity 9.8%; Pred. No. 0.034;
Matches 41; Conservative 128; Mismatches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="BACN08C07"
/clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
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/clone lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citck, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba
Proc. Natl: Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
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/organism="Mastigamoeba balamuthi"
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Email: mmuller@rockvax.rockefeller.edu
Insert Length: 525 Std Error: 0.00
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Laboratory of Biochemical Parasitology
The Rockefeller University
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Pred. No. 0.042
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/strain="ATCC 30984"
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                                                           /mol_type="genomic_DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMaol145K22"
/clone lib="XM 0.7 1.5 KB"
/note="Vector: DBCSK-; Site 1: HinclI; 0.7-1.5 kb
methylation filtered genomic_DNA library"
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                    1. .516
/organism="Zea mays"
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Search completed: July 14, 2005, 23:22:51 Job time : 11815.6 secs

Perfect score:

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Sequence:

Scoring table:

Searched:

Database :

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BD234590 Screening
AX026821 Sequence
AX319694 Sequence
AX319694 Sequence
AX116416 Sequence
AR22266 Sequence
AR411127 Sequence
AX437643 Expressio
AX311282 Sequence
AX349366 Sequence
I56772 Sequence
I56772 Sequence
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AX202478 Sequence
AX573107 Sequence
AX65746 Sequence
A63067 Sequence
BD181637 Novel mel
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U89673 Cloning vec
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BD181638 Novel mel
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AX207724 Sequence
AX211281 Sequence
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100.0%; Pred. No. 9.4e-24;
iive 0; Mismatches 0;
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Unclassified.
1 (bases 1 to 3853)
Antelman,D., Gregory,R.J. and Wills,K.N.
Retinoblastoma tusion polypeptides
Patent: US 6074850-A 5 13-JUN-2000;
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    .3853
/organism="unknown"
/mol_type="unassigned DNA"

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Sequence 5 from patent US 6379927.
AR207832 GI:21507688
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Sequence 5 from patent US 6074850.
AR098190
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AR116416
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Best Local Similarity 100.
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AR08191 Sequence
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AR098192 Sequence
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AR09814 Sequence
AR38214 Sequence
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AX0601344 Sequence
AX133940 Sequence
BD238492 Expressio
AX234391 Sequence
A9174 Sequence
BD085110 Vertebrat
AX951626 Sequence
                                                                                                       July 14, 2005, 04:39:07; Search time 749.127 Seconds (without alignments) 6468.225 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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Listing first 45 summaries
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A new small sized high-level eukaryotic expression vector
Unpublished
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/note="multiple cloning site (MCS)"
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 19 13-JUN-2000;
Location/Qualifiers
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Sequence 19 from patent US 6074850.

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Cloning vector pcDNA3ZEO DNA
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Best Local Similarity 100.0
Matches 100; Conservative
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PN 47 2010518-A/3
PN 21-MAR-2001
PF 13-MON-1997 JP 1998522958
PR 15-NOV-1996 US 08/751517,14-FEB-1997 US 08/18
DUGLAS ANTELMAN RICHARD J GREGORY, KENNETH N WILLS PC CO7H21/04, CO7K5/00, AGIK38/00, AGIK35/12
CC Strandedness: Single;
CC Topology: Linear;
FH Key
CDS
FT CDS
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Tissue specific expression of retinoblastoma protein.
BD009729
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Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 3 21-MAR-2001;
CANJI INC
OS Unidentified
PN JP 2001503638-A/3
PN JP 2001503638-A/3
PN JP 201503638-A/3
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                1 (bases 1 to 3853)
Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 5 30-APR-2002;
Location/Qualifiers
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JP 2001503638-A/3.
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100.0%; Pred. No. 9.3e-24;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 33 13-JUN-2000;
Location/Qualifiers
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Antelman,D., Gragory,R.J. and Wills,K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 33 30-APR-2002;
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Sequence 33 from patent US 6074850.
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Matches 100, Conservative
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Matches 100; Conservative
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PN JP 2001503638-A/4

PN JP 2001503638-A/4

PD 21-MAR-2001

PF 13-NOV-1996 US 08/751517,14-FEB-1997 US 08/801092 PI

DOUGLAS ANTELMAN, RICHARD J GREGORY, KENNETH N WILLS PC

COTHELY O4, COTKS/00, A61K39/00, A61K35/12

CC Strandedness: Single;

CC Topology: Linear;

PH Key Location/Qualifiers

FT source / Organism='Unidentified'.
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Tissue specific expression of retinoblastoma protein.
BD009730
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Antelman, D., Gregory, R.J. and Wills, K.N.
Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 4 21-MAR-2001;
CANJI INC
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Location/Qualifiers
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100.0%; Score 100; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-24;
Matches 100; Conservative 0; Mismatches 0;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 19 30-APR-2002;
Location/Qualifiers
1. 4026
                                                                                                                                             DNA
                                                                                                                                           AR207833 4026 bp 3
Sequence 19 from patent US 6379927.
AR207833
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JP 2001503638-A/4.
unidentified
unidentified
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Unclassified.
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RESULT 7 BD009730 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS JOURNAL

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source

ORIGIN

TITLE JOURNAL FEATURES

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REFERENCE AUTHORS

DEFINITION

RESULT 6 AR207833

ACCESSION VERSION KEYWORDS

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

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PAT 22-JAN-2001
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Pred. No. 9.3e-24;
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/mol_type="unassigned DNA"
/db &ref="taxon:32630"
/noEe="Vector pVAC1"
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Cancer Research Ventures Limited (GB)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 1 from Patent WO0179510.
AX286570.
AX286570.1 GI:17048664
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Sequence 3 from Patent WO0078358.
AX060344
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Tissue specific expression of retinoblastoma protein.
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unclassified.

unclassified.

l (bases 1 to 4341)

Hawkins, R.E., Russell, S.J., Stevenson, F.K. and Winter, G.P.
Hawkins, R.E., Russell, S.J., Stevenson, F.K. and Winter, G.P.
IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
REDICAL RES COUNCIL (GB)
Other publication A2 145064 940414
Other publication AU 4832493 940426
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PN JP 2015038-A/5
PN JP 201503638-A/5
PD 21-MAR-2097
PF 13-NOV-1997 JP 1998522958
PR 15-NOV-1996 US 08/751517,14-FEB-1997 US 08/1000GLAS ANTELMAN, RICHARD J GREGORY, KENNETH N WILLS PC CO7H21/04,CO7KS/00,A61K38/00,A61K35/12
CC Strandedness: Single;
FC Topology: Linear;
FH Key Location/Qualifiers
FT source /organism='Unidentified'.
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Antelman, D., Gregory, R.J. and Wills, K.N.
Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 5 21-MAR-2001;
CANJI INC
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100.0%; Score 100; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-24;
Matches 100; Conservative 0; Mismatches 0;
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/organism="synthetic construct"

/organism="synthetic construct"

/mol type="unassigned DNA"

/db xref="taxon:32630"

/note="This sequence is artificial and is based on well

sstablished comm ercially available vectors that are cited

with their vendor within the patent applicatio"
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/db_xref="taxon:32630"
/note="pCDNA3.1/GS vector_by_Invitrogen_Corporation"
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Patent: WO 0119853-A 1 22-MAR-2001;
THE UNIVERSITY OF SHEFFIELD (GB)
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Fikes,J.D., Hermanson,G.G., Sette,A.,
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PD 09-JUL-2002
PF 13-MAY-1999 JP 2000548449
PR 13-MAY-1999 US 09/078904,15-MAY-1998 US 60/085751 PI
JOHN D FIKES,GARY G HERMANSON, ALESSANDRO
SETTE,GLENN Y ISHIOKA,
PI BRIAN LIVINGSTON, ROBERT W CHESNUT
PC CL2N15/09, A61K31/711, A61K39/00, A61K39/12, A61K39/16, A61P31/16, A6
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	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	
OM nucleic - nucl	- nucleic search, using sw model	
Run on: J	<pre>July 14, 2005, 04:35:42 ; Search time 140.988 Seconds (without alignments) 4198.742 Million cell updates/sec</pre>	
Title: Perfect score: 1 Sequence: 1	US-09-482-682-43_COPY_1_100 100 1 gacggatcgggagatctcccctgctccctgcttgtgtgtt 100	
Scoring table: I	IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched: 4	4390206 segs, 2959870667 residues	
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SUMMARIES	ID	ADM41035	ADH11349	ADM41037	ADM41034	ADM41036	AAV40006	AAV40007	AAV63466	AAQ62391	AAS17704	ABN83143	AAF24901	AAD39652	AAF83146	ADB33528	AAZ38633	AAS12839	ADH11417	ADF10526	ACC44637
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facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
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                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNC-53 vertebrate protein homologue, UNC-53; Caenorhabditis elegans; cell shape regulator; cell motility regulator; cell migration; cell behaviour regulator; phenotype; signal transduction pathway; signal integrator protein; neuronal regeneration; revascularisation; wound healing; chronic neurodegeneration; disease; acute traumatic injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.g. promoting neuronal regeneration, treating chronic neuro-degenerative diseases or acute traumatic injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Verhasselt P;
Vandekerckhove JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrate UNC-53 protein homologue related nucleotide sequence
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                                                                                                                                                                                            100.0%; Score 100; DB 12; Length 1506; 100.0%; Pred. No. 4e-26; o; Mismatches 0; Indels 0;
                                                                                                                                                           Sequence 1506 BP; 454 A; 277 C; 361 G; 414 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                        61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 410-411; 479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH11349 standard; DNA; 1600 BP
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                                                                                                                                                                                                                                      Matches 100; Conservative
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                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                 specification
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cell shape, motility, or the direction of cell migration for use as a cherapeutic; (7) a method for determination of whether a protein is an inhibitor or enhancer of regulation of cell behaviour, growth, shape or inhibitor or enhancer of regulation of cell behaviour, growth, shape or motility or the direction of migration by contacting a host cell captured by homologue of UNC-53 and determining a change of phenotype; (8) a method for identification of vertebrate homologues of C. elegans cuc-53 gene by hybridising a probe of 15-50 bp of the unc-53 sequence to a DNA library; and (9) a method for identification of a protein which is cative in the signal transduction pathway of a cell of which a vertebrate component comprising; (i) contacting an extract of a cell with an antibody to the UNC-53 homologue; (ii) identifying an antibody/homologue complex; and (iii) analysing such a complex to identify any non-antibody protein bound to the complex. UNC-53 is a signal transducing or signal integrator protein involved in controlling directionality of cell migration and cell shape in C. elegans. Vertebrate compless of UNC-53 can be used to promoce neuronal regeneration, revascularisation or wound healing, to treat chronic neurodegenerative sequence is used in the exemplification of the present invention.
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Pred. No. 4.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1600 BP; 397 A; 409 C; 398 G; 396 T; 0 U; 0 Other;
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Best Local Similarity 100.0%;
Matches 100; Conservative C
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mammalian host, and for producing chimeric mammals that can be used to

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            selectively destroying native cells in a tissue of foctal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for cells replace destroyed cells of the tissue. The method is useful for mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                                                                                       1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
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                                                                                                                                                                                                                                                                                                       Gaps
replacement cells within a foetal non-human mammal, which comprises
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                                                                                                                                                                                                                                                                    Length 1782;
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Pred. No. 4.2e-26;
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replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells in the cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a

The present invention describes a method for engrafting foreign

Disclosure; SEQ ID NO 2; 48pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
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              develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
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                                                                                                                                                     Length 2241;
                                                                                                                     Sequence 2241 BP; 498 A; 630 C; 609 G; 504 T; 0 U; 0 Other;
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                                                                                                                                                     Score 100; DB 12;
Pred. No. 4.5e-26;
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100.0%; Pred. No. *...
0; Mismatches
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                                                                                    specification
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e.g. hyper-proliferative disease such as cancer and restenosis
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                                                                                                                                                                                                                                                                                                                                       Plasmid pCTMI
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15-FEB-1999
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Matches 100;
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                                               GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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                                  Gaps
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                                                                                                                                                                                                               E2F; transcription factor; human; retinoblastoma protein RB; bladder cancer; restenosis; angioplasty; diabetic retinopathy; thyroid hyperplasia; Grave's disease; psoriasis;
                Length 2294;
Sequence 2294 BP; 466 A; 680 C; 641 G; 507 T; 0 U; 0 Other;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                               "tripartite leader sequence"
                                                                                                                                                                                                                                        benign prostatic hypertrophy; Li-Fraumeni syndrome;
peripheral vascular disease; therapy; plasmid pCTM; ss.
                                                                                61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                 to AatII"
               100.0%; Score 100; DB 12;
100.0%; Pred. No. 4.5e-26;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "pUC19 backbone H3 complement (2857. .3717)
                                                                                                                                                                                                                                                                                                                                                                                                       'note= "SP6 promoter"
                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "CMV promoter"
                                                                                                                                                                                                                                                                                                                               location/Qualifiers
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                                                                                                                                                                                                                                                                                unidentified bacteriophage; T7.
unidentified bacteriophage; SP6.
Macaca mulatta; polyoma virus.
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                                                                                                                                       AAV40006 standard; DNA; 3853 BP
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97US-00801092
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(first entry)
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                                Matches 100; Conservative
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                                                                                                                                                                                                                                                                Human cytomegalovirus.
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                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                          mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-1997;
                                                                                                                                                                                               Plasmid pCTM
                                                                                                                                                                        27-AUG-2003
15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-1998
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                                                                                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                       AAV40006;
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                                                                                                                                                                                                                                                                                                                 Chimeric
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                                            This is the nucleotide sequence of pCTM, a plasmid which contains a CMV promoter, a tripartite adenovirus leader flanked by T7 and SP6 promoters, and a multiple cloning site with a bovine growth hormone polyA site and downstream SV40 polyA site. It has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastoma protein (BP, see AAW62465) and BZF transcription factor (see AAW62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, specifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the EZF promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GACGGATCGGGAGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3853;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3853 BP; 936 A; 986 C; 942 G; 989 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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peripheral vascular disease; therapy; plasmid pCTMI; ss.
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/note= "pUC19 backbone H3 to AatII"
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Pred. No. 5.2e-26;
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"hybrid SV40 late intron"
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/note= "CMV promoter"
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/note= "SP6 promoter"
1851. .4026
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unidentified bacteriophage; SP6.
Macaca mulatta; polyoma virus.
Example 1; Fig 4; 91pp; English
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(first entry)
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Macaca mulatta; polyoma virus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACGGATCGGGAGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
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                                                                                                                                                                                                                                                                                                  New fusion polypeptide of, e.g. transcription factor - used to treat, e.g. hyper-proliferative disease such as cancer and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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thyroid hyperplasia; Grave's disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4026 BP; 978 A; 1021 C; 982 G; 1045 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       benign prostatic hypertrophy, Li-Fraumeni syndrome, peripheral vascular disease; therapy; plasmid pCTMIE; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CCGCATAGITAAGCCAGTAICIGCICCCIGCTIGIGIGII 100
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100.0%; Pred. No. 5.3e-26;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            retinoblastoma
 complement (3032. .3890)
                                                                                                                                                                                                                                       Wills KN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription factor; human;
                               "AMP-ORF"
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unidentified bacteriophage; T7.
unidentified bacteriophage; SP6
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                                                                                                                           97WO-US021821,
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nes 100; Conservative
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/note= '
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                                                                                                                                                                                                        (CANJ-) CANJI INC.
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                                                                                                                                                                         14-FEB-1997;
                                                            WO9821228-A1
                                                                                                                           13-NOV-1997;
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                                                                                          22-MAY-1998.
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15-FEB-1999
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This is the nucleotide sequence of pCTMIE, a plasmid that was constructed by amplifying the SY40 enhancer from SY40 viral DNA by PCK, digesting the amplified broduct with BglII and insertino Bamil-digested plasmid pCTMIE with BglII and insertino Bamil-digested plasmid pCTMIE see AA440007). Plasmid pCTMIE has been used as a vector for the expression of fusion protein of the invention that comprise retinoplastoma protein (BP, see AA462465) and E2F transcription factor (see AA462464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, pspecifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the E2F promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4249 BP; 1020 A; 1074 C; 1048 G; 1107 T; 0 U; 0 Other;
                                                                                                                      "tripartite leader sequence"
                                                                                                                                                                                                                               "72 bp tandem repeat enhancer"
                                                                                                                                                                                                                                                                   note= "72 bp tandem repeat enhancer"
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note= "hybrid SV40 late intron"
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"hybrid SV40 late intron"
                                                                                                                                                                                                                                                                                                       antigen binding site"
                                                                   *tag= a
note= "CMV promoter"
307. 1074
                                                                                                                                                                                                                                                                                                                                                                               "SP6 promoter"
                                                ocation/Qualifiers
                                                                                                                                                                                            note= "early mRNA"
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14-FEB-1997;
             taurus.
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                        Chimeric.
                                                          promoter
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                                                            GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                            Vector; pVAC1; pRc/RSV; leader sequence; termination signal; fusion protein; pSfi/Not.Tag1; pelB leader; human; immunoglobulin; VH1; single chain; Fv; murine antibody; retroviral; envelope; plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating immune response to a disease marker - by administering a vector which expresses the disease marker to interact with the immune
                      Gaps
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0
 Length 4249;
                     Indels
                                                                               61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                          61 CCGCATAGITAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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100.0%; Score 100; DB 2;
100.0%; Pred. No. 5.4e-26;
ive 0; Mismatches 0;
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/note= "Claim 9"
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/note= "Claim 7"
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/note= "Claim 8
606. .716
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                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                         606. .780
                    Matches 100; Conservative
                                                                                                                                                                                            (revised)
 Query Match
Best Local Similarity
                                                                                                                                                                                                                          Vector pVAC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-1993;
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                                                                                                                                                                                           25-MAR-2003
18-NOV-1994
                                                                                                                                                                                                                                                                           vaccine; sa
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                                                                                                                                                                                                                                                                                              Synthetic.
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This sequence represents the vector pVAC1. This vector is based on the commercially available vector pRc/RSV. Leader sequences and termination signals were introduced into the vector to allow for production of fusion proteins. The vector, pSfi/Not.Tagl, was modified to replace the pelb leader with the human immunoglobulin VHI leader sequence that permits the encoding of an SfiI cloning site without modification of the amino acid sequence. This fragment was then cloned as an EcoRI/Blunt-HindIII fragment into NotI/Blunt- HindIII cut vector pRc/RSV to give pVACI. The single chain Fv for an individual patient can be inserted within the VHI leader sequence. This plasmid when encoding a single chain murine

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The invention relates to a nucleic acid construct for delivery into living cells in vivo, to induce an immune response to a disease peptide antigen, where the construct directs expression of a fusion protein comprising the peptide antigen and the first domain of FrC. Also included are a nucleic acid vector comprising the above construct, a host cell comprising the above construct or vector and a method of producing a nucleic acid construct for inducing an immune response. The method comprises identifying a nucleic acid sequence encoding a disease peptide antigen comprising epitopes characteristic of the disease, cloning the nucleic acid sequence, introducing the cloned nucleic acid into a vector which allows the antigen to be expressed as a fusion with a first domain FrC from tetanus toxin, and optionally isolating the construct from the response, particularly to tumour antigens. The present sequence is vector puAc1 which encodes a vaccine of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTL; PCR primer; pVAC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid construct, useful to immunize against various diseases including cancer, expresses the first domain of tetanus toxin FrC fused to a disease peptide antigen to provide a vaccine.
antibody/retroviral envelope fusion protein can be used as a plasmid vaccine and it induces a strong humoral response to the antibody moiety in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                               1 GACGGALCGGGAGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                           1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                      Gaps
                                                                            Sequence 4341 BP; 1032 A; 1099 C; 1091 G; 1119 T; 0 U; 0 Other;
                                                                                                                                                      ö
                                                                                                                 Length 4341;
                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                       CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                                                                                                                                                                                                                                                  61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                             100.0%; Score 100; DB 2; ilarity 100.0%; Pred. No. 5.4e-26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vector pVAC1 encoding a DNA vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 4; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   AAS17704 standard; DNA; 4341 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CANC-) CANCER RES VENTURES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-APR-2001; 2001WO-GB001719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-2000; 2000GB-00009470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stevenson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-066370/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium tetani.
                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
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                                                                                                                                                      Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS17704;
                                                                                                               Query Match
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AAS17704
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GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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                                                                                                                                                                                                                                                                                                                                                                              28-DEC-2000.
                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                               AAF24901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W;
                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel nucleic acid construct for inducing an immune response in vivo to an antigen, capable of directing the expression of a fusion protein that comprises an antigen and an adjuvant sequence derived from a plant viral coat protein. The construct of the invention has cytostatic and virucide activity. The nucleic acid construct is useful for inducing an immune response in a patient, for vaccinating a patient against an infectious disease caused by an antigen derived from a pathogen e.g. a virus, for treating a cancer patient or a patient with a predisposition to cancer and for treating a patient having a B cell malignancy, where the construct is encapsidated, and optionally, a second nucleic acid sequence encoding a further immunomodulatory which is acid sequence encoding a further immunomodulatory in medical treatment, and in the preparation of a vaccine for treating or preventing a disease state associated with the antigen. The sequence
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                                                                               1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                          1 GACGGATCGGGAGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                  plant viral coat protein; pVAC1; cytostatic; virucide;
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid construct for delivery into living cells as a vaccine, useful for treating e.g. cancer, directs the expression of a fusion protein comprising an antigen and an adjuvant sequence derived from
Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
                              Length 4341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 100; DB 6; Length 4341;
100.0%; Pred. No. 5.4e-26;
ive 0; Mismatches 0; Indels 0;
                                                     Indels
                                                                                                                                                   61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                      61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                           / Match 100.0%; Score 100; DB 6; Local Similarity 100.0%; Pred. No. 5.4e-26; nes 100; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shows the complete sequence of vector pVAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CANC-) CANCER RES VENTURES LTD.
                                                                                                                                                                                                                                                                                                                     Plasmid pVAC1 complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 7; 84pp; English
                                                                                                                                                                                                                                     ABN83143 standard; DNA; 4341 BP
                                                                                                                                                                                                                                                                                                                                                  Immune response; plant viral c
cancer; B cell malignancy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2001; 2001WO-GB005142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2000; 2000GB-00028319.
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Savelyeva N, Stevenson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant viral coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-500202/53.
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                                                                                                                                                                                                                                                                                          10-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                ABN83143;
                            Query Match
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                                                      Matches
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Gaps

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Best Local Similarity 100. Matches 100; Conservative

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The specification describes a microsphere comprising dihydrazide derivatised hyaluronic acid crosslinked to a nucleic acid (NA). The microspheres cause reduced inflammatory responses, and have increased safety and biodegradability. The microspheres are useful for transfecting a cell of a subject and for tracating subject having myocardial ischemia, by increasing cardiac angiogenesis. They are also useful for treating haemophilia. The present sequence represents the plasmid pCDNA3.1/Gs, into which is inserted a polynucleotide sequence which is crosslinked to hyaluronic acid. The polynucleotide sequence encodes a vascular endothelial growth factor (VEGF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hyaluronic acid micro spheres for use in gene therapy of myocardial ischemia and hemophilia, comprising dihydrazide derivatized hyaluronic acids crosslinked to nucleic acids.
1 caccearcecearcrecearcecearcecrarecrearcrearacaarcreare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4597 BP; 1062 A; 1214 C; 1206 G; 1115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsphere; dihydrazide; hyaluronic acid; inflammatory myocardial ischemia; cardiac angiogenesis; haemophilia; vascular endothelial growth factor; VEGF; ss.
                                                                                                                  61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the plasmid pCDNA3.1/GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 36-38; 38pp; English.
                                                                                                                                                                                                                                                                                                                                       BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2000; 2000WO-US016837.
                                                                                                                                                                                                                                                                                                                                   AAF24901 standard; DNA; 4597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-071363/08.
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AAD39652
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The invention provides a nucleic acid molecule (I) comprising at least the functional part of blasticidin resistance (BS) gene, or its homolog, linked through a recognition sequence to at least one selected gene. (I) is useful in treatment comprising: (I) providing cells/tissues transfected with (I); (2) surgical administration of the cells/tissues to the patient to be treated; and optionally (3) monitoring the status of the cells/tissues by the patient. Therapeutic compositions comprising cells/tissues transformed with (I) is useful in identifying the role of genes in healthy and diseased tissue, in tissue engineering and in cosmetic surgery. Tissue engineering can be used to treat arthritis, joint replacement, skin grafts for burn victims, and replacement coronary arteries. Cosmetic tissue surgery includes rhinoplasty. The present sequence represents the nucleotide sequence of the vector pIRES/BS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion protein; amyloid precursor protein; APP; transcription factor; notocropic; neuroprotective; APP inhibitor; amyloid precursor protein inhibitor; Alzheimer's disease; beta-secretase; gamma-secretase; human; gene; ds.
                                                                                                                                                                                                                                                                                            Novel nucleic acid molecule useful for therapeutic and cosmetic tissue engineering, comprising at least a functional part of blasticidin resistance gene linked through a recognition sequence, to a selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression vector nucleotide sequence SEQ ID NO:27
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Pred. No. 5.6e-26;
if Mismatches 0;
                                                                                                                                                                                                       Kafienah W;
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                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Fig C; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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                                                                    11-SEP-2000; 2000WO-GB003462.
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                                                                                                                                                                                                       Barker MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        containing the BS gene
                                                                                                                                                           (UYSH-) UNIV SHEFFIELD
                                                                                                                                                                                                                                                 WPI; 2001-290354/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003072041-A2
                                                                                                                                                                                                       Hollander AP,
                                                                                                                11-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                         22-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a recombinant vector which comprises DNA, consisting of an insertion cassette contained between at least two insertion sites, that encodes a small nuclear (sn) RNA. The invention is used to identify snRNA modifications that inhibit expression of transcription products (and the identified snRNA are used to suppress expression) for delivering antisense sequences to the nucleus and to create transgenic animals. The present DNA sequence is human snRNA, Ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant vector containing sequence for small nuclear RNA, useful e.g. for identifying variant snRNA that suppresses expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blasticidin resistance, BS gene, gene therapy; tissue engineering, cosmetic surgery, arthritis, joint replacement; skin graft; rhinoplasty;
                                                                                                                                                                                  vector; insertion cassette; small nuclear RNA; snRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 100; DB 6; Length 4639; 100.0%; Pred. No. 5.5e-26; rive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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                                                                                                                                   Human small nuclear RNA (snRNA) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 18pp; English
AAD39652 standard; DNA; 4639 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF83146 standard; DNA; 4840 BP
                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-2001; 2001US-00804481.
                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-2000; 2000US-0188304P
                                                                                         (first entry)
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Best Local Similarity 100.
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-499510/53.
                                                                                                                                                                             Human; recombinant transgenic animal;
                                                                                                                                                                                                                                                                                            US2002058287-A1.
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                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                         22-OCT-2002
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                                                                                                                                                                                                                                                                                                                                      16-MAY-2002
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27-FEB-2002; 2002US-0360274P.
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(MERI ) MERCK & CO INC.

Flores OA, Hazuda DJ, Inglese J; Shi X, Simon AJ, Zuck PD; Espeseth AS, Ferrer M, Miller MD, Register B,

WPI; 2003-689968/65.

DNA encoding a fusion protein of amyloid precursor protein, useful in screening for anti-Alzheimer agents, comprises a fused transcription

Disclosure; Fig 32B-F; 193pp; English.

The present invention describes a DNA molecule (I) that encodes a fusion protein (FP) comprising: (i) an amino acid sequence of amyloid precursor protein (APP), either the wild type, Swedish or NFEV versions; and (ii) a transcription factor (TF), fused in frame to the C-terminus of (i). Also described: (I) an expression vector containing (I); (2) a eukaryotic cell containing (I); and (3) methods for identifying a compound (A) that chibits processing of APP, using the cells of (2). (I) has nootropic and neuroprotective activities. (I) can be used to produce eukaryotic cells that express FP and are useful in screening for agents that inhibit processing of APP. The agents are potentially useful for the treatment or processing of APP. The agents are potentially useful for the treatment or inhibitors of: (a) beta- and gamma-secretases; and (b) cytoplasmic/extracellular APP signaling in a single assay. Cell-based assays may be free of interference from alpha-secretase activity and are homogeneous (no chromatography, immunoprecipitation or washing required) so well suited to high-throughput screening. The present invention. 

Sequence 5015 BP; 1167 A; 1297 C; 1279 G; 1272 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 100; DB 10; Length 5015; 100.0%; Pred. No. 5.6e-26; Live 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 100; Conservative Query Match

1 GACGGATCGCGAGGTCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60 ઠ 유

GACGGATCGGGAGATCTCCCCATATGGTCGACTCTCAGTACAATCTGCTCTGATG 60

61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100

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CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100

Search completed: July 14, 2005, 07:01:37 Job time : 141.038 secs

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BZ050047 jnr44a12.
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CC817461 1000004518
CC817461 100000413
CC818551 100000413
CC81874 100000423
CC819049 100004521
CC817069 10000501
CC817069 10000501
CC817652 10000382
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CC81781 100004510
CC81781 100004510
CC817759 100003812

OM nucleic

Run on:

Sequence:

Searched:

Database

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Result

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/db_xref="taxon:5807"
/lab_host="B. coli XL2 Blue MRF'"
/lab_host="B. coli XL2 Blue MRF'"
/lofore lib="CptOWAgDNA2"
/note="Vector: PCR-Script Amp SK+; Site 1: SrfI; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   יטע בעה GSS 12-MAY-2000
CpG0047A CpIOWAgDNA2 Cryptosporidium parvum genomic, genomic survey
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Famil: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' the insert, to correct miscalled bases and assign uncalled (N)
bases throughout the sequence, and to terminate when base-calling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Alveodata; Apicomplexa, Coccidia; Eimerlida; Cryptosporidiidae; Cryptosporidium.

1 (bases 1 to 602)
Strong, W.B. and Nelson, R.G. Preliminary profile of the Cryptosporidium parvum genome expressed sequence tag and genome survey sequence analys Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Cryptosporidium parvum"
/mol_type="genomic DNA"
/strain="IOWA"
                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: shotgun
High quality sequence stop: 602.
Location/Qualifiers
                                                                                                                                                                                                                                            CC817837
CC819240
CC818384
                                                                                                                                                               CC817074
CC820036
CC817652
CC817682
                                                                                                                                                                                                                                                                                                                      CC817720
CC819820
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Cryptosporidium parvum
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B67169.1 GI:2642750
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Seq primer: T7
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
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PUBMED
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
B67169
 BZ052029 jnr1303.
BZ050328 jnr1303.
BZ050328 jnr1303.
BZ0504067 jnr38b09.
BZ050505 jnr13009.
AL715724 AL715724
AL714571 AL714571
CK1120360 207j04.pl
CK1120360 207j04.pl
CK117844 209p08.pl
CK117844 209p08.pl
CK11237 ISB1-1188
CL14397 ISB1-1188
CL12353 ISB1-84J1
AQ914559 nbeb00499
BZ051815 jnr57d03.
BZ052857 jnr13g03.
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CIT-HSP-2
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jnr66£08.
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jng98d01.
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3997.736 Million cell updates/sec
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                                                                                                                                                                                                                                              gacggatcgggagatctccc......tgctccctgcttgtgtgtt 100
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                                                                                                                             July 14, 2005, 05:15:57; Search time 952.146 Seconds
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AQ075099 (
BZ049113
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BZ052015
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                          34239544 segs, 19032134700 residues
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Maximum Match 100%
Listing first 45 summaries
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AW409112
AL715724
AL714571
CK119397
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CL141237
CL140877
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BZ051815
BZ052857
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AQ863966
AQ075099
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BZ053587
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Gapop 10 0, Gapext 1.0
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Match Length DB
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92b_est2:

92b_est43:

92b_est44:

92b_est6:

92b_9881:

92b_9881:
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an

genome: a analysis

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BZ054067 117 bp DNA linear GSS 09-OCT-2002 jnr38b09.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
                                                                                                               BZO50328 69-OCT-2002
jnr42c12.b1 B.oleracea001 Brassica oleracea genomic, genomic survey
                                                                                                                                                                                                                                                                               Brassica oleracea
Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; sosids; eurosids II; Brassicales; Brassicaceae; Brassica. [ (bases 1 to 717)  
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 CGGATCGATAGGTCCCTGGACTAGTTATGGTGCACTCTCAGTACAATCTGCTCTGATGCC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /close 11b= Well oleracea001"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCC
                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 696)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
Washington University School of Medicine
Bail: submissions@watson.wustl.edu
Plate: jnr42 row: c column: 12
Seq primer: -21UPpOT forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Brassica oleracea"
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/db_xref="taxon:3712"
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High quality sequence stop: 180.
Location/Qualifiers
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Matches 67; Conservative
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BZ050328
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jnr13g03.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
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/note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
(http://sequence-www.stanford.edu/group/techdev/shear.htm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                   CAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTTT
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Mash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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                                                                                                                                                                                                                                                                                 Length 602;
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9e-09;
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2.4e-10;
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Washington University School of Medicine
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                            ch 60.0%; Score 60; DB Similarity 100.0%; Pred. No. 2.4 60; Conservative 0; Mismatches
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Plate: jnr13 row: g column: 03
Seg primer: -28RPpOT reverse
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High quality sequence start: 32
High quality sequence stop: 551.
Location/Qualifiers
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BZ052929.1 GI:23654922
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EST 18-APR-2002
CDNA Danio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 343)
Coimbra, K., Well, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J. P., Weissenbach, J. and Perit, C. A subrracted cDNA library from the zebrafish (Danio rerio)
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Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                     65 GCGGTATACACACCGCATATGGTGCACTCTCAGTACAATCTGCNCTGATGCCGCATAGTT
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                                                                                             11 GAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTT
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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          Length 348;
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        Score 53.6; DB 2;
Pred. No. 4.1e-08;
0; Mismatches 15;
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Pred. No. 4.8e-08;
0; Mismatches 11;
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/organism="Danio rerio"
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/db_xref="taxon:7955"
/clone="BNOAA018ZF12"
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EST.
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             53.6%;
80.5%;
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84.5%;
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Unpublished (2002)
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                                                      Conservative
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Best Local Similarity
Matches 60; Conserv
                                Similarity
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AL714571/c
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                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="texon:3712"
/clone lib="B.oleracea001"
/note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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P.O.Box 1038, Johannesburg, Gauteng, 2000, South Africa
Fax: 2711 489 9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.6%; Score 55.6; DB 8; Length 717; 77.9%; Pred. No. 9.1e-09; ive 0; Mismatches 19; Indels
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db xref="taxon:9606"
/tiseue_type="Salivary Gland"
/clone_lib="Salivary Gland Library"
/note="Vector: pAMP10"
                                                            Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Bmail: submissions@watenson.wustl.edu
Plate: jnr38 row: b column: 09
Seq primer: -28RPpOT reverse
                                                                                                                                                                                                                                                                                                     'organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bmail: micheler@mail.saimr.wits.ac.za.
Location/Qualifiers
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High quality sequence stop: 543.
Location/Qualifiers
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Matches 67; Conserv
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ORIGIN

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COMMENT

ORIGIN

Gaps

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53.4%; Score 53.4; DB 7; Length 761; 84.5%; Pred. No. 5.6e-08;
                        /tissue_type="inflorescence meristem"
/dew_stage="about one week after bolting"
/lab_host="E. coli SCS-1/pSE111"
/clone_lib="AtM1"
                                                                                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ihnestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
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Insert Length: 766 Std Error: 0.00
       /clone="MPMGp2011009212"
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Seq primer: pQE65.
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5-PRIME, MRNA sequence.
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                                                                                                                                                                                                                                                                                                                                /tissue_type="inner_ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner_ear_subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                              Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

(Cypriniformes; Cyprinidae; Danio.

(Coimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio) embryonic inner ear Unpublished (2002)

Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.4%; Score 53.4; DB 1; Length 345; larity 84.5%; Pred. No. 4.8e-08; Conservative 0; Mismatches 11; Indels
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Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inhestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                       /note="subtracted cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Kersten@molgen.mpg.de
Insert Length: 761 Std Error: 0.00
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CK119397/c
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/clone_llb="Atml"
//note=_wetcor: pQB-30NAST-attB (AY386205); Site_1: Sall;
Site_2: Not1; About 1 week after bolting, cDNA synthesis
site_2: Not1; About 1 week after bolting, cDNA synthesis
susing SuperscriptThm-system (Invitrogen) with an
oligo(dT)-primer containing Not1 restriction site and a
Sall adapter. The main library (plate numbers begin with
1) of 38,000 clones was rearrayed into the sublibrary
(plate numbers begin with 201) containing 5,000 putative
expression clones. Average insert size is 1 kb. Note: The
rearrayed sublibrary (plate numbers begin with 201) was
sequenced. Library generation and sequencing was granted
in context of GABI-LAPP; data are also accessible at
https://gabi.rzpd.de"
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5-PRIME, mRNA sequence.
CKL20360
CKL20360.1 GI:47830676
EST.
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/dav_breft="s.coli SCS-1/pSE111"

/clone lib="ARM1"

/clone lib="ARM1"

/note="Vector: pQE-10NAST-attB (AY386205); Site_1: Sall;
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Fellner,T., Immink,R.G.H., Cahill,D.J. and Kersten,B. Generation of a cDNA expression library from Arabidopsis inflorescence meristem
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Site 2: Not1; About 1 week after bolting, cDNA synthesis using SuperscriptTW-system (Invitrogen) with an oligo(dT)-primer containing Not1 restriction site and a Sal1 adapter. The main library (plate numbers begin with 1) of 38.000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5.00 putative expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at https://gabi.rzpd.de"
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Generation of a cDNA expression library from Arabidopsis
inflorescence meristem
Unpublished (2003)
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53.4%; Score 53.4; DB 7; Length 766;
Best Local Similarity 84.5%; Pred. No. 5.6e-08;
Matches 60; Conservative 0; Mismatches 11; Indels
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/lab_host="E. coli SCS-1/pSE111"
/clone_lib="AtM1"
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Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ihnestr. 73 , D-14195 Berlin, Germany
Tel: +49(0)30/84131128
Fax: +49(0)30/84131128
Fax: +49(0)30/84131128
Fixer: Kersten@molgen.mpg.de
Insert Length: 788 Std Brror: 0.00
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/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="GABI:953578"
/db_xref="taxon:3702"
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REFERENCE

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FEATURES

RESULT 10

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CL141237
ISB1-118J17_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-118J17,
expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at https://gabi.rzpd.de"
                                                                                                                                                                                                                                  514 TTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 455
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
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1 (bases 1 to 898)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
Thysical map of the xenopus tropicalis genome
Unpublished (2003)
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llarity 84.5%; Pred. No. 5.8e-08;
Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequencing Center
Washington University School of Medicine
Baall: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTACACTATAGGG
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/db_xref="taxon:8364"
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RESULT 12 CL140877/c

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Class: BAC ends
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E (bases 1 to 899)
S Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.

D upublished (2003)
Contact: Richard K Wilson Genome Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: 77 TAATACGACTCACTATAGGG
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1581-118812_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-118812, GL140877
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 1009)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Amardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
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Washington University School of Medicine
                                                                                                                                        Xenopus tropicalis (western clawed frog)
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/db_xref="texaon:8364"
/clone="ISB1-118B12"
/clone_lib="ISB1"
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Insert Length: 75000 Std Error: 0.00
Seg primer: T7 TAATACGACTCACTATAGGG
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High quality sequence stop: 681.
Location/Qualifiers
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                                                                                                CL140877.1 GI:40634512
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/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone lib="CUGI Rice BAC Library (EcoRI)"
/clone lib="CUGI Rice BAC Library (EcoRI)"
/note="Vector: pBACINGigo; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pagetimportant food_crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ914559 B14 bp DNA linear GSS 02-DEC-1999 nbeb0049M21r CUGI Rice BAC Library (ECORI) Oryza sativa (japonica cultivar-group) genomic clone nbeb0049M21r, genomic survey
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Brematophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Britartoideae; Oryzae; Oryza.

1 (bases 1 to 814)
Ming,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 TTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 TCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 76
                                                                                      1. .1009
/organism="Xenopus tropicalis"
/organism="Senomic DNA"
/mol_type=genomic DNA"
/db xref="texon:8364"
/clone="ISB1-84115"
/clone="Ib="ISB1"
/note="Vector: pBelobAC11; ISB-1 Xenopus tropicalis BAC Library Segment 1"
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db.tref="taxon:3994"
/clone="nbeb0049M21r"
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Pred. No. 5.9e-08;
0; Mismatches 11;
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100 Jordan Hall, Clemson, SC 29634, USA
121: 864 656 7288
Pax: 864 656 4293
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Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 21
High quality sequence stop: 361.
Location/Qualifiers
High quality sequence start: 167
High quality sequence stop: 324.
Location/Qualifiers
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GSS.
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1 Similarity 84.5%;
60; Conservative
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Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 $. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/BST Resource Center (www.genome.clemson.edu)."
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 675)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Mssh,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica eleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the Shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 TCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 814;
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Pred. No. 6.7e-08;
0; Mismatches 18; Indels
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Genome Sequencing Center
Washington University School of Medicine
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Plate: jnr57 row: d column: 03
Seg primer: -21UPpOT forward
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/db_xref="taxon:3712"
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High quality sequence stop: 94.
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Score 53; DB 8; Length 675; Pred. No. 7.6e-08;

53.0%; 75.6%;

Query Match Best Local Similarity

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                       3 CGGATCGGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCC
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	on: July 14, 2005, 04:2	Title: US-09-482-682-43_COPY_4141_4241  Perfect score: 101 Sequence: 1 acagcaaggggaggattgg	, 242276 ing chos	length: 0 Length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<del>.</del>	4: gb_om:* 5: gb_ov:* 6: gb_pat:* 7: ob ph:*		4 C/ C/ C/	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Result Query No. Score Match Length DR ID	1 101 100.0 3986 12 PCDNA3ZEO 2 101 100.0 4597 6 AX060344 3 101 100.0 5082 6 A31754 101 100.0 5082 6 A31754	101 100.0 5432 6 BD234590 101 100.0 5432 6 AX02651 101 100.0 5446 6 BD195386 101 100.0 5446 6 AX319694	9 101 100.0 5590 12 AB038602 AB038602 0 101 100.0 5639 12 AY437643 AY437643 1 101 100.0 5651 6 AX211282 AX211282 S 2 101 100.0 5651 6 AX249366 AXX49366 S	101 100:0 5/31 6 AX2024/8 AX2024/8 EXX2024/8 E	8 101 100. 9 101 100.

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TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 101
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JP 2001522222-A/8.
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="pCDNA3.1/GS vector by Invitrogen Corporation"
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Bogaert, T.A. and Deraeymaeker, M.
Bogaert, T.A. and Deraeymaeker, M.
VERTEBRATE HOWOLOGUES OF UNC-53 PROTEIN OF C. ELEGANS
Patent WO 9824810-A 10 11.-UUN-1998;
BOGAERT THIERRY ANDRE OLIVIER (BE); DERAEYMAEKER MARC (BE)
Location/Qualifiers
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/organism="unidentified"
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100.0%; Pred. No. 2.5e-18;
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/db_xref="taxon:32644"
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Sequence 10 from Patent WO9824810.
A91754
A91754.1 GI:6740671
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Sequence 3 from Patent WO0078358.
AX060344
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CIZNIS/12, CIZNS/10, CIZNIS/85, CO7K14/435, CO7K16/18, A61K38/17,
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PI PETER VERHASSELT,NATHALIE JEANNE RAYMONDE PUJOL,LUC PI
JACQUES SIMON MAERTENS,
PI WALTER LUYTEN,HUGO GEERTS,JOEL STEFAAN VANDEKERCKHOVE,JOHAN
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Strandedness: Double;
Topology: Circular;
Vertebrate homologues of UNC-53 protein of C elegans FH
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
JP 200152222-A/8
13-NOV-2001
03-DEC-1997 JP 1998E25231
04-DEC-1996 GB 9625283.8
CHRIST JULES PLATTEEUW, CARLOS MANUEL BUESA ARJOL, MARC
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Platteeuw, C.J., Arjol, C.M.B., Deraeymaeker, M., Verhass Pujol, N.J. X., Luc, Maertens, J.S., Luyten, W., Geerts, H. Vandekerckhove, J.S., Geysen, J. and Bogaert, T.A.O.E. Vertebrate homologues of UNC-53 protein of C elegans Patent: JP 2001522222-A 8 13-NOV-2001;
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protein of C elegans.
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Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 101; Conservative 0; Mismatches 0;
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/organism="unidentified"

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/db xref="taxon:32644"
                                                                                                                                    Vertebrate homologues of UNC-53 BD085110
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BD195386 5446 bp DNA linear PAT 17-JUL-2003 Composition and methods for administering Pneumococcal DNA.
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Composition and methods for administering Pneumococcal DNA Location/Qualifiers
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S Briles, D. E., Mcdaniel, L. S. and Curiel, D. T.
Composition and methods for administering Pneumococcal DNA
Composition and methods for administering Pneumococcal DNA
D 2002514061-A 3 14-MAY-2002;
UNIVERSITY OF ALABAMA AT BIRMINGHAM
OS Unidentified
PN JP 2002514061-A/3
PD 14-MAY-2002
PF 04-DEC-1996 US 08/759505
PR 04-DEC-1996 US 08/759505
PR 04-DEC-1996 US 08/759505
PR 04-DEC-1996 US 08/759505
PR 04-DEC-1996 US MCDANIEL, DAVID T CURIEL PC
C12P21/06,C12N15/00,C07H21/02,C07H21/04
CC Strandedness: Single;
CC Topology: Linear;
CC Composition and methods for administering Pneumococcal DN
Key
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/organism='Unidentified'
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/organism="synthetic_construct"
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/db xref="taxon:32630"
/noTe="pcDNA3 vector sequence"
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Cell proliferation assay
Patent: WO 0181614-A 5 01-NOV-2001;
Chemicon International (US)
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2002514061-A/3.
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PC CLINIAL/21,
CC CLINIAL Sequence: Mutagen
FR Key
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    .5432
    /organism='Artificial Sequence'.

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Patent: DE 19856261-C 9 30-MAR-2000;
HOECHST MARION ROUSSEL DE GMBH (DE)
Location/Qualifiers
1. :543.
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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100.0%; Pred. No. 2.4e-18;
tive 0; Mismatches 0;
l (bases a complete and a complete assay of Abeta-peptide Screening assay of Abeta-peptide Patent: JP 2002531141-A 2 24-SEP-2002; AVENTIS PHARMA DEUTSCHLAND GMBH ON JP 2002531141-A/2 PD 24-SEP-2002 PP 27-NOV-1999 JP 2000586944 PR 07-DEC-1998 DE 198 56 261.6
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100.0%; Score 101; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 101; Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
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Sequence 9 from Patent DE19856261.
AX026821
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AB038602
AB038602.1 GI:13094141
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Submitted (21-FEB-2000) Kazuya Hashinaka, Miyazaki Medical College,
Submitted (21-FEB-2000) Kazuya Hashinaka, Miyazaki Medical College,
Department of Biochemistry, 5200 Kihara, Kiyotake, Miyazaki
B89-1692, Japan (E-mail-hasinaka@postl.miyazaki-med.ac.jp,
Tel:81-985-85-0985, Fax:81-985-85-2401)
Location/Qualifiers
L. 5590
/organism="Cloning vector pLCPVRGNR104"
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                                                                         1204 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA 1263
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CGRLGVADRYQDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
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                                   1 ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
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Cloning vector pLCPVRGNR104
other sequences; vectors.
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 0; Mismatches
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2 (bases 1 to 5590)
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complement(4834. .5493)
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Expression vector pcGlobin 2, complete sequence.
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2 (bases 1 to 5639)
2 (bases 1 to 5639)
2 Direct Submission
2 Submitted (14-OCT-2003) Department of Biology, College of Natural Sciences, Chungnam National University, 305-764, Daejeon 305-764,
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Expression vector pcGlobin 2
other sequences; artificial sequences; vectors.
1 (bases 1 to 5639)
Ro, H., Kim, E.J. and Rhee, M.
A new vector system, pcGlobin 2 for in vitro synthesized RNA injection into zebrafish embryos
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                                                                                                                                                                                                                                                                                         Length 5590;
/codon_start=1
/transl_table=11
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complement(4643. :5503)
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1larity 100.0%; Pred. No. 2.4e-18;
Conservative 0; Mismatches 0;
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PAT 30-AUG-2001

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1826 ACAGCAAGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA 1885
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 1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
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                                                                                                1886 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 1926
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<963. .1670
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Sequence 5 from Patent WO02102854.
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1397 ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA 1456
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                                                      1886 recerrereadecedaaadaaceadereedeereradeede 1926
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                                                                                                                                                                                                                                                                                                                                                   Jeppesen, C.B. Conjugates of follicle stimulating hormones Patent: WO 0158493-A 6 16-AUG-2001;
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Sequence 4 from Patent WO0202597.
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Length 5731;

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PAT 29-MAR-2003

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Search completed: July 14, 2005, 14:03:30 Job time: 757.618 secs
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                                                                                         polyA_signal
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/translation="DPEEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT
PRETYCVVONSHEDPEVKFWMYVDGYEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
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YPSDIAVEKESNQGENYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHE
ALHNHYTQKSLSLSPGK"
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                                                                                                                                                                                                              circular SYN 03-JUL-2003
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Submitted (13-JUN-2003) Marcelle C., Lgpd, Institut de Biologie du
Developpement, Campus de Luminy Case 907 F-13288 Marseille, 13288,
FRANCE
                                                                                                                                                                                          1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGGATGCGGTGGGCTCTA 60
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/organia="unidentified cytomegalovirus"
/mol type="other DNA"
/db_xref="taxon:205912"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences; vectors.
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|organism="Expression vector pCLGFPA"
|mol_type="other DNA"
|db_xref="taxon:236984"
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In ovo electroporation of avian somites
Unpublished
C. Chases I to 6084)
Marcelle, C.
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Organism="Oryctolagus cuniculus"

mol_type="other DNA"
                                                                                                                      100.0%; Score 101; DB 6;
100.0%; Pred. No. 2.4e-18;
iive 0; Mismatches 0;
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/ Mol_type="other DNA"

/ db xref="taxon:10633"

2908...3723

/ organism="Requorea victoria"

/ mol_type="other DNA"

/ db xref="taxon:6100"
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'organism="Bos taurus"
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'db_xref="taxon:9913"
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740. .887
/gene="beta actin"
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TITLE
JOURNAL
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1734. .1776
//note="multiple cloning site; MCS
under control of CMV enhancer/chicken beta-actin promoter"
1782. .1996
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2011 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 2051
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3757 .3807
/note="late"
                                                                                                    /note="bovine growth hormone" 2442. .2836 2908. .3723
/gene="beta actin"
1734. .1776
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July 14, 2005, 04:35:42; Search time 142.398 Seconds (without alignments) 4198.742 Million cell updates/sec
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
                                                                                OM nucleic - nucleic search, using sw model
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l acagcaagggggaggattgg........ccagctggggctctaggggg 101 US-09-482-682-43\_COPY\_4141\_4241 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesegn2003cs:\* geneseqn2003ds:\* geneseqn2003as:\* geneseqn2003bs:\* N\_Geneseq\_16Dec04:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2004as: genesegn1980s:\* genesegn1990s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:

	Description	Adhl1353 Vertebrat	Aaf24901 Nucleotid	Adr12380 Vector pM	Adb33528 Expressio	Adh11417 Plasmid p	Adm97811 & X UAS b	Adi34681 Nucleotid	Adh11233 Vertebrat	Abn86685 Nucleotid	Ade21866 Plasmid v	Ado05277 pcDNA3 pl	Aaz89476 Transgeni	Aav38297 Plasmid p	Aas18619 Renilla l	Abl53540 Vector pc	Adn36314 Plasmid p	Abl58494 Recombina	Abl58493 Recombina	Abl58489 Recombina	Abl58490 Recombina
SUMMARIES	ID	ADH11353	AAF24901	ADR12380	ADB33528	ADH11417	ADM97811	ADI34681	ADH11233	ABN86685	ADE21866	AD005277	AAZ89476	AAV38297	AAS18619	ABL53540	ADN36314	ABL58494	ABL58493	ABL58489	ABL58490
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	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101
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Aai66195 Human FSH	Abk40237 DNA encod	Abl58492 Recombina	Abl58491 Recombina	Abt40262 pCXFc DNA	Ada89054 Plasmid p	Adg74306 Fibroblas	Aadil615 Six finge	Adm97787 Gal4-DBD	Aal44423 West nile	Aal44424 West nile	Aad56212 Human AB-	Aad56211 Human AB-	Aad56210 Human AB-	Aad56213 Human AB-	Aad56215 Human PSM	Aad56214 Human AB-	Abk96469 Plasmid p	Abk96470 Plasmid p	Abk15579 DNA encod	Abk15580 DNA encod	Aad13062 pcDNA3-Bl	Aai66194 Human FSH	Abk40236 DNA encod	Abk51585 Nuclear t
AA166195	ABK40237	ABL58492	ABL58491	ABT40262	ADA89054	ADG74306	AAD11615	ADM97787	AAL4423	AAL44424	AAD56212	AAD56211	AAD56210	AAD56213	AAD56215	AAD56214	ABK96469	ABK96470	ABK15579	ABK15580	AAD13062	AAI66194	ABK40236	ABK51585
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100.0	100.0	100.0	100.0	100.0	.100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101
21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

UNC-53 vertebrate protein homologue; UNC-53; Caenorhabditis elegans; cell shape regulator; cell motility regulator; cell migration; cell behaviour regulator; phenotype; signal transduction pathway; signal integrator protein; signal integrator protein; neuronal regeneration; revascularisation; wound healing; chronic neurodegenerative disease; acute traumatic injury; Vertebrate UNC-53 protein homologue related nucleotide sequence. ADH11353 standard; DNA; 3482 BP. fibrotic disease; gene; ds (first entry) 11-MAR-2004 ADH11353; RESULT 1 ADH11353 

WO9824810-A2. Unidentified.

97WO-EP006956. 96GB-00025283 03-DEC-1997; 04-DEC-1996; 11-JUN-1998.

(JANC ) JANSSEN PHARM NV.

Verhasselt P; Vandekerckhove JS; Platteeuw CJ, Buesa Arjol CM, Deraeymaeker M, Pujol NJR, Maertens LJS, Luyten W, Geerts H, Pujol NJR, Maertens LJS Geysen J, Bogaert TAOE;

WPI; 1998-362411/31. P-PSDB; ADH11354. Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.g. promoting neuronal regeneration, treating chronic neuro-degenerative diseases or acute traumatic injuries.

Disclosure; Page 414-417; 479pp; English.

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derivative or bioprecursor of UNC-53. Also described: (1) a cDNA sequence encoding a vertebrate homologue of the C. elegans UNC-53 protein; (2) a nucleic acid which hybridises to the cDNA of (1), (3) vector comprising the cDNA as in (1); (4) a host cell containing the vector as in (3); (5) a transgenic cell, tissue or animal comprising the vector as in (3); (6) a compound identified as an enhancer or inhibitor of the regulation of the repulation of cell shape, motility or the direction of cell migration for use as a compound identified as an enhancer of regulation of whether a protein is an inhibitor or enhancer of regulation of cell behaviour, growth, shape or motility or the direction of migration by contacting a host cell containing a change of phenotype; (8) a method for identification of vertebrate homologues of (0) and containing a change of c. elegans unc-53 gene by hybridising a probe of 15-50 bp of the unc-53 sequence to a DNA library; and (9) a method for identification of a protein which is active in the signal transduction pathway of a cell of which a vertebrate homologue of UNC-53 is a component comprising; (i) identifying an inthal challed that a component comprising of (i) identifying an early that has a component comprising (ii) identifying an early and the signal contacting and cell with an antibody to the UNC-53 homologue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody/homologue complex; and (iii) analysing such a complex to identify any non-antibody protein bound to the complex. UNC-53 is a signal transducing or signal integrator protein involved in controlling directionality of cell migration and cell shape in C. elegans. Vertebrate homologues of UNC-53 can be used to promote neuronal regeneration, revascularisation or wound healing, to treat chronic neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
present invention describes a vertebrate protein homologue of an UNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases or acute traumatic injuries or fibrotic diseases. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3482 BP; 767 A; 956 C; 913 G; 846 T; 0 U; 0 Other;
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Matches 101; Conservative
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The specification describes a microsphere comprising dihydrazide derivatised hyaluronic acid crosslinked to a nucleic acid (NA). The microspheres cause reduced inflammatory responses, and have increased safety and biodegradability. The microspheres are useful for transfecting a cell of a subject and for treating a subject having myocardial ischemia, by increasing cardiac angiogenesis. They are also useful for treating haemophilia. The present sequence represents the plasmid pcDNNA:1/GS, into which is inserted a polymucleotide sequence which is crosslinked to hyaluronic acid. The polymucleotide sequence encodes a

Sequence 4597 BP; 1062 A; 1214 C; 1206 G; 1115 T; 0 U; 0 Other;

vascular endothelial growth factor (VEGF)

Hyaluronic acid micro spheres for use in gene therapy of myocardial ischemia and hemophilia, comprising dihydrazide derivatized hyaluronic acids crosslinked to nucleic acids.

Example 1; Page 36-38; 38pp; English

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Microsphere; dihydrazide; hyaluronic acid; inflammatory response; myocardial ischemia; cardiac angiogenesis; haemophilia; vascular endothelial growth factor; VEGF; ss.
                                            1334 TGGCTTCTGAGGCGGAAACCACCTGGGGGCTCTAGGGGG 1374
                                   TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 101
                                                                                                                                                      Nucleotide sequence of the plasmid pCDNA3.1/GS.
                                                                                                  ВР
                                                                                                 AAF24901 standard; DNA; 4597
                                                                                                                                     (first entry)
                                                                                                                                     20-APR-2001
                                                                                                                   AAF24901;
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(COLL-) COLLABORATIVE GROUP LTD

WPI; 2001-071363/08

Chen W;

99US-0140260P.

18-JUN-1999;

19-JUN-2000; 2000WO-US016837

WO200078358-A2

Synthetic

28-DEC-2000.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying modulators of untranslated region-dependent expression of a VEGF gene, useful for treating cancer, comprises contacting a compound with a cell or translation mixture containing a reporter gene linked to
                                                             1 ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
                                 Gaps
                                ;
                                                                                                                                                                                                                                                                                                                                             ss; cytostatic; VEGF modulator; angiogenesis inhibitor;
UTR-dependent expression; vascular endothelial growth factor;
untranslated region; cancer; angiogenesis; vector.
100.0%; Score 101; DB 4; Length 4597; 100.0%; Pred. No. 1.7e-22; tive 0; Mismatches 0; Indels 0
                                                                                                                                                    1840 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGGGG 1880
                                                                                                                        61 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; SEQ ID NO 94; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2003; 2003US-0441637P.
                                                                                                                                                                                                                            ADR12380 standard; DNA; 4825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PTCT-) PTC THERAPEUTICS INC
                                                                                                                                                                                                                                                                                     (first entry)
               Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                   Vector pMCP1
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    Query Match
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2601 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA 2660
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operably linked to an untranslated region (UTR) of the VEGF gene, and detecting expression of the reporter gene. A compound is identified as modulator if the level of expression of the reporter gene in the presence of the compound is altered as compared to that in the absence of the compound or in the presence of a control. Compounds identified by MI are useful for treating, preventing or ameliorating cancer or its symptoms, and/or for inhibiting angiogenesis. This sequence corresponds to the vector pMCPL, a mammalian expression vector designed to integrate into the genome at sites containing the FRT recombination site using the flp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion protein; amyloid precursor protein; APP; transcription factor; nootropic; neuroprotective; APP inhibitor; amyloid precursor protein inhibitor; Alzheimer's disease; beta-secretase;
                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                            1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGGATGCGGTGGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a fusion protein of amyloid precursor protein, useful ir
screening for anti-Alzheimer agents, comprises a fused transcription
                                                                                                                                                                                                                         Sequence 4825 BP; 1236 A; 1135 C; 1204 G; 1250 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                            Length 4825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hazuda DJ, Inglese J;
on AJ, Zuck PD;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2661 TGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 2701
                                                                                                                                                                                                                                                                                                                                                                                                                           61 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression vector nucleotide sequence SEQ ID NO:27
                                                                                                                                                                                                                                                            100.0%; Score 101; DB 13;
100.0%; Pred. No. 1.8e-22;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flores OA, Hazuda
Shi X, Simon AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 32B-F; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-secretase; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB33528 standard; DNA; 5015 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2002; 2002US-0360274P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-2003; 2003WO-US005458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                              Local Similarity 100.
1es 101; Conservative
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egister B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Register
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-689968/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003072041-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Espeseth AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA 1249
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that express FP and are useful in screening for agents that inhibit processing of APP. The agents are potentially useful for the treatment or prevention of Alzelmer's disease. Cells that express FP can screen for inhibitors of: (a) beta- and gamma-secretases; and (b) cytoplasmic/extracellular APP signaling in a single assay. Cell-based assays may be free of interference from alpha-secretase activity and are homogeneous (no chromatography, immunoperecipitation or washing required) so well suited to high-throughput screening. The present sequence represents a plasmid nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                               1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.g. promoting neuronal regeneration, treating chronic neuro-degenerative diseases or acute traumatic injuries.
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNC-53 vertebrate protein homologue; UNC-53; Caenorhabditis elegans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Verhasselt P;
Vandekerckhove JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell shape regulator; cell motility regulator; cell migration; cell behaviour regulator; phenotype; signal transduction pathway; signal transduction pathway; neuronal regeneration; signal integrator protein; neuronal regeneration; revascularisation; wound healing; chronic neurodegenerative disease; acute traumatic injury;
                                                                                                                                                                           Sequence 5015 BP; 1167 A; 1297 C; 1279 G; 1272 T; 0 U; 0 Other;
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                           Length 5015;
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                                                                                                                                                                                                                                                                                                                                                                      1250 TGGCTTCTGAGGCGGGAAAGAACCAGCTGGGGGCTCTAGGGGGG 1290
                                                                                                                                                                                                                                                                                                                                                   TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 101
                                                                                                                                                                                                           Score 101; DB 10;
Pred. No. 1.8e-22;
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Luyten W, Geerts H,
                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                             100.0%; Score 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 96; SEQ ID NO 10; 479pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pCB201 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibrotic disease; human; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J, Buesa Arjol CM,
Maertens LJS, Luyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH11417 standard; DNA; 5082
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                                                                                                                                                                                                                             Best Local Similarity 100.0%; Matches 101; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pujol NJR, Maercand Pujol NJR, Bogaert TAOE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-362411/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ADH11424.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9824810-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH11417;
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                                                                                                                                                                                                           Query Match
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       888888888888
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The present invention describes a vertebrate protein homologue of an UNC-
53 protein of Caenorhabditis elegans or a functional equivalent,
64 derivative or bioprecursor of UNC-53. Also described; (1) a cDNA sequence
65 encoding a vertebrate homologue of the C. elegans UNC-53 protein; (2) a
66 cnucleic acid which hybridises to the CDNA of (1); (3) vector comprising
67 cnucleic acid which hybridises to the cDNA of (1); (3) vector comprising
68 compound identified as an enhancer or inhibitor of the regulation of
69 cell shape, motility, or the direction of cell migration for use as a
60 cell shape, motility, or the direction of cell behaviour, growth, shape or
60 inhibitor or enhancer of regulation of cell behaviour, growth, shape or
61 charapeutic; (7) a method for determining a change of phenotype;
62 cell shape, motility or the direction of ell behaviour, growth, shape or
63 cell shape or of migration of cell behaviour, growth, shape or
64 cell shape of UNC-53 and determining a change of phenotype;
65 cell shape of UNC-53 and probe of 15-50 bp of the unc-53 sequence to
66 cell with an antibody protein pathway of a cell of which a vertebrate
67 conclusion of the UNC-53 is a component comprising: (i) identifying an extract of a cell with an antibody protein bound to the complex. UNC-53 is a
68 signal transducing or signal integrator protein involved in controlling contractionality of cell migration and cell shape in C. elegans. Vertebrate complexes a complexes and (ii) analysing such a complex to the complexe of promote neuronal regeneration elemental controlling contraction and cell shape in C. elegans. Vertebrate complexes and controlled controled controlled controlled controlled controlled controlled control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases or acute traumatic injuries or fibrotic diseases. The
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ö 9 1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGTTCTA 0; Gaps Sequence 5082 BP; 1164 A; 1365 C; 1311 G; 1242 T; 0 U; 0 Other; 100.0%; Score 101; DB 2; Length 5082; 100.0%; Pred. No. 1.8e-22; ive 0; Mismatches 0; Indels 0; 2934 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 2974 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 101 101; Conservative Similarity 61 Query Match Best Local Matches 엄 ò g δ

& X UAS beta-lactamase vector SEQ ID NO: 64. BP ADM97811 standard; DNA; 5218 (first entry) 01-JUL-2004 ADM97811; ADM9781 RESULT 

enzyme, sensor cell; signal transduction detection system; promoter; targeting sequence; targeted drug; ds; vector.

Synthetic. Unidentified.

WO2004031415-A2.

05-SEP-2003; 2003WO-US028078 15-APR-2004.

05-SEP-2002; 2002US-0408297P.

(VERT-) VERTEX PHARM INC.

Sanders PS; Zeh K, Whitney MA,

WPI; 2004-330208/30.

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4177 ACAGCAAGGGGGAGGATGGGAAGACAATAGCAGGCATGCTGGGGATGCGGGGCTTG
                                                                                                                               The present invention relates to a method of developing a sensor cell, for determining the activity of a target gene in the cell, which comprises providing a homogeneous population of cells, where each of the cells comprises a signal transduction detection system and introducing into the population of cells an isolated DNA construct comprising a promoter operatively linked to a targeting sequence. The method is useful in developing a sensor cell for determining the activity of a target gene in the cell. The sensor cell and the methods are useful in developing new and therapeutic drugs directed to the targets. The present sequence is a vector used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid molecules having one or more recombination sites and encoding an amino acid sequence tag, useful for recombinational and/or topoisomerase-mediated cloning methods for producing fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (I) comprising one or more recombination sites, and one or more nucleic acid sequences
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Developing a sensor cell, useful in determining the activity of a target gene and in developing therapeutic drugs, comprises providing cells comprising a signal transduction detection system and introducing DNA construct into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                            Sequence 5218 BP; 1231 A; 1361 C; 1335 G; 1291 T; 0 U; 0 Other;
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0
                                                                                                                                                                                                                                                                                                                                                                               Length 5218;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of plasmid pcDNA6/Biotag(TM)-D-TOPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGGGG 4277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinational cloning; recombination; topoisomerase;
fusion protein production; ds.
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 101; DB 12;
100.0%; Pred. No. 1.8e-22;
ative 0; Mismatches 0;
                                                                                               Example 7; Page 231-234; 234pp; English.
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19-JUL-2002; 2002US-0396627P.
10-OCT-2002; 2002US-0417172P.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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which encode an amino acid sequence tag. (I) can also comprise one or more topolsomerases. The amino acid sequence tag is an amino acid sequence that is capable of being post-translationally modified, and is an amino acid sequence that is capable of being post-translationally modified by biotinylation, at a capable of being post-translationally modified by biotinylation, attachment of 4-phosphopanthethelme, attachment of lipoic acid or attachment of flavins, and is an amino acid sequence that is capable of being biotinylated, wherein the amino acid sequence that is capable of being biotinylated is all or a portion of the Klebsiella pneumoniae or being biotinylated is all or a portion of the Rebsiella pneumoniae or can accepted ecarboxylase a subunit, all or a portion of the Escherichia coli biotin carboxyl carrier protein component of acetyl-CoA carboxylase. The methods and compositions of the present invention are useful for identifying, concentrating, purifying and/or producing fusion proteins that comprise an amino acid sequence tag. The nucleic acid molecules can also be used in recombinational cloning and/or topolsomerase. mediated cloning methods to produce polynucleoride constructs which encode the fusion proteins. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1425 ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTTA 1484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.g
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Vandekerckhove JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrate UNC-53 protein homologue related nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5302 BP; 1254 A; 1361 C; 1349 G; 1338 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5302;
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Pred. No. 1.8e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH11233 standard; DNA; 5425 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
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The present invention describes a vertebrate protein homologue of an UNC-derivative or bioprecursor of UNC-53. Also described: (1) a cDNA sequence derivative or bioprecursor of UNC-53. Also described: (2) a concoling a vertebrate homologue of the C. elegans UNC-53 protein; (2) a mucleic acid which hybridises to the CDNA of (1); (3) vector comprising the vector as in (3); (5) a transgenic cell, tissue or animal comprising the vector as in (3); (6) a compound identified as an enhancer or inhibitor of the regulation of cell shape, motility, or the direction of cell migration for use as a cherapentic; (7) a method for determination of whether a protein is an inhibitor or enhancer of regulation of cell migration for use as a compound identification of welther a protein is an inhibitor or enhancer of regulation of cell migration for use as a complicy or the direction of migration by contacting a host cell inhibitor or enhancer of regulation of vertebrate homologues of C. elegans unc.53 gene by hybridising a probe of 15-50 bp of the unc-53 sequence to complex in the signal transduction pathway of a cell of which a vertebrate complex in the signal transduction pathway of a cell of which a vertebrate complex in the signal transduction pathway of a cell of which a vertebrate complex in antibody/homologue complex; and (11) analysing such a complex to antibody/homologue complex; and (11) analysing such a complex to antibody/homologue complex; and (11) analysing such a complex to directionality of cell migration and cell shape in C. elegans. Vertebrate complex of accidentify any non-antibody protein bound to the complex. UNC-53 is a component protein involved in controlling charaction and cell signal integrator protein involved in controlling charaction or wound healing, to treat charaction are recovered in controlling controlling or signal integrator protein involved in controlling charaction or wound healing, to treat charaction are recovered in controlling or signal involves of promote neuronal regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3217 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGGGGCTCTA 3276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Major histocompatibility complex; MHC; antigen presenting cell; APC; antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic; cancer; viral infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
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treating chronic neuro-degenerative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases or acute traumatic injuries or fibrotic diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a pcDNA3 plasmid vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 101;
                                                                        Disclosure; Page 231-237; 479pp; English.
  promoting neuronal regeneration, treediseases or acute traumatic injuries.
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                                                                                                                                               The invention relates to a new nucleic acid molecule (I) encoding a fusion polypeptide useful as a vaccine composition. (I) comprises a first nucleic acid sequence encoding a first polypeptide or peptide that promotes processing via the Major Histocompatibility Complex (MHC) class I pathway (MHC-I-PP) and/or promotes development or activity of an inferenting call (APC). The second nucleic acid sequence is linked in frame to the first nucleic acid sequence or to a linker nucleic acid sequence and encodes an antigenic polypeptide or peptide. The methods and compositions of the present invention are useful as therapeutic vaccine for cancer and for major viral infections, such as hepatoma and cervical cancer, that cause morbidity and mortality. They can also be used in treating animal diseases, such as equine herpesvirus, bovine viruses, Marek's disease, retroviral and lentiviral diseases and rabies, in the veterinary medicine context. The present sequence represents the curle and present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1189 ACAGCAAGGGGGAGGATTGGGAAGACAATTAGCAGGCATGCTGGGGGATGCGGGGCTCTA 1248
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                                                           Nucleic acid molecule encoding a fusion polypeptide that promotes processing via the Major Histocompatibility Complex class I pathway and/or promotes activity of an antigen presenting cell, useful as vaccine for cancer and viral infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chimeric fusion; translocation; antigenic; cytostatic; immunotherapy; gene therapy; cancer; tumour; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 101; DB 6; Length 5431; 100.0%; Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid vector pcDNA3 nucleotide sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No. --
                                                                                                                           Claim 24; Page 22-23; 127pp; English.
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                                     WPI; 2002-619261/66.
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                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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The present invention describes a nucleic acid (I) encoding a chimeric fusion or fusion polypeptide comprising a first domain with a cranslocation polypeptide, and a second domain comprising an antigen having at least one antigenic peptide. Also described: (I) an expression vector comprising (I) operatively linked to a promoter and optionally, to one or more regulatory elements that enhance expression of the nucleic acid in a cell; (2) a particle comprising (I) or the expression vector; (3) a cell that has been modified to comprise (I) or the expression vector; (3) a cell that has been modified to comprising a first domain with a translocation polypeptide, and a second domain comprising an antigen having at least one antigenic peptide; (5) a pharmaceutical composition capable of inducing or enhancing an antigen specific immune response.

Comprising (I) expression vector, particle, cell, cell of the particle, cor the chimeric polypeptide; (7) increasing the number of CDB + CTLs specific for a selected desired antigen in a subject by administering the composition described above; (7) increasing the number of CDB + CTLs specific thy administering the composition described above; (8) inhibiting the growth of a tumour in a subject by administering the composition described above; and (8) inhibiting the growth of a tumour in the composition described above; and (8) inhibiting the growth of a tumour in the composition described above; and (8) inhibiting the growth of a tumour in the composition described above; and (8) inhibiting the growth of a tumour in the composition described above; and (8) inhibiting the growth of a tumour in the composition described above; and (8) inhibiting the growth of a tumour in the composition described above; and (8) inhibiting the growth of a tumour in the composition described above; and (8) inhibiting the growth of a tumour in the composition described above; and (8) inhibiting the database of the composition described above; and (8) inhibiting the composition described above; and (8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic activity, and can be used in immunotherapy, and gene therapy. The nucleic acids (1), compositions and methods are useful for treating cancer. The present sequence represents a plasmid vector nucleotide
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comprising a first domain with a translocation polypeptide, and a second
domain with an antigen having at least one antigenic peptide, useful for
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                                                                                                                                                                                               Disclosure; SEQ ID NO 8; 68pp; English.
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20-OCT-2000; 2000WO-US041422.
04-APR-2001; 2001US-0281003P.
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                                                                                             treating cancer
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Claim 30; Page 7-8; 16pp; German.
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                                                                                                                                                                                                                                                           Novel chimeric polypeptide e.g., Pseudomonas aeruginosa exotoxin A domain II/human papilloma virus-16 E7 peptide useful for inducing or enhancing antigen specific immune response, or for inhibiting growth of tumor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acid encoding a chimeric polypeptide comprising a translocation domain of a bacterial toxin and at least one antigenic peptide. The preferred translocation domain is domain II of Pseudomonas aeruginosa exoctoria A (ETR(dII)) and the preferred antigen is human papilloma virus type 16 (HPV-16) E7 which is a model tumour nearingenic peptide comprises an epitope that binds to and is presented on the cell surface by major histocompatibility complex (MHC) class I proteins. The nucleic acid of the invention is useful as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  composition for enhancing antigen specific immune response, increasing the number of CD8+ cytotoxic T lymphocytes (CTLs) and for inhibiting the growth of a tumour. The present sequence is pcDNA3 plasmid vector used in
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100.0%; Pred. No. 1.8e-22;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 8; 48pp; English.
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Matches 101; Conservative
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                                                                                                                                                                               WPI; 2004-356187/33
(HUNG/) HUNG C.
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This invention describes a novel method for the detection of human gammaserctase by detection of a partial protein formed by cleavage of a fusion protein encoded by a transgene containing a first nucleotide sequence which encodes a protein comprising the amino acid sequence (A) and a second nucleotide sequence which encodes a signal peptide. The products of the invention have neuroprotective and nootropic activity. The method is used to detect activity of gamma-secretase. The transgene and/or vectors are useful for the production of a transgenic call or C. elegans. Transgenic C. elegans is useful in a method for the calcivity. The methods and transgenes activity. The methods and transgenes are useful in research of also useful in a method to identify inhibitors of the gamma-secretase activity. The methods and transgenes are useful in research of Alzheimer's disease. Inhibitors of gamma-secretase are useful in sequence encodes a transgenic anyloid precursor protein (APP) which is sequence encodes a transgenic anyloid precursor protein (APP) which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1190 ACAGCAAGGGGGAGGATGGGAAGACAATAGCAGGCATGCTGGGGATGCGGGGTGGGCTTA 1249
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Streptococcus pneumoniae; sepsis; otitis media; meningitis; bacteraemia;
pneumonia; vaccine; genetic immunisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5432 BP; 1251 A; 1410 C; 1390 G; 1381 T; 0 U; 0 Other;
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infection or sepsis.
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give (Now) to the course to test the multiple cloning site of pcDNA3 and course for multiple cloning site of pcDNA3 into knullifed, digested with kpnl and ligated into kpnl-digested pcDNA3 upstream of the multiple cloning site of pcDNA3 and downstream of the human cytomegalovirus immediate early (HCWV-IE) promoter to create pGT41. A full-length coding sequence of Streptococcus promoter to create a fusion between rsv6 and bppA. Intramuscular into pGT41 to create a fusion between rsv6 and bppA. Intramuscular captured into pGT41 to create a fusion between rsv6 and bppA. Intramuscular captured protection against an otherwise lethal challenge with a pKSD2601, induced protection against an otherwise lethal challenge with a capsulope DNA in eukaryotic cells is claimed. The plasmid includes promoter for driving expression in a eukaryotic cell (e.g. HCMV-IE), DNA promoter for driving expression in a eukaryotic cell (e.g. HCMV-IE), DNA crooding a leader sequence (e.g. of RSVG) which facilitates expression, translation through or transport of the expression product in a cukaryotic cell membrane, and DNA encoding a pneumonoccal epitope such as suitable carrier or diluent, and optionally one or more cytokines or DNA encoding them, or a bacterial delivery system. The vaccine is used to elicit an immunological response in a host, including humans, susceptible to preumococcal infection or sepsis. The plasmid can also be used to express a pneumococcal epitope of interest in vitro. (Updated on 17-OCT-
(see AAV38298) that codes for respiratory syncytial virus
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Sequence 5446 BP; 1255 A; 1417 C; 1390 G; 1384 T; 0 U; 0 Other;
                                        100.0%; Score 101; DB 2; Length 5446; 100.0%; Pred. No. 1.8e-22;
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Renilla luciferase; sea pansy; cell proliferation disorder; immune disorder; hypogammaglobulinaemia; haematologic condition; anaemia; neoplasm; cancer; human immunodeficiency virus; HIV; tissue white cell infiltrative disorder; organ failure; myotrophic condition; gonadal failure; bone disorder; muscle disorder; osteoporosis; endocrine condition; vascular disorder; atherogenesis;
                                                                                   Renilla luciferase vector pcDNA3.
           AAS18619 standard; DNA; 5446 BP
                                                                                                                                                                                                                                                                                                              25-APR-2000; 2000US-00559874.
02-JUN-2000; 2000US-00586339.
                                                                                                                                                                                                                                                                                       25-APR-2001; 2001WO-US013512.
                                                           (first entry)
                                                                                                                                                                                                                                      WO200181614-A2.
                                                           26-FEB-2002
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                                                                                                                                                                                     pcDNA3; ds.
                                                                                                                                                                                                              Synthetic.
                                 AAS18619;
AAS18619
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WO200216549-A2.

Chimeric.

CHEM-) CHEMICON INT

WPI; 2002-041420/05.

Leng J;

28-FEB-2002.

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The invention describes a novel method for measuring proliferation of a cell or population of cells. The method comprises obtaining light cell or population deta from a cell containing a Renillal luciferase over a period of time, cell proliferation of a cell or a appulation of cells can be containing the Renilla luciferase enzyme is useful for diagnosing a cell proliferative disorder including: neoplasm or cancer, viral clisorder or disease e.g. Human immunodeficiency virus (HIV), immune disorders e.g. Human immunodeficiency virus (HIV), immune clisorders e.g. hypogammaglobulinaemia and haematologic conditions e.g. manemias, tissue white cell infiltrative disorders, organ failure, conditions of bone and muscle c.g. osteoporosis, endocrine conditions and vascular disorders e.g. orsteoporosis, endocrine conditions and vascular disorders e.g. certoporosis, endocrine conditions and vascular disorders e.g. certoporosis, endocrine conditions and vascular disorders e.g. certoporosis, endocrine conditions and vascular disorders e.g. cell which does not have a cell proliferative disorder. The vector is also useful for determining the effect of an agent on cell to that of a cell publicative disorder. A difference is also useful for determining a cell potained from a sample with the cordition, by transfecting a cell potained from a sample with the cordition, by transfecting a cell obtained from a sample with the cordition cell to interact, and comparing the light emission data from the agent of the cell to interact, and comparing the light emission data from the cell of modulating cell proliferation under conditions that allow the agent of the cell to interact, and comparing the light emission data from the cell of modulating cell proliferation under cell in the absence of the agent of the the light emission data from the light emission data from the light emission data from the light emission data from the light emission data from the light emission data from the light emission data from the light emission data from the 
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Determining cell proliferation for monitoring treatment of a subject, comprises obtaining light emission data from cell containing Renilla luciferase for specific time, and detecting a change in the data.
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                                                                                                    Example 1; Fig 1A-B; 52pp; English
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Matches 101; Conservative
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Unidentified.
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(YEDA ) YEDA RES & DEV CO LTD
23-AUG-2001; 2001WO-IL000790.
     25-AUG-2000; 2000US-0227853P.
                  Quintana FJ;
                      WPI; 2002-227369/28.
                 Cohen IR,
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Treating or preventing an ongoing autoimmune disease e.g. diabetes, comprises vaccination with a DNA sequence comprising a CpG motif.

Example 1; Page 48-52; 53pp; English.

The present sequence is that of vector pcDNA3, a multipurpose cloning and expression vector containing the cytomegalovirus (CMV) immediate-early promoter, a polylinker and the bovine growth hormone polyadanylation site. The vector also expresses neomycin resistance in eukaryotic cells. Human heat shock protein 60 (hap60) full-length cDNA was cloned into pcDNA3 under the control of the CMV promoter, creating plasmid pHsp60. In order to explore the potential of a DNA-based therapy of insulin dependent diabetes mellitus (IDDM), the effect of immunisation of NOD mice, which spontaneously develop IDDM, with pHsp60 was examined. Surprisingly, pcDNA3 plasmid was as effective at inhibiting the development of diabetes as was the pHsp60 plasmid. Despite the absence of Hsp60, pcDNA3 induced specific effects on the autoimmunity to Hsp60 intrinsic to the NOD diabetoganic process; down-regulation of T-cell proliferation and the induction of IgG2D antibodies to Hsp60 autoimmunity and on the NOD diabetes. The invention therefore peptide analogue p2777. A CpG oligonucleotide (see ABL53541), present in the pcDNA3 amplicillin resistance gene, reproduced the effects of pcDNA3 con Hsp60 autoimmunity and on the NOD diabetes. The invention therefore provides a method for the treatment or prevention of autoimmune diseases by administering a DNA vaccine which includes a CpG motif and which and a population and page of the pcDNA3 motified antigen associated with autoimmune diseases, especially

Sequence 5446 BP; 1255 A; 1417 C; 1390 G; 1384 T; 0 U; 0 Other;

Gaps 0; Query Match 100.0%; Score 101; DB 6; Length 5446; Best Local Similarity 100.0%; Pred. No. 1.8e-22; Matches 101; Conservative 0; Mismatches 0; Indels 0;

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Search completed: July 14, 2005, 07:01:38 Job time : 143.448 secs

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CN161285
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               GenCore version 5.1.6
(c) 1993 - 2005 .Compugen Ltd.
                                                                                                                                                                                                                                                                                             34239544 segs, 19032134700 residues
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                                                                                                                                                                      US-09-482-682-43_COPY_4141_4241
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                                                                             nucleic search, using sw model
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Maximum DB
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CN778129
295 bp mRNA linear EST 20-MAY-2004 pgn2c.pk001.h10.f Chicken Lymphoid cDNA library (pgn2c) Gallus gallus cDNA clone pgn2c.pk001.h10.f 3'end of pat.pk0008.d12 5',
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/lab host="B.coli EMDH108"
clone lib="chicken Lymphoid cDNA library (pgn2c)"
/note="vector: pCMVSPORT 6"
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/db_xref="taxon:9011"
/clone="pgn2c.pk001.hl0.f 3'end of pat.pk0008.dl2"
/sex="Male and Female"
                         CB728069
CB72859
CB727859
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Morgan, R. W. and Burnside, J.
Chicken ESTS from lymphoid tissue- 3' sequence
Unpublished (2004)
Contact: Robin W. Morgan
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1341
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Location/Qualifiers
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                            CB728069
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CB728070
CB726527
CB726522
CB7128
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Gallus gallus
1. .295
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from

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Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: TWM8058 row: C column: 15 Seq primer: GTAATACGACTCACTATAGGG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX993205
Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP272ml0, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACAGCAAGGGGGGGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A., Nonneman,D.J., Wray,J.E. and Keele,J.W.
Porcine EST collection using a normalized library constructed tembryos representing early developmental stages
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clome_lib="WARC 4FIG"
/note="Vector: poDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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Contect: Smith TPL
USDA, ARS, US Meat Animal Research Center
NO BOX 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
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Pred. No. 2.4e-09;
0; Mismatches 11;
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BX993205.1 GI:49724663
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP272m10"
/clone_lib="MHPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sus scrofa"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity 87.5%;
Matches 84; Conservative
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Matches 82;
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AUTHORS
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/dav_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_nost="B.coll DH10B"
/clone lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
                                                                                                                         CF315931 378 bp mRNA linear EST 15-AUG-2003 HD--05-A13.b1 OsHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
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                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Enhartoidaae; Oryzae; Oryza

1 (bases 1 to 378)
1 (bases 1 to 378)
1 (kim,J.K., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 ACAGCAAGGGGGGGGATTGGGAATAGCAGGCATGCTGGGGATGCGGTGTGTTT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, MyongJi University
YongIn, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCR4-ToPO; Site_1: EcoRI; Callus was treated with ABA(120u) for Ihr. Oligo-capped mRNA was reverse transcribed and then used for PCR: mRNA was derived from rice Histone Deacetylase overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
|mol_type="mRNA"
|cultivar="Nackdong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.2%; Score 85; DB 7; Length 378
100.0%; Pred. No. 6.4e-15;
ive 0; Mismatches 0; Indels
       248 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:39947"
/clone="HD--05-A13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 rGGCTTCTGAGGCGGAAAGAACCAG 377
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                                                                                                                                                                                                   HD--05-A13, mRNA sequence.
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                                                                                                                                                                                                                                                CF315931.1 GI:33687692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nahm B.H.
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Best Local Similarity
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CN161285
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EST 14-JAN-2004

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Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: TWM8036 row: C column: 13
Seq prime: GTAATACGACTCACTATAGGG.
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (Dases I to 753. Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
Contact: Smith TPL
                                                                CK462023 755 bp mRNA linear 932791 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                                                                          CK462023.1 GI:40833304
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Matches 77; Conservative
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Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/Dacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/Dacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by AgResearch Ltd., New Zealand and The
Institute of Genomic Research (TIGR), USA.
Plate: 281 row: G column: 22
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                    772 bp DNA linear GSS 18-MAR-2003 CH240 281G22.TJ CHORI-240 Bos taurus genomic clone CH240_281G22, BZ851581
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  9
                                     109 ACAGCAAGGGGAGGACTGGGAAGACAATAGCAGGCATGCTGGGGAAAA-GAGGGCTCTA 51
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpreted to 172)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Chen, D., Riggs, F., de Jong, P.,
Crawford, A.M. and McEwan, J.C.
Bovine BAC End Sequences from Library CHORI-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; GHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
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                                                                                  96
                                                                                                           61 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_281G22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Blood"
/clone_lib="CHORI-240"
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1. .772
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BZ851581
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTT
                                                                                                                                              /clome_lib="MARC 4FIG"
/note="Vector: pcDNA3.1; Site_1: ECORI, Site_2: NOtI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                              62.0%; Score 62.6; DB 7; Length 755; 76.2%; Pred. No. 3.8e-08; ive 0; Mismatches 24; Indels
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840970 MARC 3PIG Sus scrofa cDNA 5', mRNA sequence.
CF366325
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/organism="Sus scrofa"
                           /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                   /tissue_type="pooled"
/lab_host="DH108"
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Unpublished (2003)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Best Local Similarity
'''' 70; Conserve
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          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: SR68023 row B column: 14
Seq primer: GTAATACGACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 648)
Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.B. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 526 ACACCAGGGGGGGGGGTTGGGAAAAAAAAAAAAGCCTTCCTGGGGGGATCCGGGGGGCTTTT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tIssues including brain, liver, muscle, placenta/endometrium, ovary, testes, and bone marrow."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.8%; Score 59.4; DB 7; Length 683; llarity 74.3%; Pred. No. 3.4e-07; Conservative 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB419493 648 bp mRNA linear 592356 MARC 6BOV BOS taurus CDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAGGGGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4396
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                    tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
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/db_xref="taxon:9913"
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/lab host="DH10B"
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  Contact: Smith TPL
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Best Local Similarity
Matches 75; Conserva
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases I to 666)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A. Davies, B. Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR010518 666 bp DNA linear GSS 05-JUL-2004 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP232a16, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tIssues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
                                                                                                                                                                                                                                                                                                        5 CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGCTTCTATGGC
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Pred. No. 5.8e-07;
0; Mismatches 24; Indels (
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Pred. No. 1.1e-05;
0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTGAGGCGAAAAAACCACTTGGGGCTTTAGGGGG 635
                                                                                                                                                                                                                                                                                                                                                                                                              TTCTGAGGCGGAAAGAACCAGCTGGGGGCTCTAGGGGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGTATGCGGTGGAAAGATCCAGCAGGGCTGGAG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR010518
CR010518.1 GI:49743509
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="MHPP232a16"
/clone_lib="MHPP"
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Mus musculus
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                                                                                                                                                                                         Secty Match
Best Local Similarity 75.3%;
Matches 73; Conservative 0
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REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

ORIGIN

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286 ATAGTAAGGGGGGGGGCGGGAAGATAACAGTAGGTACGTCGGGGGACGTGGCGGGTCTCA 345
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                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae
AMGNNUC:MRBE3-00121-F5-A rat brain E15 (10374) Rattus norvegicus CDNA clone mrbe3-00121-£5 5', mRNA sequence.
CB763949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db xref="taxon:10116"
/clone="mrbe3-00121-f5"
/tissue type="brain E15"
/clone_lib="rat brain E15"
/note="vector: pBCB; Site_1: BstXI; Site_2: Not1; rat brain E15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAGCAAGGGGGGGATTGGGAAGACAATAGCAGGCATGCTGGGGGATGCGGTGGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881
Plate: 00121 row: f column: 5.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
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Pred. No. 0.00071;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"

    433
/organism="Rattus norvegicus"

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/db_xref="taxon:10116"
/clone="mrbe3-00121-g12"
/tissue_type="brain E15"
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Location/Qualifiers
                                                                                                                         Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                         Contact: Dan Fitzpatrick
Amgen, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2003)
Contact: Dan Fitzpatrick
                                                                          CB763949.1 GI:29852340
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Amgen Rat EST Program
Unpublished (2003)
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
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Best Local Similarity 67.3%;
Matches 68; Conservative (
                                                                                                                                                                                                                                       (bases 1 to 422)
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    Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, D.J., Biggs, P.J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.

Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR159589 119 bp DNA linear GSS 06-JUL-2004 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP67p12, genomic survey sequence.
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                   ch 48.7%; Score 49.2; DB 9; Similarity 70.2%; Pred. No. 0.00039; 66; Conservative 0; Mismatches 28;
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CR159589.1 GI:49938438
GSS; genome survey sequence; MICER.
                                                                                                                                                                                                             organism="Mus musculus"
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                                                                                                                                                                                                                                  /mol_type="genomic DNA"
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/clone_lib="MHPP"
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Mus musculus
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Best Local Similarity
Matches 66; Conserva
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RESULT 11 CR159589/c LOCUS

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REFERENCE AUTHORS JOURNAL

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ACCESSION VERSION KEYWORDS SOURCE RESULT 12 CB763949 LOCUS

Matches

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Gaps

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EST 16-MAY-2003

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Rattus norvegicus (Norway rat)
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Job time : 968.667 secs
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Best Local Simi
Matches 68;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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AMGNNUC:WRBE3-00120-C9-A rat brain E15 (10374) Rattus norvegicus
cDNA clone mrbe3-00120-c9 5', mRNA sequence.
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/clone_lib="rat brain E15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
/clone_lib="rat_brain_E15 (10374)"
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brain_E15"
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Plate: 00120 row: c column: 9.
Location/Qualifiers
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                                                                                        Length 433;
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                                                                                                                          33; Indels
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                                                                                                                                                                                                                                                     346 CGGTCCTCGAGGTGGAAAGAATTAGTCGGGGTCTGAGGGGG 386
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Pred. No. 0.00071;
0; Mismatches 33;

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    /organism="Rattus norvegicus"

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Rattus norvegicus
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
                                                                                    th 47.7%;
Similarity 67.3%;
68; Conservative
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Matches 68; Conserv
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CB742761
LOCUS
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AUTHORS
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                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/clone="mrbo3-00121-c7"
/tissue_type="brain B15"
/clone_Tb="rat brain B15"
/clone_Tb="vector: pBCB; Site_1: BstXI; Site_2: Not1; rat brain B15"
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One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00121 row: c column: 7.
Location/Qualifiers
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Pred. No. 0.00071;
0; Mismatches 33;

    .449
    /organism="Rattus norvegicus"

                                                                                  1 (Dases 1 to 449)
Amgen EST Program.
Amgen Ret EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
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ilarity 67.3%;
Conservative (
Rattus norvegicus
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20 101 100.0 1014 4 CFAJ4121 AJ224121 Canis fam	30 101 100.0 1044 1 AY452662 31 101 100.0 1054 1 AF104441 32 101 100.0 1054 1 AF104442 33 101 100.0 1058 6 103356 34 101 100.0 1064 1 AY628199 35 101 100.0 1064 1 AY53127	101 100.0 1073 1 101 101 101 101 101 101 101 101 101	101 100.0 1075 1 AY729027 101 100.0 1075 1 PATNIPN2 101 100.0 1075 1 PATNIPNA 101 100.0 1075 1 PATNIPNIA	45 IUI 100.0 1080 1 AFOZ/139 ALIGNMENTS	AR3 AR3 AR3 AR3 AR3 Unk	unsch, C.A., osen, C.A., taphylococcu atent: US 65 1	/mol_type="genomic DNA"  ORIGIN  Query Match 100.0%; Score 101; DB 6; Length 142;  Best Local Similarity 100.0%; Pred No. 8 72-20.	); Mismatches GGATACATTTGAATGT) GGATACATATTTGAATGT) GGAAAATTTGAATGT) CGAAAAGTGCCACCTGACC CGAAAAGTGCCACCTGACCTCGACCCTCGACCCTCGACCCCTCGACCCTCGACCTCGACCCTCGACCCTCACCTCACCTCACCTCACCTCACCTCACCTCACCAC	RESULT 2 ARS38046/C LOCUS LOCUS LOCUS LOCUS AR538046 LOCUS LOCUS AR538046 AR538046 VERSION AR538046 VERSION AR538046 VERSION AR538046.1 GI:53929263 KEYWORDS SOURCE Unknown.
GenCore version 5.1.6  Copyright (c) 1993 - 2005 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: July 14, 2005, 04:39:07; Search time 756.618 Seconds (Without alignment)	2-43_COPY_8283_8383 tctcatgagcgaaaagtgccacctgac		um DB seq length: 0 um DB seq length: 2000000000	FOST_PIOCESSING; MAXIMUM MATCh 100% Listing first 45 summaries Database . GanDmbl.*		₽ Tp	SUMMARIES Result Query No. Score Match Length DB ID	1 101 100.0 142 2 101 100.0 142 3 101 100.0 248 5 101 100.0 251 6 101 100.0 251 7 101 100.0 344 8 101 100.0 400 101 100.0 456	101   100.0   456   6 E01374   E01374     101   100.0   456   6 E01302   E01372     101   100.0   456   6 E01302   E01372     101   100.0   456   6 AX260098   AX260058     101   100.0   693   6 AX360150   AX360150     101   100.0   693   6 AX360150   AX360150     101   100.0   998   AY559171   AY559176     101   100.0   1011   SWTEMAQGE   X97254     101   100.0   1012   CECI1F10   C292776     101   100.0   1012   CECI1F10   C392776     101   101   101   101   101   101   101     101   101   101   101   101   101     101   101   101   101   101   101     101   101   101   101   101   101     101   101   101   101   101     101   101   101   101   101   101     101   101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101     101   101   101   101   101   101     101   101   101   101   101   101   101     101

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BCT 26-APR-1993

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Kemper, B., Jensen, F., von Depka-Prondzynski, M., Fritz, H.J., Borgmeyer, B. and Mizuuchi, K. Resolution of Holliday structures by endonuclease VII as observed in interactions with cruciform DNA Cold Spring Harb. Symp. Quant. Biol. 49, 815-825 (1984) 85153063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales; Enterobacteriaceae; Escherichia.

1 (bases 1 to 251)
Uorutaa, G and Karen, T.
SYNTHESIS OF SELECTIVE AGED PROFEIN OR POLYPEPTIDE IN BACTERIA Patent: JP 1981154999-A 1 30-NOV-1981;
                                                                                                            PMMOENDO 240 bp DNA linear BCT 26-APR-1
Plasmid pMM110 region of endo VII cleavage sites near cruciform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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PD 30-NOV-1981
PP 09-APR-1981 JP 1981052488
PR 11-APR-1980 US 80 139225
PI UORUTAA GIRUBAATO, KAREN TARUMATSUJI
C C12P21/00, COTH21/00, C12N1/00, C12N15/00//C12R1/19; CC strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC anti:sense: No.
CC arti:sense: No.
CC fragment type: N. Terminal Fragment;
CC *source: clone=pKT241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 101; DB 1; Length 240; 100.0%; Pred. No. 8.7e-20; tive 0; Mismatches 0; Indels (
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DNA coding for Escherichia coli penicillinase.
E00018
 source text: Plasmid pMM110 DNA. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Plasmid pMM110"
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/db_xref="taxon:2599"
/plasmid="Plasmid pMM110"
                                                                                                                                                                                                                                                          other sequences; plasmids.
1 (bases 1 to 240)
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JP 1981154999-A/1.
Escherichia coli
Escherichia coli
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Matches 101; Conservative
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Plasmid pMM110
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DEFINITION
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PMMOENDO/c
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Unknown.
Unclassified.
1 (bases 1 to 142)
Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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JP 1981154999-A/2
30-NOV-1981
11-APR-1980 US 80 139225
UORUTAA GIRUBAATO, KAREN TARUMATSUJI
C12P21/00,C07H21/00,C12N1/00,C12N15/00//C12R1/19; CC
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Best Local Similarity 100.0%; Score 101; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 8.7e-20;
Matches 101; Conservative 0; Mismatches 0; Indels
                                                                                         Staphylococcus aureus polynucleotides and sequences Patent: US 6737248-A 2608 18-MAY-2004;
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/product='E.coli penicilinase'
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DNA coding for Escherichia coli penicillinase.
E00019
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/db_xref="taxon:562"
                                                                                                                                                                                /mol_type="genomic DNA"
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/organism="Escherichia
                                                                                                                               Location/Qualifiers
                                                                                                                                                1. .142
/organism="unknown"
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PN 4P 1981154999-A/2
PP 10-NOV-1981 JP 198
PR 11-APR-1980 US 80
PI UORUTAA GIRUBAATO,
PC C12P21/00, CO7721/0
strandedness: Double;
CC topology: Linear;
CC topology: Linear;
CC *source: clone=pKT
FH Key
FT CDS 21
FT CDS 221

    (bases 1 to 228)
    Vorutaa, G. and Karen, T.

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Escherichia coli
Escherichia coli
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KEYWORDS
SOURCE
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E00019/c
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PAT 29-SEP-1997

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primer_bind
ORIGIN
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L18624.1 GI:308338
STS; PCR primer; STS sequence; microsatellite marker;
microsatellite repeat; repeat polymorphism; sequence tagged site.
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Patent: US 4338397-A 1 06-JUL-1982;
President and Fellows of Harvard College; Cambridge, MA
                              210. .>252
/product='E.coli penicilinase' FT
                                                                                                                                                                              Query Match 100.0%; Score 101; DB 6; Length 251; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 101; Conservative 0; Mismatches 0; Indels
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Human chromosome 8 STS UT5345, sequence tagged site.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  101644 251 bp ss-DNA Sequence 1 from Patent US 4338397.
                                                                                                     /organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
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/mol_type="unassigned DNA"
                                                           al 190. .196.
Location/Qualifiers
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Gilbert, W. and Talmadge, K.
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Homo sapiens
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Best Local Similarity
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HUMUT5345
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PF 21-NOV-1997 JP 1998523916
PR 22-NOV-1996 US 60/031626,14-OCT-1997 US 60/061953 PI
PATRICK J DILLON,GIL H CHOI,RODNEY A WELCH
PC C12N15/11,C12N15/63,C07K16/12,G01N33/569,G06F17/30,G11B7/00 CC
Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
CC Nucleotide sequence of Escherichia coli pathogenicity islands
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Nucleotide sequence of Escherichia coli pathogenicity islands.
BD195256
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Original source text: Homo sapiens DNA.
Submitted by: Utah Center for Human Genome Research University of Utah. Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
Ballard, L., Melis, R., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Rodriguez, P., Albertsen, H., Lalouel, J.-M. and White, R. Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome
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Dillon, P.J., Choi, G.H. and Welch, R.A.
Nucleotide sequence of Escherichia coli pathogenicity islands
Patent: JP 2002513277-A 43 08-MAY-2002;
HUMAN GENOME SCIENCES INC, WISCONSIN ALUMNI RESEARCH FOUNDATION
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Gel: Acrylamide 7%, Formamide 32%, Urea 34%
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llarity 100.0%; Pred. No. 8.7e-20;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e-mail: sts@corona.med.utah.edu
Primer A: GAGCAAAACAGGAAGGCAAAATGC
Primer B: TTCGGGGAAATGTGCGCGGAACC
32P-label: B Primer
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
/map="8"
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Denaturation: 94C 10sec
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08-MAY-2002
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Extension: 72C 20sec
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/db_xref="taxon:32630"
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AUTHORS
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PI TOCHIFUSA NORIYUKI,
PI TOCHIFUSA NORIYUKI,
PI KITAZAWA TOSHIKI, OJIDA KAZUHIDE, MATSUSHIRO AIZO PC
CI2NIS/100, CI2NI/20, CI2PI/00, (CI2NI/20, CI2RI:19), (CI2P2I/00, PC
CI2RI:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC *Source: Strain-HB101;
CC *Source: clone=pV2G1;
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E00892 456 bp DNA linear PAT 29-SEP-1997 Synthetic DNA encoding fused polypeptide between E coli beta-lactamase and human beta-urogastrone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ę
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product='beta-urogastrone mature peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product='beta-urogastrone precursor' FT 209. .277
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                         Score 101; DB 6; Length 400; Pred. No. 8.7e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACTGACGTC 65
                               ce 1. .400
/organism='Unidentified'
Location/Qualifiers

    .456
    /organism="synthetic construct"
/mol_type="genomic DNA"

Location/Qualifiers
                                                                                                                                                                                                                                                                                                  100.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches

    .400
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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E00892/c
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                                                                                                                                                                                                                                                                                                            PAT 29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                     other sequences; artificial sequences.

1 (Bases I to 456)

POLYPEPTIDE SECRETION EXPRESSION VECTOR, MICROORGANISM TRANSFORMED BY SAID VECTOR AND PRODUCTION OF POLYPEPTIDE USING SAID PACENT: JP 1987083890-A 1 17-APR-1987;

EARTH CHEM CORP LTD

OS Artificial gene

OC Artificial gequence; Genes.

PN JP 1987083890-A/I
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                                                                                   1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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09-OCT-1985 JP 1985225393
YOSHIKAWA KAZUTOSHI, MOMOTA YUTAKA, KAJIFUSA NORIYUKI,
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  Length 456;
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                                                                                                                                                                                                                                                                                                              linear
                                        0; Indels
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/product='beta urogastrone'
209. .277
278. .486
/product='beta urogastrone'
                                                                                                                                                              61 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                    GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                            E01156 456 bp DNA 1
DNA fragment which secrets beta urogastrone.
Score 101; DB 6;
Pred. No. 8.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .456
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                        0; Mismatches
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hypothetical: No;
anti-sense: No;
*source: clone=pUG201;
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100.0%;
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synthetic construct
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AX260098.1 GI:16509129
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JP 1987190083-A/1
20-AUG-1987
                                                                                                                                                                                                                                                   topology: Linear;
hypothetical: No;
                                                                                                                                                                                                                                                                              anti-sense: No;
   synthetic construct
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mat_peptide
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AX260098/c
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VERSION
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AUTHORS
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DNA linear PAT 29-SEP-1997

DNA encoding beta-urogastron fused with DNA encoding a promoter and signal peptide of beta-lactamase.
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                                                                                                                                                                                                                                                                                                                06-AUG-1987
31-JAN-1986 JP 1986021032
OKAI HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, ADACHI SHOJI, MATSUBARA AKIMASA, OLIDA KAZUHIDE, YANO MAKI, MIHARA SHIGERU, MATSUSHIRO AIZO, YANAIHARA NOBORU
C12P21/00,C12R1591);
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                                                                                                                  EVILYA.1 GI:2169533
JP 1987179398-A/1.
synthetic construct
synthetic construct
synthetic construct
synthetic construct
other sequences, artificial sequences.

I bases I to 456
Okai, H., Kumakura, T., Kawamoto, S., Adachi, S., Matsubara, A.,
Ojida, K., Yano, M., Mihara, S., Matsushiro, A. and Yanaihara, N.
PRODUCTION OF BETH-UROGASTRONE
PACHEL: JP 1987179398-A I 06-AUG-1987;
EARTH CHEM. CORP. LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E01302

MA encoding human beta-urogastrone fused with DNA encoding promoter and signal peptide of beta-lactamase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide 278. .436
    /product='beta-urogastron'
    /product='beta-urogastron'
    /product='beta-urogastron'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
100.0%; Score 101; DB 6; 100.0%; Pred. No. 8.7e-20; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .456
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                              Artificial gene
Artificial sequence, Genes.
Homo sapiens
UP 1987179398-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125. .170
200. .203
209. .277
278. .436
                                                                                                                                                                                                                                                                                                                                                                                           strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                       topology: Linear;
hypothetical: No;
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E01302.1 GI:2169561
JP 1987190083-A/1.
synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-sense: No;
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Matches 101; Conservative
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RBS
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E01274/c
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JOURNAL
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14-FEB-1986 JP 1986031415
OKAI HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, KOIDE TAKAO, MOMOTA YUTAKA

C12N15/00,C07H21/04,C12N1/00,C12P21/02,(C12N1/00,C12R1:19), PC
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                                               Okai, H., Kumakura, T., Kawamoto, S., Koide, T. and Momota, Y.
POLYPEPTIDE-EXPRESSION VECTOR, HOST TRANSFORMED WITH SAID VECTOR
AND PRODUCTION OF POLYPEPTIDE USING SAID HOST
PATENT: JP 1987190083-A 1 20-AUG-1987;
EARTH CHEM CORP IID
OS Artificial gene
OC Artificial sequence; Genes.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 101; DB 6; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 101; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
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other sequences, artificial sequences.
1 (bases 1 to 456)
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Patent: WO 0172774—A 60 04-OCT-2001,
Cyclacel Limited (GB)
Location/Qualifiers
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Sequence 60 from Patent WO0172774.
AX260098
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200. .203
209. .277
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; Myrtales; Lythraceae; Cuphea.

1 (bases 1 to 693)
Toepfer, R., Bautor, J., Bothmann, H., Filsak, E.,
Schulte, W., Voetz, M., Ralek, J. and Schell, J.,
PROMOTERS
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                                                                                                                            1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                          Gaps
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                   Query Match 100.0%; Score 101; DB 6; Length 466; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 101; Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
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100.0%; Score 101; DB 6;
Best Local Similarity 100.0%; Pred. No. 8.8e-20;
Matches 101; Conservative 0; Mismatches 0;
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MAX PLANCK GESELLSCHAFT (DE)
Other publication CA 2169093 950316
                                                                                                                                                                                                                                                                                                                        Sequence 112 from Patent W00172774. AX260150
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Drosophila melanogaster
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Sequence 11 from Patent W09507357.
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SOURCE
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ORGANISM
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AUTHORS
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AUTHORS
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JOURNAL
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JOURNAL
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/mol_type="unassigned DNA"
/mol_xref="taxon:3930"
/clone="CLKASIG8"
/clone_lib="Genomic Lambda Fix II"
Other publication AU 7615494 950327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: July 14, 2005, 14:03:30 Job time: 756.618 secs
                             Location/Qualifiers
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version 5.1.6
- 2005 Compugen Ltd.
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July 14, 2005, 04:35:42; Search time 142.398 Seconds (without alignments) 4198.742 Million cell updates/sec

1 agggttattgtctcatgagc........gaaaagtgccacctgacgtc 101 US-09-482-682-43\_COPY\_8283\_8383 Perfect score: Sequence: Title:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\* N Geneseq 16Dec04:\* geneseqn2004as: geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:

		nescribcion	Aav76919 Staphyloc	Aan10032 Sequence	Aan10031 Sequence	Aav31229 E. coli J	Aan60624 Plasmid p	Aan71080 Sequence	Aan70833 Beta-urog	Aan81765 Sequence	Aba90413 Drosophil	Aax21173 Polynucle	Aax21149 Polynucle	Aba90456 Drosophil	Adh58311 Electroph	Aas30560 DNA encod	Aas27819 DNA encod	Abk42984 Genomic s	Aal07344 Human rep	Aal03229 Human rep	Aal06588 Human rep	Aal07340 Human rep
** SUMMARIES	£	TT	AAV76919	AAN10032	AAN10031	AAV31229	AAN60624	AAN71080	AAN70833	AAN81765	ABA90413	AAX21173	AAX21149	ABA90456	ADH58311	AAS30560	AAS27819	ABK42984	AAL07344	AAL03229	AAL06588	AAL07340
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Aba14573 Human ner	Aas34681 Human DNA	Ada41574 Human sec	Acc50905 Human sec	Abz71508 Secreted	Adb91869 Human sec	Adb61140 Connectiv	Adb94622 Novel hum	Adc74663 Human sec	Ada57709 BAC fragm	Adn41551 Novel hum	Aas30559 DNA encod	Aas27818 DNA encod	Abk42983 Genomic s	Aas41807 Genomic s	Aas41855 Genomic s	Aak85485 Human imm	Aak85434 Human imm	Aal07343 Human rep	Aal06587 Human rep	Aal07339 Human rep	Aal03228 Human rep	Aba14572 Human ner	Aas34680 Human DNA	Adb61139 Connectiv
ABA14573	AAS34681	ADA41574	ACC50905	ABZ71508	ADB91869	ADB61140	ADB94622	ADC74663	ADA57709	ADN41551	AAS30559	AAS27818	ABK42983	AAS41807	AAS41855	AAK85485	AAK85434	AAL07343	AAL06587	AAL07339	AAL03228	ABA14572	AAS34680	ADB61139
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101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101
c 21	c 22	c 23	c 24	c 25	c 26	C 27	c 28	c 29	c 30	c 31	c 32	c 33	c 34	c 35	c 36	c 37	c 38	c 39	c 40	c 41	c 42	c 43	C 44	C 45

## ALIGNMENTS

RESULT 1

Staphylococcus aureus contig SEQ ID #2608. BP AAV76919 standard; DNA; 142 (first entry) 16-MAR-1999 AAV76919; AAV76919/c 

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelld infection; food poisoning; osteomyelltis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

Staphylococcus aureus

EP786519-A2.

30-JUL-1997

97EP-00100117. 07-JAN-1997; 96US-0009861P. 05-JAN-1996; (HUMA-) HUMAN GENOME SCI INC.

Rosen CA; Fannon MR, Dillon PJ, Barash SC, Choi GH, WPI; 1997-374922/35. Kunsch CA,

Polynucleotide(s) and proteins derived from Staphylococcus aureus -stored on computer readable medium and used in the production of anti-S.aureus vaccines.

Claim 1; Page 2287; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or

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industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. sureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eylld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the computer
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                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning vehicle; bacterial vector; transformed host; penicillinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of the pKT218 EcoRI-PstI penicillinase gene fragment.
                                                                                                                                                                                                Length 142;
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                                                                                                                                                                      Sequence 142 BP; 45 A; 25 C; 26 G; 45 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 7
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0; Mismatches 0;
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Matches 101; Conservative
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Best Local Similarity
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                                                                                                                                              readable medium
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misc_feature
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The closest identifiable promoter for the penicilinase gene in pKT241 (AAN10031) is located in the region 14 to 20 nucleotides before its

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translational start signal. In the examples, the 3' end of pKT241 was attached to the signal DNA sequence of the DNA fragment (19) for rat preproinsulin (see AAN10033). The closest identifiable promoter for the penicillinase gene in pKT218 (AAN10032) is located in the region 14 to 20 mucleotides before its translational start signal. In the examples, the 3' end of pKT218 was attached to the signal DNA sequence of the DNA fragment (CB6) for rat preproinsulin (see AAN10034)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The closest identifiable promoter for the penicilinase gene in pKT241 (AAM10031) is located in the region 14 to 20 nucleotides before its translational start signal. In the examples, the 3' end of pKT241 was attached to the signal DNA sequence of the DNA fragment (19) for rat perproinantin (see AAN10033). The closest identifiable promoter for the penicillinase gene in pKT218 (AAN10032) is located in the region 14 to 20 nucleotides before its translational start signal. In the examples, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGGGTTATTGTCTCATGAGGGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthesis of mature protein or polypeptide - by using bacterial host transformed by cloned vehicle contg. DNA fragment etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning vehicle; bacterial vector; transformed host; penicillinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of the pKT241 EcoRI-PstI penicillinase gene fragment.
                                                                                                                                                                                                                                                                                                                                                                  Length 228;
                                                                                                                                                                                                                                                                                        Sequence 228 BP; 72 A; 37 C; 46 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 75
                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 101; DB 1;
100.0%; Pred. No. 2.3e-21;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/label= sticky end
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/label= sticky
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ID AAN10031 standard; DNA; 251 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Fig 2; 34pp; English
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                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Lou.
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Talmadge K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1981-80125D/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAP10038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-OCT-1981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP38182-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}{c} \egin{array}
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AAV31229/c RESULT

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The plasmid produces secreted beta-urogastrone in a transformed expression system. Similar plasmids may be constructed where the seceretion signal may be coupled with eg. somatostatin, insulin, growth hormone, interferon, IL-2, gastric inhibitory peptide, influenza B SA, epidermal growth factor and thymosine-beta4. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant vector for polypeptide secretion - contains signal peptide sequence directly bonded to peptide-coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 101; DB 1; Length 456; Best Local Similarity 100.0%; Pred. No. 2.6e-21; Matches 101; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                               GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= d
/label= Beta-lactamase signal peptide
278. 436
/*tag= e
                                                                                                                  105 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                                Plasmid pUG201 sequence encoding beta-urogastrone.
                                                                                                                                                                                                                                                                                                                                                                                                    Beta-lactamase signal peptide; pGH54; pGH55; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kajifusa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Table 4; 79pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuwakura T,
                                                                                                                                                                                                                               BP
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AAN60624 standard; DNA; 456
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209. .439
/*tag= c
209. .277
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200. .203
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                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohgai H, Momota H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1986-182911/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAP60678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1984;
                                                                                                                                                                                                                                                                                                       25-MAR-2003
29-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a E. coli strain J96 contig containing pathogenicity island (PAI) sequences, and represents a nucleic acid molecule of the invention. PAIs are large fragments of DNA which comprise pathogenicity determinants. The sequences of the invention are taken from PAI IV and PAI V. PAI IV is located at approximately 64 min (near phev) on the E. coli chromosome and is greater than 170 kb. PAI V is located at approximately 94 min (at phex) on the E. coli chromosome and is approximately 94 min (at phex) on the E. coli chromosome and is approximately 160 kb in size. Antibodies specific to the proteins encoded by the PAI open reading frames of the invention can be used in kits to detect uropathogenic E. coli. The proteins are used in vaccines to elicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                            New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to elicit an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; vaccine; protective immune response; ds.
                                                                                                                                                                    Gaps
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     DNA
3' end of pKT218 was attached to the signal DNA sequence of the fragment (CB6) for rat preproinsulin (see AAN10034)
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0
                                                                                             Length 251;
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                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 400 BP; 106 A; 77 C; 91 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                               GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                       Sequence 251 BP; 74 A; 45 C; 50 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                   115 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 75
                                                                                         Query Match
100.0%; Score 101, DB 1;
Best Local Similarity 100.0%; Pred. No. 2.3e-21;
Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 101; DB 2;
100.0%; Pred. No. 2.5e-21;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E. coli J96 pathogenicity island contig #43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Page 140-141; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon PJ, Choi GH, Welch RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    response to pathogenic E. coli.
                                                                                                                                                                                                                                                                                                                                                                                AAV31229 standard; DNA; 400 BP
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97US-0061953P.
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Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9822575-A2
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14-OCT-1997;
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Gaps

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Oshiden

Kitazawa T,

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AAN70833 standard; DNA; 456
                          AAN70833;
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                                                                                                                                            promoter
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AAN81765/c
                                                                                                                                                             RBS
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         Sequence encodes beta-urogastrone under the control of a tac promoter. The peptide may be expressed from plasmid pUGT 150s in a transformed E.coli host. The plasmid may carry several separately expressing sequences comprising a tac promoter, SD site, signal peptide, and coding sequence, to produce beta-UG in high yield. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                       Expression vector contg. multiple information units is used to transform host all for increased prodn. of polypeptides.
1 AGGCTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 101; DB 1; Length 456; 100.0%; Pred. No. 2.6e-21; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     /*tag= b
/transl_except= (pos:434. .436,aa:Arg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 101
                                   GGGTTCCGCCCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                               113 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTTCCGCGCACATTCCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 553; 34pp; Japanese.
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                      Sequence encoding beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                   86JP-00031415.
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                                                                                              AAN71080 standard; DNA; 456
                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                     (EART ) EARTH SEIYAKU KK.
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Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                                       pUGT 150s; beta-UG; ds
                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1987-273761/39.
                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                JP62190083-A
                                                                                                                                                                                                                                                                                                                                  14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                   14-FEB-1986;
                                                                                                                                  25-MAR-2003
10-MAR-2003
                                                                                                                                                   13-MAY-1991
                                                                                                                                                                                                                                                                                                                 20-AUG-1987
                                                                                                                                                                                                                 Synthetic
                                                                                                                 AAN71080;
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                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                             CDS
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An example of a sequence detected by a probe consisting of polyinosine, polydeoxyinosine, oligoinosine and/or oligodeoxyinosine is labeled. The seDNa and probe are hybridized and the existence of DNA in the product is detected. It can be used to detect the presence of malignant tumour. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of DNA and/or RNA - by converting to single strand form and using probe contg. labelled inosine deriv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 101; DB 1; 
; Pred. No. 2.6e-21; 
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 11; 11pp; Japanese.
                                                                                                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SEKI ) SEKISUI CHEM IND CO LTD
BP.
                                                                                                                                                                                                  дв.
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209.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
                                                                                                                                                                                                  Tumour; inosine; DNA probe;
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(first entry)
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200..204
                                                                                                                      (first entry)
                                                                                                                                                             Seta-urogastrone sequence
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Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                              (revised)
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13-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1986;
                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP62244398-A
                                                                            25-MAR-2003
10-MAR-2003
                                                                                                                      18-JAN-1991
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(23)

Key CDS

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The present invention relates to Drosophila cell cycle progression proteins (AAM41972-AAM47608) and their coding sequences (ABA90566-ABA90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting the cell division cycle, or capable of inhibiting the cell division cycle, or capable of treating a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as (such as psoriasis), antiinflammatory, antifungal and antiparasitic disorders disorders (such as malaria)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGGCTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                        Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide sequence from the genome of Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 466 BP; 135 A; 87 C; 93 G; 150 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101; DB 6;
Pred. No. 2.6e-21;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Scc.
100.0%; Pred
0; M
                                                                                                                                                                                                                                                                                                                  Claim 1; Page 99; 213pp; English.
                                                                                                                                                                                  Midgley C;
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                                                                       23-MAR-2001; 2001WO-GB001297
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                                                                                                        24-MAR-2000; 2000GB-00007268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX21173 standard; DNA; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Matches 101; Conservative
                                                                                                                                             (CYCL-) CYCLACEL LTD
                                                                                                                                                                                  Glover DM,
                                                                                                                                                                                                                     WPI; 2002-055132/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum
WO200172774-A2
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                                  04-OCT-2001
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                                                                                                                                                                                  Deak P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antiproliferative, cytostatic, cardiant, immunosuppressive; meiosis, antinflammatory; antipsoriatic; dermatological; antifungal; mitosis; antiparastic; antimalarthritic; call divisio; cell cycle progression protein; tumour; proliferative disorder; cardiovascular; autoimmune; dermatological disorder; de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
             Sequence of HB101 (pGH201) encoding new beta-urogastrone deriv. Met(21),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secretion inhibiting action, or cell proliferation promoting action. The deriv. has the same biological or pharmacological activities as beta-urogastrone. It is not susceptible to denaturation by oxidn. and is chemically stable. Deriv. has resistance to proteclytic enzymes such as protease. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New beta-urogastrone deriv. - has gastric acid secretion inhibition and proliferation promotion activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deriv. has various biological activities such as gastric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                       ds.
                                                                                                                                                                                                                   /*tag= b
/product= "New beta-urogastrone deriv."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                   secretion; cell proliferation; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 685; 76pp; Japanese.
                                                                                                                                           Location/Qualifiers
209. .277
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                                                                                                                                                                                                                                                                                                                                                                                                                             (EART ) EARTH SEIYAKU
                                                                                                                                                                                                   278.
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                                                                   Gastric acid
                                                                                                                                                                                                                                                                         JP63012298-A.
                                                                                                                                                                                                                                                                                                                                                   30-JUN-1986;
                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-1986;
                                                                                                                                                                                                                                                                                                              19-JAN-1988
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                                                                                                        Synthetic
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Antiproliferative, cytostatic; cardiant; immunosuppressive; meiosis; antiinflammatory, antipporiatic; dermatological; antifungal; mitosis; antiparasitic; antimalarial; antirhumatic; antiarthritic; cell division; cell cycle progression protein; tumour; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90366-ABA90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting the cell division cycle, or capable of inhibiting a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as (glomerulonephritis and rheumatorid arthritis), dermatological disorders (such as psoriasis), antiinflammatory, antifungal and antiparasitic
                                                                                                                                                              AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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                                                                                                                Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila cell cycle progression protein coding sequence #91.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiovascular; autoimmune; dermatological disorder; ds
                                                                                                                                                                                                         GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 58
                   ; Score 101; DB 2;
; Pred. No. 2.7e-21;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΰ
                                                                                                                                                                                                                                                                                                                                                                        BP
                        100.0%;
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Conservative (
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                                                                                                                                                                                                                                                                                                                                                                     ABA90456 standard; DNA; 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders (such as malaria)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-055132/07
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Best Local Similarity
Matches 101; Conser
                                             Similarity
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                     Query Match
Best Local Simil
Matches 101; C
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                                                                                                                                                                                                                                                                                                                                                                                                                     ABA90456;
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                                                                                                                                                                                                                                                                                                                            RESULT 12
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ID ABA9
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                                 for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                            AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphils. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGGCTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
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                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 101; DB 2; Length 487; 100.0%; Pred. No. 2.6e-21;
                                                                                                                                                                                                                                                                                                                                                Sequence 487 BP; 125 A; 127 C; 113 G; 121 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTTCCGCGCACATTTCCCCCGAAAGTGCCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                  biosynthetic products such as enzymes
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                                                                                                                                    Claim 1; Page 1106; 1150pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 101; Conservative
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WPI; 1999-081273/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9859034-A2
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AAX21149

RESULT 11 AAX21149/

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Query Match

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Gaps

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Indels

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Sequence 535 BP; 145 A; 108 C; 122 G; 155 T; 0 U; 5 Other;

biosynthetic products such as enzymes

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing the affinity of an extendable oligonucleotide (EO) for a target nucleic acid, for providing primers having improved specificity, comprises hybridization of the EO to a template oligonucleotide (TO) and
                                                                                                                                                                                                                                               ds; primer library; extendable oligos; EO; ligation chain reaction; LCR; rolling circle amplification; strand displacement amplification; isothermal DNA amplification; biotechnology; agriculture; medical research; pUCI9 plasmid.
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                                                                                                                                                                                                                   Electropherogram of a DNA sequencing reaction using E154 & T422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
                   295 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
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                                                                                                                 ADH58311 standard; DNA; 605 BP
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                                                                                                                                                                                  (first entry)
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Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                  Synthetic.
Escherichia coli.
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antianaemic; dermatological; immunosuppressive; antiinflammatory; antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic; osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; systemic lupus extytematosus; rheumatoid arthritis; carcinowascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative; ds.
                                                                                                 Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
                                                                           DNA encoding novel prostate gland antigen, Seg ID No 418.
        AAS30560 standard; DNA; 776 BP
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2000US-0225267P
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                                                    21-NOV-2001 (first entry)
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05-SEP-2000;
06-SEP-2000;
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14-JUL-2000;
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14-AUG-2000;
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2000US-0246610P.
2000US-0246611P.
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2000US-0241785P.
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06-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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02-OCT-2000;
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13-OCT-2000;
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The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prognosis, prognosis, prognosis, prognosis, prognosis, prostatitis, acute bacterial prostatitis, chronic non-bacterial prostatitis, chronic non-bacterial prostatitis, benign prostatic chronic non-bacterial prostatitis, benign prostatic chronic non-bacterial prostatitis, benign prostatic chromatosis, granulomatous prostatic is malacophakia, benign prostatic chromas, compared to the prostation of the prostation of transitional cell carcinomas, ductal carcinomas, in, (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid cuthitis), bhod-related disorders (sighte cell anaemia), hyperproliferative disorders, urinary system disorders (arrhythmias), respiratory compared disorders, urinary system disorders (arrhythmias), respiratory confisorders (laferances), liver disorders (alsorders (laferances), liver disorders  disorders (laferances), liver disorders, disorders (laferances), liver disorders (laferances), liver disorders, disorders, disorders (laferances), liver disorders, liver disorders (laferances), liver disorders, disorders, disorders, disorders (laferances), liver disorders, liver disorders, liver disorders, liver,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful to prevent skin aging, for preventing hair loss, to maintain organs before transplantation, and as food additive or preservative
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2000US-0250391P.
2000US-0251030P.
2000US-0251988P.
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2000US-0251479P.
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2000US-0249300P.
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08-DEC-2000; 2000US-0251989P
08-DEC-2000; 2000US-0251990P
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Matches 101; Conservative
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01-DEC-2000; 2
05-DEC-2000; 2
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17-NOV-2000;
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06-DEC-2000;
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1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAAATAAACAAATAG 60

61 GGGTTCCGCGCACATTCCCCCGAAAGTGCCACCTGACGTC 101 GGGTTCCGCGCACATTCCCCGAAAGTGCCACCTGACGTC 446

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ò g AAS27819/c ID AAS27819 standard; DNA; 776 BP

RESULT 15

0; Gaps

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Neuroprotective, cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; ds; acquired immune deficiency syndrome.
                                                DNA encoding novel signal transduction pathway protein, Seg ID 1479.
                                                                                                                                                                                                                                                                                                                                                                        2000US-0215135P.
2000US-0216647P.
2000US-0216880P.
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08-SEP-2000;
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2000US-0232397P
2000US-0232398P
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2000US-0249207P
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The invention relates to novel isolated polypeptides (I), and

The invention relates to novel isolated polypeptides (I) are useful for

Glagnosing, preventing and treating diseases including immune system

disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ

transplant rejections and graft versus host disease, infectious diseases

(e.g. hepatitis (2), bleeding disorders, haemoglobin abnormalities and

other blood-related disorders (sickle cell anaemia), myeloproliferative

(e.g. daucher's disease and caneer), neurodegenerative disorders

(c.g. qaucher's disease and caneer), neurodegenerative disorders (e.g.

Alzheimer's disease, Parkinson's disease), chromosomal abnormalities

(Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.

Alzheimer's disease, Parkinson's disease), chromosomal abnormalities

(Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.

Glomerulonephritis), cardiovascular disorders (e.g. Addison's

crespiratory disorders, dermatological disorders (e.g. Addison's

crespiratory disorders), liver disorders, gastrointestinal disorders

(inflammatory disorders), liver disorders (cirrhosis), as stimulators of

B-cell responsiveness to pathogens, activators of T-cells, to induce

Cinflammatory disorders), liver disorders (cirrhosis), as stimulators of

Higher affinity antibodies, and as a means to induce tumour proliferation

cin pathologies e.g. acquired immune deficiency syndrome (AIDS), AAS26976-

Company and por the invention pathway protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1479; 880pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM;
                                                                                 2000US-0250391P.
2000US-0251030P.
2000US-0251988P.
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2000US-0251479P.
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08-DEC-2000; 2000US-0251990P
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61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101 486 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 446 ઠે

Search completed: July 14, 2005, 07:01:38 Job time : 142.448 secs

1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60

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Best Local Similarity 100. Matches 101; Conservative

CC817070 100002J15 CC818640 100004P22 CC818642 100004J12 CC818623 100004J12 AL694813 100005107 AL694813 100005107 AL694813 100005107 CC817633 100004M08 CC817639 100004M08 CC817595 100004K04 CC817595 100004K04 CC817595 100004K04 CC8187699 100004H16 CC817679 100004H16 CC817699 100004H116 CC817699 100004H116 CC817699 100004H116 CC817699 100004H116

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CCB19923 100006J13
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Compugen Ltd.
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Mebeloma cylindrosporum

Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

Agaricales; Cortinariaceae; Hebeloma.

I (bases 1 to 300)

Wipf,D., Benjdia,M., Tegeder,M. and Frommer,W.B.

Construction of a functional cDNA library from the ectomycorrhizal fungus Hebeloma cylindrosporum

Unpublished (2001)

Contact: Wipf D

ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 293287

Email: daniel.wipf@zmbp.uni-tuebingen.de
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                                                                                                                             BM078095 300 bp mRNA linear EST 30-NOV 83374 Hebeloma cylindrosporum functional cDNA library Hebeloma cylindrosporum cDNA 5', mRNA sequence.
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/mol_type="mRNA"
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/tissue type="Mycelia"
/lab host="E. coli XL1-Blue"
ALIGNMENTS
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High quality sequence stop: 300
POLYA=No.
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DEFINITION

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VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

ORIGIN

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rR0009140 309 bp DNA linear GSS 25-FEB-2004
F.rubripes GSS sequence, clone 010H20aC4, genomic survey sequence.
AL000426
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Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y.,
Williams, G. and Brenner, S.
Direct Submission
Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CBIO 1SB. Email: biohelpehgmp.mrc.ac.uk
Vector: pBluescript II KS
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                                                                                     A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.J., Bouchireb, N., Cottage, A., Yeo, G.S., Umrania, Y., Williams, G. and
                           1 (bases 1 to 300)
Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and
Frommer, W.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pDR 196 (unpublished); Site_1: EcoRI;
Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tisue type="Mycelia"
/lab_host="E. coli XL1-Blue"
/clone lib="Hebeloma cylindrosporum functional cDNA
library"
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                                                                                                                                                                                                                   ZMBP - Center for Molecular Biology of Plants University of Tuebingen Auf der Morgenstelle 1, 72076 Tuebingen, Germany Tel: 49 7071 2976160 Fax: 49 7071 29387 Email: daniel.wipf@zmbp.uni-tuebingen.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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    300
    /organism="Hebeloma cylindrosporum"

     Agaricales; Cortinariaceae; Hebeloma
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Genome Res. 9 (10), 960-971 (1999)
99455097
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SSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="H1"
/db_xref="taxon:76867"
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    no homology below le-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 101; Conservative
                                                                                                                                                                                                 Contact: Wipf D
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SET788 Hebeloma cylindrosporum functional cDNA library Hebeloma cylindrosporum functional cDNA library Hebeloma cylindrosporum cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                        Hebeloma cylindrosporum
Hebeloma cylindrosporum
Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Cortinariaceae; Hebeloma.
1 (bases 1 to 300)
Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU964094 1inear EST 13-NOV-2002 EST226 Hebeloma cylindrosporum functional cDNA library Hebeloma cylindrosporum cDNA, mRNA sequence.
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Frommer, W.B.
A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis.
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Site_2: XhoI"
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Location/Qualifiers
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Contact: Wipf D
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
Fax: 49 7071 297817
Email: daniel.wipf@zmbp.uni-tuebingen.de
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                                                                        61 GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                  114 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Hebeloma cylindrosporum"
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|ab_host="E. coli XL1-Blue"
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'strain="H1"
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BU964094/c

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Rm. 308, Bi
84112, USA
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CC819240/c
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 bp mRNA linear EST 04-SEP-2003 nonym: hlcc2) Homo sapiens cDNA clone
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 391)
Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="313 (synonym: hlcc2)"
/note="Vector: pTriplEx2; Site_l: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No si sequence available.

This clone (DKEZp313J611) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                  39 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAG
                                                                                                                                                                                                                                                                                                       One pass dye-terminator sequencing of cosmid cloned genomic
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                                                                                                                                                                                                                               Length 309;
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                                                                                                                                                                                                                             100.0%; Score 101; DB 9;
100.0%; Pred. No. 8.2e-19;
iive 0; Mismatches 0;
                                                  Location/Qualifiers
1. .30
/organism="Taxifugu rubripes"
/mol_type="genomic DNA"
/db xref="rtaxon:31033"
/clone="0.0H20acon:4"
/clone=11b="cosmid 010H20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313J1611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
/lab_host="DH10B"
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Matches 101; Conservative
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AL597149
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/lab hose="E. Col; strain XL10-Gold, T1-resistant, F-"
/lab hose="E. Col; strain XL10-Gold, T1-resistant, F-"
/clone lib="Oxytricha plasmid UUGC10 library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chamically-competent E. Coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                             CC819240 11-JUL-2003 17-JUL-2003 100005D19R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC100005D19 R, genomic survey
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Sterkiella histriomuscorum
Eukaryota, Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 414)
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Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes
Unpublished (2003)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., 5
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                                                                                                                                      288 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 328
                                                                                                61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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/mol_type="genomic DNA"
/db_xref="taxon:94289"
/clone="UUGC100005519"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Plate: 0005 row: D column: 19
Seg primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
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Fax: 801 585 7177
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Fax: 801 585 7177
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                                                                                                                                                       Haplochromis chilotes
Haplochromis chilotes
Haplochromis chilotes
Haplochromis chilotes
Bukaryota; Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Rutanyota; Meaplochromis; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidei; Cichlidae; Haplochromis.
E 1 (bases 1 to 417)
Watanabe, M., Kobayashi, N., Shin-i, T., Kohara, Y. and Okada, N.
Orf sequences of cichlid in Lake Victoria are essentially same
L Unpublished (2004)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact Fradasu Shin-i
Contact Padasu Shin-i
Tenis 1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Weiser Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
        417 bp mRNA linear EST 23-APR-2004 BJ684174 HCEST library Haplochromis chilotes cDNA clone no90c12, BJ684174
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Sterkiella histriomuscorum
Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichida, Oxytrichidae, Sterkiella.

1 (bases 1 to 491)
Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'organism="Haplochromis chilotes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="jaw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="no90c12"
                                                                                                                      BJ684174.1 GI:46527295
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Best Local Similarity 100.
Matches 101; Conservative
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BI805285 495 bp mRNA linear EST 02-OCT-2001 S035A01 Stem library from Oryza Bativa (3-5 leaf stage) Oryza sativa cDNA clone S035A01, mRNA sequence.
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I (bases I to 495)

Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
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Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-8698051
Fax: 0086-571-86961525
Email: webmastereGestarray.org, URL: http://www.estarray.org
Seq primer: M13 forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 101; DB 9; Length 491; Best Local Similarity 100.0%; Pred. No. 8.4e-19; Matches 101; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Contact: Haitao Dong, Debao Li
Bioinfomatics and Gene Network Research Group
Email: ddunn@genetics.utah.edu
Plate: 0006 row: J column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends estop: 491.
High quality sequence stop: 491.
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Pred. No. 8.4e-19;
100.08; FIL
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                Best Local Similarity 100.
Matches 101; Conservative
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Fax: 801 585 7177
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84112, US
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/lab hose="E. Col; strain XL10-Gold, T1-resistant, F-"
/clone lib="Goxytricha plasmid UUGC10 library"
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DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWM92 (gi|473114|gp|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Sterkiella histriomuscorum
Sterkiella histriomuscorum
Bukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichida; Oxytrichidae; Sterkiella.

1 (bases 1 to 495)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes
Unpublished (2003)
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
                                                                                                                                                   Length 495;
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                                                                                                                                               100.0%; Score 101; DB 4;
100.0%; Pred. No. 8.4e-19;
tive 0; Mismatches 0;
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Fax: 801 585 7177
Email: ddunnagenetics.utah.edu
Plate: 0004 row: B column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                        /note="Vector: pSport2"
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Location/Qualifiers
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CC818374.1 GI:32897661
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Best Local Similarity
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CC818374/c
                                                                                                                                                                                      Matches
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ORGANISM
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100.0%; Score 101; DB 9; Length 495;

Query Match

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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
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/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWM42 (gi|4732114|gp|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                 392 AGGGTTATTGTCTCATGAGGGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 333
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                                                        Sterkiella histriomuscorum
Eukaryota, Alveolata; Ciliophora; Spirotrichea; Stichotrichida;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 496)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax unpublished (2003)
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100004L13R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100004L13 R, genomic survey
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Indels
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/organism="Sterkiella histriomuscorum"
/organism="genomic DNA"
/dmol_type="genomic DNA"
/db_xref="taxon:94289"
/clone="UUGC100004L13"
/clone="UUGC100004L13"
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   Mismatches
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Plate: 0004 row: L column: 13
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/Mol type=genomic DNA"
// Ab Aref="taxon:94289"
// Clone="UUGCIO003C16"
// Lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
// Lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
// Lone="UUGCIO003C16"
// Lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
// Lone="Detail: PWD42N; Purified macronuclear chromosomal
// Note="Vector: PWD42N; Purified macronuclear chromosomal
// Now Oxytricha trifallax was blunt end-repaired with
// Lab NA polymerase and T4 polynucleotide kinase. Adaptor
// Coligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
// PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible
// derivative of plasmid R1 The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Sterkiella histriomuscorum
Eukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
                                                                                                                                                                                          Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella.
1 (bases 1 to 515)
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100002D21R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100002D21 R, genomic survey
     histriomuscorum genomic clone UUGC100003C16 R, genomic survey
                                                                                                                                                                                                                                                         1 (bases 1 to 515)
Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
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                                                                                                                                            Sterkiella histriomuscorum (Oxytricha trifallax)
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
                                                                                                                                                                      Sterkiella histriomuscorum
                                                                                                                                                                                                                                                                                                                                       macronuclear chromosomes
Unpublished (2003)
                                                                                   CC817752.1 GI:32897039
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Matches 101; Conservative
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Fax: 801 585 7177
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CC817128/c
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/clone lib="Waytricha plasmid UUGCIO library"
/clone lib="WetCr: PWD4Zny; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gild732114 [gb]AF129072.1], a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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Sterkiella histriomuscorum
Eukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella.
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                                                                                                                                                                   CC819854 503 bp DNA linear GSS 17-JUI 100006N08R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC10006N08 R, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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|db_xref="taxon:94289"
|clone="UUGC100006N08"
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331 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 291
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Plate: 0006 row: N column: 08
Seg primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genet
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CC819854/c
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/lab hose="E. Col; strain XL10-Gold, T1-resistant, F-"
/clone lib="Coytricha plasmid UUGCIO library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polynucleotide kinase. Adaptor
oligomotleotides were ligated to the blunt ends in high
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pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Sterkiella histriomuscorum
Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 519)
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Stichotrichida, Oxytrichidae, Sterkiella.
1 (bases 1 to 518)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads, from plasmid inserts of Oxytricha trifallax
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Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
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University of Utah Genome Center
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Location/Qualifiers
                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                      macronuclear chromosomes
Unpublished (2003)
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CC817162.1 GI:32896449
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/clone libe "Oxytricha plasmid UUGCIO library"
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DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
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molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                             Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                 Email: ddunn@genetics.utah.edu
Plate: 0002 row: J column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends etop: 519.
High quality sequence stop: 519.
University of Utah
                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                 Rm. 308, B:
84112, USA
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Perfect score:

Run on:

Seguence:

Scoring table:

Searched:

Database :

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AR116416 Sequence
AR2226 Sequence
AR411127 Sequence
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155540 Sequence
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BD181637 Novel mel
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BD181638 Novel mel
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AX207724 Sequence
AX349365 Sequence
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 U89673 Cloning vec
           BD234590 Screening
AX026821 Sequence
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AX573107 Sequence
AX685746 Sequence
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Antelman,D., Gregory,R.J. and Wills,K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 5 13-JUN-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       DNA
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AR098190
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AR20783 Sequence
BD009729 Tissue sp
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AR098191 Sequence
AR20783 Sequence
AR20783 Sequence
AR20783 Tissue sp
AR098192 Sequence
AR20783 Sequence
AR20784 Sequence
AR20784 Sequence
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AS3814 Sequence
AX13340 Sequence
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AX154 Sequence
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AX24391 Sequence
BD288492 Expressio
AX24391 Sequence
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                                                                   July 14, 2005, 04:39:07; Search time 749.127 Seconds (without alignments) 6468.225 Million cell updates/sec
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Compugen Ltd.
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        GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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PAT 14-FEB-2001

PAT 20-JUN-2002

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JOURNAL FEATURES

REFERENCE AUTHORS

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PAT 14-FEB-2001
                                                   cloning vector; expression vector; multiple cloning site; Plasmid. synthetic construct synthetic construct
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                                                                                                                                                  Peters,H., Hundhausen,T., Kroenke,M. and Marget,M.
A new small sized high-level eukaryotic expression vector
Unpublished
                                                                                                                                                                                                                  Peters, M. Submission
Direct Submission
Submitted (07-AUG-1995) H. Peters, Inst. f. Immunologie, Michaelisstr. 5, D- 24105 Kiel, FRG
Related sequences: M21295 and K03104.
Location/Qualifiers
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    .2125
/note="cloning vector (pcDNA3) (Invitrogen)"

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; Pred. No. 9.3e-24;
0; Mismatches 0;
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Antelman,D., Gregory,R.J. and Wills,K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 19 13-JUN-2000;
Location/Qualifiers
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                                                                                                               other sequences; artificial sequences.
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Cloning vector pcDNA3ZEO DNA
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AR098191.1 GI:12807448
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100.0%;
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                                     X90639.1 GI:949972
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Best Local Similarity 100.0
Matches 100; Conservative
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N JP 200150368-A/3

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PN JP 200150368-B/3

PP 13-NOV-1997 JP 1998522958

R 15-NOV-1996 US 08/751517,14-FEB-1997 US 08/801092 PI
DOUGLAS ANTELMAN, RICHARD J GREGORY, KENNETH N WILLS PC
COTPLI/04,COTKS/00/A51K38/00,A61K38/12

CC Strandedness: Single;
CC Strandedness: Single;
CC Topology: Linear;
FH Key
CD 209. .862.
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Tissue specific expression of retinoblastoma protein.
BD009729
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1 (bases 1 to 3853)
Antelman, D., Gregory, R.J. and Wills, K.N.
Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 3 21-MAR-2001;
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Pred. No. 9.4e-24;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 5 30-APR-2002;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.49
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/wol_type="unassigned DNA'
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JP 2001503638-A/3.
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Best Local Similarity 100.
Matches 100; Conservative
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100.0%; Score 100; DB 6;
100.0%; Pred. No. 9.3e-24;
ive 0; Mismatches 0;
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Antelman,D., Gregory,R.J. and Wills,K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 33 13-JUN-2000;
Location/Qualifiers
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 33 30-APR-2002;
Location/Qualifiers
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/wol_type="unassigned DNA"
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No Unidentified

No 19 2001503638-A/4

PD 21-MAR-22001

PF 13-NOV-1996 US 08/751517,14-FEB-1997 US 08/

DOUGLAS ANTELMAN, RICHARD J GREGORY, KENNETH N WILLS PC

CO7121/04,C07785/00,461K38/102

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source /organism='Unidentified'.
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Tissue specific expression of retinoblastoma protein.
BD009730
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unclassified.
1 (bassel 1 to 4026)
Antelman, D., Gregory, R.J. and Wills, K.N.
Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 4 21-MAR-2001;
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100.0%; Score 100; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-24;
Matches 100; Conservative 0; Mismatches 0;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 19 30-APR-2002;
Location/Qualifiers
                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
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Sequence 19 from patent US 6379927.
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/organism="unidentified"
/mol_type="genomic DNA"
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JP 2001503638-A/4.
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1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
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Location/Qualifiers
                                                                                           Length 4341;
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                                                                                     ; Score 100; DB 6;
; Pred. No. 9.3e-24;
0; Mismatches 0;
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other sequences; artificial sequences.
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Cancer Research Ventures Limited (GB)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 1 from Patent WO0179510.
AX286570.
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Sequence 3 from Patent WO0078358.
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Best Local Similarity 100.0%;
Matches 100; Conservative 0
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Hawkins, R.E., Russell, S.J., Stevenson, F.K. and Winter, G.P.
IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
BEATENT: WO 94080008-A 58 14-APR-1994;
MEDICAL RES COUNCIL (GB)
Other publication CA 2145064 940414
Other publication AP 4822493 940426
Other publication AP 8501699T 960227.
Location/Qualifiers
1. 4341
                                                                                                                                                                                                                                                                    unclassified.
unclassified.
unclassified.
l (bases 1 to 4249)

S Antelman, D., Gregory, R.J. and Wills, K.N.
Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 5 21-MAR-2001;
CANJI INC
CANJI INC
OS Unidentified
PN JP 2001503638-A/5
PD 21-MAR-2001
PP 13-NOV-1997 JP 1998522958
PR 13-NOV-1997 JP 1998522958
PR 13-NOV-1997 JP 1998522958
COTH2L/O4, COTKSO, A61K38/00, A61K35/12
CC Strandedness: Single;
CC Topology: Linear;
FH Key Lords/O0, A61K38/00, A61K35/12
CC Topology: Linear;
FT source Lords/Ovalifiers
FT Source Lords/Organism='Unidentified'.
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Tissue specific expression of retinoblastoma protein.
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ative 0; Mismatches 0;
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JP 2001503638-A/5.
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Matches 100; Conservative
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A38214
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PAT 22-JAN-2001

REFERENCE AUTHORS

FEATURES

COMMENT

PAT 21-NOV-2001

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Search completed: July 14, 2005, 14:03:30 Job time: 749.127 secs
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="whis sequence is artificial and is based on well
established comm ercially available vectors that are cited
with their vendor within the patent applicatio"
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I (bases 1 to 5053)
Fikes, J.D., Hermanson, G.G., Sette, A., Ishioka, G.Y., Livingston, B. and Chesnut, R.W.
Stression vectors for stimulating an immune response and methods of using the same
Patent: JP 2002520000-A 18 09-JUL-2002;
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Patent: WO 0119853-A 1 22-MAR-2001;
THE UNIVERSITY OF SHEFFIELD (GB)
Location/Qualifiers
1. .4840
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other sequences; artificial sequences.
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Sequence 1 from Patent WO0119853.
AX133340.
AX133940.1 GI:14139881
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JP 2002520000-A/18.
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OS Artificial Sequence

OS Artificial Sequence

PN JP 200252000-A/18

PD 9-JUL-2002

PF 13-MAY-1999 JP 2000548449

PR 13-MAY-1998 US 09/078994,15-MAY-1998 US 60/085751 PI
JOHN D FIKES,GARY G HERMANSON, ALESSANDRO

SETTE,GLENN Y ISHIOKA,

PC CINNS/CON, ROBERT W CHESNUT

PC CINNS/CON, A61K31/711, A61K39/00, A61K39/12, A61K39/29,

PC A61P31/14, A61P31/20, A61P37/02, C12N15/00

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Location/Qualifiers

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/organism='Artificial Sequence'.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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July 14, 2005, 04:35:42; Search time 140.988 Seconds (without alignments) 4198.742 Million cell updates/sec Run on:

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Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

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geneseqn1980s:\*
geneseqn1990s:\*
geneseqn2000s:\*
geneseqn2001as:\*
geneseqn2001as:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs

### SUMMARIES

Description	Adm41035 Fungus nu	Adhl1349 Vertebrat	Adm41037 Cytomegal	Adm41034 Human nuc	Adm41036 Cytomegal	Aav40006 Plasmid p	Aav40007 Plasmid p	Aav63466 Plasmid p	Aag62391 Vector pV	Aas17704 Vector pV	Abn83143 Plasmid p	Aaf24901 Nucleotid	Aad39652 Human sma	Aaf83146 Complete	Adb33528 Expressio	Aaz38633 pEP2 expr	Aas12839 DNA segue	Adh11417 Plasmid p	Adf10526 Plasmid p	Acc44637 Murine rD
ΙD	ADM41035	ADH11349	ADM41037	ADM41034	ADM41036	AAV40006	AAV40007	AAV63466	AAQ62391	AAS17704	ABN83143	AAF24901	AAD39652	AAF83146	ADB33528	AAZ38633	AAS12839	ADH11417	ADF10526	ACC44637
DB	12	7	12	12	12	7	0	0	7	9	9	4	9	4	10	m	4	N	ដ	10
% Query Match Length DB	1506	1600	1782	2241	2294	3853	4026	4249	4341	4341	4341	4597	4639	4840	5015	5053	5070	5082	5162	5162
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
Result No.	п	7	e	4	Ŋ	9	7	Φ	6	10	11	12	13	. 14	15	16	17	18	19	20

Ads75099 Plasmid p Abv77540 Plasmid p Abv77540 Plasmid p Abv77548 Plasmid p Abv77549 Plasmid p Adv77549 Plasmid p Adv77549 Plasmid p Adv17639 Plasmid p Adv18668 Nucleotid Adv21866 Plasmid p Adv21866 Plasmid p Adv21864 Plasmid p Abl53440 Vector pc Adv36314 Plasmid p Abl58498 Recombina Abk88868 Topoisome Abk88868 Topoisome Adv688791 Plasmid p	Ado06720 Recombina Ab158490 Recombina Ab158490 Recombina Aag88310 Plasmid p Aai66195 Human FSH Ab40237 DNA encod
ADS75099 ACC44692 ABV77540 ABV77549 AD134681 AD133 AD186685 AD77539	ADO06720 ABL58489 ABL58490 AAQ88310 AAI66195 ABK40237
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51172 51172	5543 5614 5614 5618 5651 5651
	100.0 100.0 100.0 100.0
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10000000000000000000000000000000000000	4 4 4 4 4 0 1 2 2 4 5 2 4 5

#### ALIGNMENTS

Fungus nucleotide sequence SEQ ID NO:3 ADM41035 standard; DNA; 1506 BP. (first entry) 17-JUN-2004 ADM41035; RESULT 1 ADM41035 

engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; fungus; gene; ds.

WO2004027029-A2.

01-APR-2004.

17-SEP-2003; 2003WO-US029251.

19-SEP-2002; 2002US-0411790P.

(XIME-) XIMEREX INC.

Thompson SC; Beschorner WE, Sosa CE,

WPI; 2004-295402/27.

Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.

Disclosure; SEQ ID NO 3; 48pp; English.

The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for

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32 protein of Geanorhabditis elegans or a functional equivalent,
derivative or bioprecursor of UNC-53. Also described: (1) a CDNA sencoding a vertebrate homologue of the C. elegans UNC-53 protein; (2) a
encoding a vertebrate homologue of the C. elegans UNC-53 protein; (2) a
nucleic acid which hybridises to the cDNA of (1); (3) vector comprising
the CDNA as in (1); (4) a homologue cell containing the vector as in (3); (5)
a transgenic cell, tissue or animal comprising the vector as in (3); (5)
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facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                               1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                     GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNC-53 vertebrate protein homologue; UNC-53; Caenorhabditis elegans; cell shape regulator; cell motility regulator; cell migration; cell behaviour regulator; phenotype; signal transduction pathway; asignal transducing protein; signal integrator protein; neuronal regeneration; revascularisation; wound healing; chronic neurodegeneration; disease; acute traumatic injury;
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Vandekerckhove JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.
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                                                                                                                                                                                                100.0%; Score 100; DB 12; Length 1506; 100.0%; Pred. No. 4e-26;
                                                                                                                                                           Sequence 1506 BP; 454 A; 277 C; 361 G; 414 T; 0 U; 0 Other;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                            61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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                                                                                                                                                                                                                                      0; Mismatches
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Matches 100; Conservative
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                                                                                                                     specification
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a compound identified as an enhancer or inhibitor of the regulation of cell shape, motility, or the direction of cell migration for use as a therapeutic; (7) a method for determination of whether a protein is an inhibitor or enhancer of regulation of cell behaviour, growth, shape or expressing a homologue of UNC-53 and determining a change of phenotype; (8) a method for identification of vertebrate homologues of C. elegans unc-53 gene by hybridising a probe of 15-50 bp of the unc-53 sequence to a DNA library; and (9) a method for identification of a protein which is active in the signal transduction pathway of a cell of which a vertebrate homologue of UNC-53 is a component comprising; (i) contacting an extract of a cell with an antibody to the UNC-53 homologue; (ii) identifying an artibody/homologue complex; and (iii) analysing such a complex. UNC-53 is a signal transducing or signal integrator protein involved in controlling clientify any non-antibody protein bound to the complex. UNC-53 is a signal transducing or signal integrator protein involved in controlling directionality of cell migration and cell shape in C. elegans. Vertebrate homologues of UNC-53 can be used to promote neuronal regeneration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                      diseases or acute traumatic injuries or fibrotic diseases. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                           sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 2; Length 1600; 4.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1600 BP; 397 A; 409 C; 398 G; 396 T; 0 U; 0 Other;
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; Pred. No. 4.1e
0; Mismatches
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Best Local Similarity 100.0
Matches 100; Conservative
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selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present
                                                                                                                                                                                                                                                                                                sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
replacement cells within a foetal non-human mammal, which comprises
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ö 9 1 GACGGATCGCGGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTCGCTCTGATG 60 1 GACGGATCGGGAGATCTCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG ; 0 Length 1782; Seguence 1782 BP; 458 A; 399 C; 451 G; 474 T; 0 U; 0 Other; Indels 100 61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100.0%; Score 100; DB 12; 100.0%; Pred. No. 4.2e-26; iive 0; Mismatches 0; Matches 100; Conservative Similarity Query Match Local

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CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100 61 ò g

Human nucleotide sequence SEQ ID NO:2. ADM41034 standard; DNA; 2241 BP (first entry) 17-JUN-2004 ADM41034; RESULT ADM41034 

engrafting foreign replacement cell; implanting foreign replacement cell; growth, differentiation, drug development, vaccine development, tissue transplantation; human disease study; human; gene, ds.

Homo sapiens

WO2004027029-A2 01-APR-2004.

17-SEP-2003; 2003WO-US029251

19-SEP-2002; 2002US-0411790P.

(XIME-) XIMEREX INC.

Thompson SC; Sosa CE, Beschorner WE,

WPI; 2004-295402/27

Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.

Disclosure; SEQ ID NO 2; 48pp; English.

replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the feral non-human mammal host, where the foreign replacement cells in cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a The present invention describes a method for engrafting foreign

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                    develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the specification.
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                                                                                                                                                                                                                                                                                             GACGGATCGGGAGATCTCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                   Gaps
mammalian host, and for producing chimeric mammals that can be used
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                                                                                                                                                                         Length 2241;
                                                                                                                                  Sequence 2241 BP; 498 A; 630 C; 609 G; 504 T; 0 U; 0 Other;
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                                                                                                                                                                         100.0%; Score 100; DB 12; ilarity 100.0%; Pred. No. 4.5e-26; Conservative 0; Mismatches 0;
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engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds. Cytomegalovirus nucleotide sequence SEQ ID NO:4. 17-JUN-2004 (first entry) Cytomegalovirus 

BP.

ADM41036 standard; DNA; 2294

RESULT 5 ADM41036

ADM41036;

WO2004027029-A2

01-APR-2004.

17-SEP-2003; 2003WO-US029251.

19-SEP-2002; 2002US-0411790P.

(XIME-) XIMEREX INC.

Thompson SC; Beschorner WE, Sosa CE,

WPI; 2004-295402/27.

Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.

Disclosure; SEQ ID NO 4; 48pp; English.

The present invention describes a method for engrafting foreign replacement cells within a footal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells in the cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the specification

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Plasmid pCTMI.
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15-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     E2F; transcription factor; human; retinoblastoma protein RB; bladder cancer; restenosis; angioplasty; diabetic retinopathy; thyroid hyperaplasia; Grave's disease; psoriasis; benign prosetatic hypertrophy; Li-Fraumeni syndrome; peripheral vascular disease; therapy; plasmid pCTM; ss.
                                  Length 2294;
Sequence 2294 BP; 466 A; 680 C; 641 G; 507 T; 0 U; 0 Other;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function= "tripartite leader sequence"
                                                                                                                                                                                            CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                        CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= d
/note= "pUC19 backbone H3 to AatII"
complement(2857. .3717)
                                100.0%; Score 100; DB 12;
100.0%; Pred. No. 4.5e-26;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1132. .1149
/*tag= c
/note= "SP6 promoter"
1679. .3853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "CMV promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
209. .864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wills KN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified bacteriophage; T7.
unidentified bacteriophage; SP6.
Macaca mulatta; polyoma virus.
Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= e
/note= "AMP-ORF"
                                                                                                                                                                                                                                                                                              AAV40006 standard; DNA; 3853 BP.
                                                  Best Local Similarity 100.0%;
Matches 100; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US021821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-00751517
97US-00801092
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gregory RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-297858/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CANJ-) CANJI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pCTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9821228-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L5-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antelman D,
                                                                                                                                                                                                                                                                                                                               AAV40006;
                                                                                                                                                                        61
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOS
                                                                                                                                                                                                                                                                            AAV40006
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This is the nucleotide sequence of pCTM, a plasmid which contains a CMV promoter, a tripartite adenovirus leader flanked by T7 and SP6 promoters, and a multiple cloning site with a bovine growth hormone polyA site and downstream SV40 polyA site. It has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastoma protein (BP, see AM62465) and E2F transcription factor (see AM62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, profections, appecificatily canner (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the E2F promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
e.g. hyper-proliferative disease such as cancer and restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bladder cancer; restenosis; angioplasty; diabetic retinopathy; thyroid hyperplasia; Grave's disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2F; transcription factor; human; retinoblastoma protein RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3853 BP; 936 A; 986 C; 942 G; 989 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function= "tripartite leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         benign prostatic hypertrophy; Li-Fraumeni syndrome;
peripheral vascular disease; therapy; plasmid pCTMI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= e
/note= "pUC19 backbone H3 to AatII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100; DB 2;
Pred. No. 5.2e-26;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= c
'note= "hybrid SV40 late intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ′*tag= a
'note= "CMV promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T7.
SP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
0
                                                   Example 1; Fig 4; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta; polyoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV40007 standard; DNA; 4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mastadenovirus.
unidentified bacteriophage;
unidentified bacteriophage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     075. .1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1305. .1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match .
Best Local Similarity
Matches 100; Conserv
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SOS

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This is the nucleotide sequence of pCTMIE, a plasmid that was constructed by amplifying the SV40 enhancer from SV40 viral DNA by PCR, digesting the maplified product with Ball and inserting into BamHI-digested plasmid pCMMIE has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastoms protein (BP, see AAW82465) and E2F transcription factor (see AAW62444). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, specifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the E2F promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion polypeptide of, e.g. transcription factor - used to treat, e.g. hyper-proliferative disease such as cancer and restenosis.
                                                                                                                                                                               "tripartite leader sequence"
                                                                                                                                                                                                                                                                                                                                                bp tandem repeat enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                     note= "72 bp tandem repeat enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "hybrid SV40 late intron"
                                                                                                                                                                                                                                   note= "hybrid SV40 late intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
"T antigen binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "pUC19 backbone H3
complement(3255. .4113)
                                                                                                          ′*tag≃ a
'note= "CMV promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       = "SP6 promoter"
.4249
                                                                    Socation/Qualifiers
                                                                                                                                                                                                                                                                                        note= "early mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antelman D, Gregory RJ, Wills KN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "AMP-ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 8; 91pp; English
Macaca mulatta; polyoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US021821.
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97US-00801092.
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                                                                                                                                                                                                081. .1145
                                                                                                                                                                                                                                                          .1366
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                                                                                                                                                                                                                                                                                                                                                note= "72
                                                                                                                                                                               function=
                                                                                                                                           .1074
                                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                           *tag=
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                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                          164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CANJ-) CANJI INC.
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                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                      misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09821228-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-1997;
                     3os taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-1998
                                    Chimeric
                                                                                         promoter
                                                                                                                                                                                                                                                                                                               enhancer
                                                                                                                                                                                                                                                                                                                                                                   enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                    intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDS
                                                                        že,
 This is the nucleotide sequence of pCTMI, a plasmid that was constructed from pCTM (see AAV40006) by digesting pCTM with XhoI and NotI and subcloning a 180 bp intron XhoI-NotI fragment from a pCMV-beta-gal vector. Plasmid pCTMI has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastoma protein (BP, see AAW62465) and E2P transcription factor (see AAW62461). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, specifically cancer used to treat hyperproliferative conditions, specifically cancer repressing transcription of the blander) or restenosis. They are more effective in repressing transcription of the E2P promoter than RB alone and cause cell cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                              New fusion polypeptide of, e.g. transcription factor - used to treat, e.g. hyper-proliferative disease such as cancer and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2F; transcription factor; human; retinoblastoma protein RB; bladder cancer; restenosis; angioplasty; diabetic retinopathy; thyroid hyperplasia; Grave's disease; psoriasis; benign prostatic hypertrophy; Li-Fraumeni syndrome; peripheral vascular disease; therapy; plasmid pCTMIE; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4026 BP; 978 A; 1021 C; 982 G; 1045 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 100; DB 2; Length 40 100.0%; Pred. No. 5.3e-26; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
complement (3032. .3890)
                                                                                                                                                                                                                                                                         Gregory RJ, Wills KN;
                   /*tag= f
/note= "AMP-ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mastadenovirus.
unidentified bacteriophage; T7.
unidentified bacteriophage; SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV63466 standard; DNA; 4249 BP
                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 6; 91pp; English
                                                                                                                                             97WO-US021821.
                                                                                                                                                                               96US-00751517
97US-00801092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                             WPI; 1998-297858/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                     (CANJ-) CANJI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pCTMIE
                                                                                                                                                                               15-NOV-1996;
14-FEB-1997;
                                                                      WO9821228-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
15-FEB-1999
                                                                                                                                                                                                                                                                         Antelman D,
                                                                                                         22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV63466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query' Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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to AatII"

Sequence 4249 BP; 1020 A; 1074 C; 1048 G; 1107 T; 0 U; 0 Other;

셤 ò a antibody/retroviral envelope fusion protein can be used as a plasmid vaccine and it induces a strong humoral response to the antibody moiety in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)

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                                                               GACGGATCGGGAGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTCTCTGATG 60
                                                                                                                                                                                                                                              Vector; pVAC1; pRc/RSV; leader sequence; termination signal;
fusion protein; pSfi/Not.Tag1; pelB leader; human; immunoglobulin; VH1;
single chain; Fv; murine antibody; retroviral; envelope; plasmid;
                                           GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating immune response to a disease marker - by administering a vector which expresses the disease marker to interact with the immune
                          Gaps
                         ö
     Length 4249;
                        0; Indels
                                                                                   CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                                                                             CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hawkins RE, Russell SJ, Stevenson FK, Winter GP;
   100.0%; Score 100; DB 2;
100.0%; Pred. No. 5.4e-26;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                complement (1. .775)
                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "Claim 9"
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                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "Claim 7"
                                                                                                                                                       AAQ62391 standard; DNA; 4341'BP.
                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-GB002054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92GB-00020808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                            .780
Query Match
Best Local Similarity 100.0
Matches 100, Conservative
                                                                                                                                                                                                                                                                                                                                                                                         606. .716
                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                             .909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-135575/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-1992;
                                                                                                                                                                                                                             Vector pVAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9408008-A1
                                                                                                                                                                                               25-MAR-2003
                                                                                                                                                                                                         18-NOV-1994
                                                                                                                                                                                                                                                                               vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-1994
                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                            AAQ62391;
                                                                                   61
                                                                                                     61
                                                                                                                                                                                                                                                                                                                               misc RNA
                                                                                                                                                                                                                                                                                                                                                           misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                          misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system.
                                                                                                                                             AAQ6239
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commercially available vector pRc/RsV. Leader sequences and termination signals were introduced into the vector to allow for production of fusion proteins. The vector, pSfi/Not.Tagl, was modified to replace the pelb leader with the human immunoglobulin VHI leader sequence that permits the encoding of an SfiI cloning site without modification of the amino acid sequence. This fragment was then cloned as an EcoRI/Blunt-HindIII fragment into NotI/Blunt-HindIII cut vector pRc/RSV to give pVACI. The single chain Fv for an individual patient can be inserted within the VHI leader sequence. This plasmid when encoding a single chain murine

This sequence represents the vector pVAC1. This vector is based on the

Claim 10; Fig 7; 77pp; English.

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The invention relates to a nucleic acid construct for delivery into living cells in vivo, to induce an immune response to a disease peptide antigen, where the construct directs expression of a fusion protein comprising the peptide antigen and the first domain of Frc. Also included are a nucleic acid vector comprising the above construct or vector and a method of producing a nucleic acid construct for inducing an immune response. The method comprises identifying a nucleic and sequence encoding a disease peptide comprises identifying a nucleic acid sequence, introducing the cloned nucleic acid into a vector nucleic acid sequence, introducing the cloned nucleic acid into a vector which allows the antigen to be expressed as a fusion with a first domain Frc from tetanus toxin, and optionally isolating the construct from the vector. The construct or vector is used as a vaccine to induce an immune response, particularly to tumour antigens. The present sequence is vector byACI which encodes a vaccine of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTL; PCR primer; pVAC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid construct, useful to immunize against various diseases including cancer, expresses the first domain of tetanus toxin FrC fused to a disease peptide antigen to provide a vaccine.
                                                                                                                                                                                                     1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                              1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                          Gaps
                                                                                                                                            ö
                                                                    Sequence 4341 BP; 1032 A; 1099 C; 1091 G; 1119 T; 0 U; 0 Other;
                                                                                                        DB 2; Length 4341;
                                                                                                                                          Indels
                                                                                                                                                                                                                                                    61 CCGCATAGTTAAGCCAGTATCTGCTCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                         CGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                    100.0%; Score 100; DB 2;
100.0%; Pred. No. 5.4e-26;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vector pVAC1 encoding a DNA vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  AAS17704 standard; DNA; 4341 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CANC-) CANCER RES VENTURES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2000; 2000GB-00009470.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                          Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice J, Stevenson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-066370/09.
                                                                                                                       Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200179510-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAS17704;
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                             AAS17704
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1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W;
                                                                                                                         RESULT 12
                                                                                                                                       AAF24901
ID AAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel nucleic acid construct for inducing an immune response in vivo to an antigen, capable of directing the expression of a fusion protein that comprises an antigen and an adjuvant sequence derived from a plant viral coat protein. The construct of the invention has cytostatic and virucide activity. The nucleic acid construct is useful for inducing an immune response in a patient, for vaccinating a patient against an infectious disease caused by an antigen derived from a pathogen e.g. a virus, for treating a cancer patient or a patient with a predisposition to cancer and for treating a patient naving a B cell malignancy, where the construct is encapsidated, and optionally, a second nucleic acid sequence encoding a further immunomodulatory colypeptide is administered to the patient. The construct is also useful in medical treatment, and in the preparation of a vaccine for treating or preventing a disease state associated with the antigen. The sequence shows the complete sequence of vector pWACI
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                                                                                                GACGGATCGGGAGATCTCCCCAATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                   Immune response; plant viral coat protein; pVAC1; cytostatic; virucide;
                                                                                1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid construct for delivery into living cells as a vaccine, useful for treating e.g. cancer, directs the expression of a fusion protein comprising an antigen and an adjuvant sequence derived from
Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 100; DB 6; Length 4341;
100.0%; Pred. No. 5.4e-26;
tive 0; Mismatches 0; Indels 0;
                            Length 4341;
                                                      0; Indels
                                                                                                                                      61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                       CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                           100.0%; Score 100; DB 6; 100.0%; Pred. No. 5.4e-26;
                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                      Plasmid pVAC1 complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 7; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CANC-) CANCER RES VENTURES LID.
                                                                                                                                                                                                                                     ABN83143 standard; DNA; 4341 BP
                                                                                                                                                                                                                                                                                                                                                                  cancer; B cell malignancy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2000; 2000GB-00028319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2001; 2001WO-GB005142
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                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant viral coat protein.
                                                    Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-500202/53.
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       WO200240513-A2.
                                                                                                                                                                                                                                                                                            10-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                 ABN83143;
                           Query Match
                                         Local
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The specification describes a microsphere comprising dihydrazide derivatised hyaluronic acid crosslinked to a nucleic acid (NA). The microspheres cause reduced inflammatory responses, and have increased safety and biodegradability. The microspheres are useful for transfecting a cell of a subject and for treating a subject having myocardial ischemia, by increasing cardiac angiogenesis. They are also useful for treating hemophilia. The present sequence represents the plaamid pCDNA3.1/Gs, into which is inserted a polynucleotide sequence which is crosslinked to hyaluronic acid. The polynucleotide sequence encodes a vascular endothelial growth factor (VEGF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsphere, dihydrazide, hyaluronic acid, inflammatory response, myocardial ischemia, cardiac angiogenesis, haemophilia, vascular endothelial growth factor, VEGF, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4597 BP; 1062 A; 1214 C; 1206 G; 1115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                     CCGCATAGTTAAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
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                                                                                                      61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of the plasmid pCDNA3.1/GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 36-38; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COLL-) COLLABORATIVE GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2000; 2000WO-US016837.
                                                                                                                                                                                                                                                                                                                                                                 AAF24901 standard; DNA; 4597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-071363/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200078358-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-2000
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RESULT 13 AAD39652

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The invention provides a nucleic acid molecule (I) comprising at least the functional part of blasticidin resistance (BS) gene, or its homolog, linked through a recognition sequence to at least one selected gene. (I) is useful in treatment comprising:(I) providing cells/tissues transfected with (I); (2) surgical administration of the cells/tissues tronsfected with (I); (2) surgical administration of the cells/tissues tronsfected with (I); (2) surgical administration of the cells/tissues tronsfected by the patient. Therapeutic compositions comprising cells/tissues transformed with (I) is useful in identifying the role of genes in healthy and diseased tissue, in tissue engineering and in cosmetic surgery. Tissue engineering can be used to treat arthritis, joint replacement, skin grafts for burn victims, and replacement coronary arteries. Cosmetic tissue surgery includes rhinoplasty. The present sequence represents the nucleotide sequence of the vector pIRES/BS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion protein; amyloid precursor protein; APP; transcription factor; notropic; neuroprotective; APP inhibitor; amyloid precursor protein inhibitor; Alzheimer's disease; beta-secretase; gamma-secretase; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid molecule useful for therapeutic and cosmetic tissue engineering, comprising at least a functional part of blasticidin resistance gene linked through a recognition sequence, to a selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGGATCGGGAGATCTCCCCATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4840 BP; 1154 A; 1227 C; 1236 G; 1223 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 100; DB 4; Length 4840;
; Pred. No. 5.6e-26;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression vector nucleotide sequence SEQ ID NO:27
                                                                                                                                                                                                   Kafienah W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Fig C; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 100; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB33528 standard; DNA; 5015
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                                                                                                             99GB-00021418
                                                                 11-SEP-2000; 2000WO-GB003462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2003 (first entry)
                                                                                                                                                                                                   Barker MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               containing the BS gene
                                                                                                                                                       (UYSH-) UNIV SHEFFIELD
                                                                                                                                                                                                                                               WPI; 2001-290354/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003072041-A2.
                                                                                                                                                                                                 Hollander AP,
                                                                                                             11-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2003
                    22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant vector which comprises DNA, consisting of an insertion cassette contained between at least two insertion sites, that encodes a small nuclear (sn) RNA. The invention is used to identify snRNA modifications that inhibit expression of transcription products (and the identified snRNA are used to suppress expression) for delivering antisense sequences to the nucleus and to create transgenic animals. The present DNA sequence is human snRNA, Ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACGGATCGGGAGATCTCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blasticidin resistance; BS gene; gene therapy; tissue engineering; cosmetic surgery; arthritis; joint replacement; skin graft; rhinoplasty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nseful
                                                                                                                                                                              Human; recombinant vector; insertion cassette; small nuclear RNA; snRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant vector containing sequence for small nuclear RNA, e.g. for identifying variant snRNA that suppresses expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4639 BP; 1067 A; 1198 C; 1243 G; 1131 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 100; DB 6; Length 4639; 100.0%; Pred. No. 5.5e-26; o. Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete sequence of vector pIRES/BS.
                                                                                                                                  Human small nuclear RNA (snRNA) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 18pp; English
AAD39652 standard; DNA; 4639 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF83146 standard; DNA; 4840 BP
                                                                                                                                                                                                                                                                                                                                                                             12-MAR-2001; 2001US-00804481.
                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0188304P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lander ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-499510/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                      transgenic animal;
                                                                                                                                                                                                                                                                                       US2002058287-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200119853-A2.
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pIRES/BS; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-2001
                                                                                      22-OCT-2002
                                                                                                                                                                                                                                                                                                                                   16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graaf DD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF83146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 8
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                                         AAD39652
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Matches

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Gaps

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WERL J MERCK & CO INC.

WA (MERI J MERCK & CO INC.

WE Sepeseth AS, Ferrer M, Flores OA, Hazuda DJ, Inglese J;

Miler MD, Register B, Shi X, Simon AJ, Zuck PD;

XX

WH; 2003-689968/65.

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WH; 2003-689968/65.

XX

PT Greening for anti-Alzheimer agents, comprises a fused transcription

PT Greening for anti-Alzheimer agents, comprises a fused transcription

PT Greening for anti-Alzheimer agents, comprises a fused transcription

XX

Disclosure; Fig 32B-F; 193pp; English.

XX

CC The present invention describes a DNA molecule (I) that encodes a fusion

CC Transcription factor (IPF), fused in frame to the C-terminus of (I), a containing (I); and (3) methods for identifying a compound (A) that

CC containing (I); and (3) methods for identifying a compound (A) that

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61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100

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Search completed: July 14, 2005, 07:01:38 Job time : 141.038 secs THIS PAGE BLANK (USPTO)

100004F18 100003L17 100004J13 100004E20 100005C01

100002K13 100006M24 100003A09 100003G07

CC819886 CC818492 CC8118492 CC8117865 CC8117805 CC8117069 CC817069 CC817069 CC817069 CC817069 CC817069 CC817069 CC817652 CC817652 CC8176324 CC817834 CC817730 CC817730

100005D19

100003A24

100003B21

100003M12 100006H09 100004J10 100003F16

nucleic

Run on:

Sequence:

Title: Perfect :

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/db_xref="taxon:5807"
/lab_host="E. coli XL2 Blue MRF""
/lab_host="E. coli XL2 Blue MRF""
/lofoe lib="CplOWAgDNA2"
/note="Vector: PCR-Script Amp. SK+; Site 1: SrfI; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B67169 602 bp DNA linear GSS 12-MAY-2000
CpG0047A CpIOWAgDNA2 Cryptosporidium parvum genomic, genomic survey
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' the insert, to correct miscalled bases and assign uncalled (N)
bases throughout the sequence, and to terminate when base-calling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryofta; Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporidium.

1 (Base I to 602)

2 (Chase I to 602)

2 kosses I to 602)

Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Cryptosporidium parvum"
/mol type="genomic DNA"
/strain="IOWA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 602.
Location/Qualifiers
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CC817069
CC817074
CC817052
CC817652
CC817682
CC817837
CC819837
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CC819820
CC818421
                                                                                              CC817805
CC818511
CC818574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC817769
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Cryptosporidium parvum
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B67169.1 GI:2642750
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Seq primer: T7
Class: shotgun
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B67169
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BZ054067 jnr38b09.
AZ04012 sal10h5 S
AL715724 AL715724
AL714571 AL714571
CK110397 212009.pl
CK120360 207704.pl
CK120393 ISB1-118B
CL14237 ISB1-118B
CL14237 ISB1-118B
CL14237 ISB1-118B
CL123953 ISB1-8471
AQ944559 nbeb0049M
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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9b_htc::

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Result 80.

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(http://sequence-www.stanford.edu/group/techdev/shear.htm)
The randomly sheared gDNA was chromatographed on sephacry1 S-400 to remove any small fragments and DNA eluting in the void volume was blunt-ended with T4 DNA Polymerase, treated with alkaline phosphatase to prevent the ligation of multiple fragments, ligated to Srf I-digested pCR-Script Amp (SK+) vector and transformed into E. coli strain Xil0 Gold. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 primers."
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jnr13g03.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
sequence.
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/note="Vector: pOTW13; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea TO1000DH3 buds provided by

Thosmas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome
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Delehaunty, Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Mash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
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                                                                                                                                                                                                                                                    Length 602;
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Pred. No. 2.4e-10;
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Genome Sequencing Center
Washington University School of Medicine
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                                                                                                                                                                                                                              Similarity 100.0%; Score 60; 2.4. Similarity 100.0%; Pred. No. 2.4.
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Seg primer: -28RPpOT reverse
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/db_xref="taxon:3712"
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High quality sequence start: 32
High quality sequence stop: 551.
Location/Qualifiers
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Best Local Similarity 77.99
Matches 67; Conservative
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BZ050328 (99-OCT-2002 jnr42c12.bl B.oleracea001 Brassica oleracea genomic survey
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jnr38b09.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
GSS 09-OCT-2002
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 696)
Delehautty, K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Mash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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/db xref="texon:3712"
/clone_lib="B.oleracea001"
/note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas OBborn at the University of Wisconsin. Genomic DNA was provided by Rabio Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 717)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
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Washington University School of Medicine
Bmail: submissions@watson.wustl.edu
Plate: int42 row: c column: 12
Seq primer: -21UPpOT forward
Class: shotgun
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High quality sequence stop: 180.
Location/Qualifiers
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                                                                                                                           BZ050328.1 GI:23649718
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                                                                                                                                                                                         Brassica oleracea
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o mRNA linear EST 18-APR-2002 inner ear subtracted cDNA Danio
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                                                                                                                                                                     65 GCGGTATACACACCGCATATGGTGCACTCTCAGTACAATCTGCNCTGATGCCGCATAGTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (bases 1 to 333)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi,M., Hardelin,J.P., Weissenbach,J. and Petit,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
Danio rerio (zebrafish)
Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 TICACACCGCATAIGGIGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA
                                                                                                                               11 GAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
         Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL715724 Minus 343 pp Minus AL715724 Danio rerio embryonic inner ear subtracretio cDNA clone BN0AA018ZF12 5', mRNA sequence.
                                                                          15;
         Score 53.6; DB 2;
Pred. No. 4.1e-08;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53.4; DB 1;
Pred. No. 4.8e-08;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="subtracted cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="inner ear"
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/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="BN0AA018ZF12"
                                                                                                                                                                                                                                                                                                           125 AAGCCAGTATACACTCC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL715724.1 GI:20180327
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                                                                                                                                                                                                                                                   87
         53.6%;
80.5%;
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Unpublished (2002)
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Best Local Similarity 84.5
Matches 60, Conservative
                                                                       62; Conservative
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                                     Best Local Similarity
Matches 62; Conserv
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            Query Match
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AL715724/c
LOCUS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                     forganism="Brassica oleracea"
| Amol type="genomic DNA"
| Amol type="genomic DNA"
| Amol type="genomic DNA"
| Clone lib="Bolotracea001"
| Clone lib="Polotracea001"
| Inote="Vector: pOTw13; Whole genome shotgun library from prep wing buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the Sequencing Center.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 348)

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P.O. Box 1038, Johannesburg, Gauteng, 2000, South Africa
Fax: 2711 489 9226
Email: micheler@mail.saimr.wits.ac.za.
Location/Qualifiers
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Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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/clone lib="Salivary Gland Library"
/note="Vector: pAMP10"
                                                                                                                Genome Sequencing Center
Washington University School of Medicine
Manil: submissions@watson.wustl.edu
Plate: jnr38 row: b column: 09
Seq primer: -28RPpOT reverse
Class: shoctgun
High quality sequence start: 87
High quality sequence stop: 543.
Location/Qualifiers
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organism="Homo sapiens"
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/db_xref="taxon:9606"
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Department of Human Genetics
                                                                                       Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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Matches 67; Conservative
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                            TITLE
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AW409112
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/clone_lib="AtM".
/clone_lib="AtM".
/note="Vector: pQB-30MAST-attB (AY386205); Site 1: Sall;
Site 2: Not1; About 1 week after bolting, cDNA synthesis
site 2: Not1; About 1 week after bolting, cDNA synthesis
using Superscript'M-system (Invitrogen) with an
oligo(dT)-primer containing Not1 restriction site and a
Sall adapter. The main library (plate numbers begin with
1) of 38,000 clones was rearrayed into the sublibrary
(plate numbers begin with 201) containing 5,000 putative
expression clones. Average insert size is 1 kb. Note: The
rearrayed sublibrary (plate numbers begin with 201) was
sequenced. Library generation and sequencing was granted
in context of GABI-LAPP; data are also accessible at
https://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CK120360 766 bp mRNA linear EST 01-JUN-2004 207j04.pl AtMl Arabidopsis thaliana cDNA clone MPMGp2011J04207
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 766)
Peilner,T., Immink,R.G.H., Cahill,D.J. and Kersten,B.
Generation of a cDNA expression library from Arabidopsis
inflorescence meristem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             674 TTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 615
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/tissue_type="inflorescence meristem"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 TCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53.4; DB 7; Length 761;
Pred. No. 5.6e-08;
0; Mismatches 11; Indels 0
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/dev_stage="about one week after bolting"
/lab_host="E. coli SCS-1/pSE111"
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Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inhestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
Fax: +49(0)30/84131128
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Insert Length: 76 Std Error: 0.00
Plate: 207 row: J column: 4
Seg primer: pQE65.
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/db xref="taxon:3702"
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/ecotype="Columbia"
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CK120360
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Best Local Similarity 84.5%;
Matches 60; Conservative
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212069.pl AtMl Arabidopsis thaliana cDNA clone MPMGp2011009212
5-PRIME, mRNA sequence.
CK119397
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Arabidopsis thaliana
Brabidopsis thaliana
Brabryophyta, Jridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (Dases 1 to 761)
Geliner, Tr., Immink, R.G.H., Cahill, D.J. and Kersten, B.
Generation of a cDNA expression library from Arabidopsis inflorescence meristem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 TTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="embryonic"
|clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
Actinopterygii, Neopterygii, Teleostei, Ostariophysi; Cypriniformes, Cyprinidae, Danio.

1 (bases 1 to 345)

2 (ochabra, K., Weil,D.), Brottier,P., Blanchard,S., Levi,M., Hardelin,J.P., Weissenbach,J. and Petit,C.

A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.4%; Score 53.4; DB 1; Length 345; 84.5%; Pred. No. 4.8e-08; ive 0; Mismatches 11; Indels (
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Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Innestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
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Insert Length: 761 Std Erro
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/dev_stage="about one week after bolting"
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/note="V
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5-PRIME, mRNA sequence.
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Site_2: NotI; About 1 week after bolting, cDNA synthesis using SuperscriptThe system (Invitrogen) with an oligo(dT)-primer containing NotI restriction site and a SalI adapter. The main library (plate numbers begin with 1) of 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at
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Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Innestr. 73, D-14195 Berlin, Germany
Fax: +49(0)30/84131128
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Insert Length: 788 Std Error: 0.00
Plate: 209 row: P column: 8
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/db_xref="taxon:3702"
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expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at https://gabi.rzpd.de"
                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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1 (bases 1 to 898)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.
Mardis,E. and Wilson,R.
4 physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
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Mashington University School of Medicine
Bmail: submissions@waten.wustl.edu
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High quality sequence stop: 742.
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RESULT 12 CL140877/c

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ISB1-118B12_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-118B12, CAN-2004 sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

(Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                Xenopus tropicalis
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 899)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
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Washington University School of Medicine
Email: submissions@watson.wusfl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTATAGGG
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Washington University School of Medicine
Bmail: submissions@waten.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTATAGGG
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High quality sequence stop: 681.
Location/Qualifiers
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CL123953.1 GI:40617588
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CL123953/c
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Oryza sativa (japonica cultivar-group)

ISM Oryza sativa (japonica cultivar-group)

Elwaryora, Viridiplante; Streptophyra; Embryophyta; Tracheophyta; Spermatcphyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

El (bases 1 to 814)

RS Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Contact: Wing RA

Contact: Wing RA

Clemson University

Iou Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 7288

Eax: 864 656 7288

Eax: 864 656 7288

Eax: 686 650 7288

Eax: 686 650 7288

Class: BAC ends

Class: BAC ends
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Class: BAC ends
High quality sequence start: 167
High quality sequence stop: 324.

High quality sequence stop: 324.

Location/Qualifiers
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Pred. No. 5.9e-08;
0; Mismatches 11; Indels 0.
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High quality sequence stop: 361
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Best Local Similarity 84.5%;
Matches 60; Conservative (
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times, larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional clouding, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryas sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,286 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/BST Resource Center (www.genome.clemson.edu)."
Earle, 1991). The relatively small genome of rice, three
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279 TGGGCGGATTTTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGTGATGCCGCAT 338 7 TCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCAT ; 0 Length 814; 18; Indels ch 53.2%; Score 53.2; DB 8; I Similarity 78.0%; Pred. No. 6.7e-08; 64; Conservative 0; Mismatches 18; 67 AGTTAAGCCAGTATCTGCTCCC 88 Query Match Best Local Similarity Matches 64; Conserva ð 쉽 ઠે ద

ORIGIN

339 AGTTAAGCCAGCCCCGACACCC 360

BZ051815 675 bp DNA linear G jnr57d03.bl B.oleracea001 Brassica oleracea genomic, DEFINITION RESULT 15 BZ051815 ACCESSION

genomic survey

GSS

Brassica oleracea Brakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica. BZ051815 BZ051815.1 GI:23652690 Brassica oleracea sequence. VERSION KEYWORDS SOURCE ORGANISM

1 (bases 1 to 675)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002) TITLE JOURNAL COMMENT REFERENCE AUTHORS

Genome Sequencing Center
Washington University School of Medicine
Baail: submissions@watson.wustl.edu
Plate: jnr57 row: d column: 03
Seq primer: -21UPpOT forward Contact: Richard K. Wilson

Class: shotgun FEATURES

High quality sequence start: 29 High quality sequence stop: 94. Location/Qualifiers . .675

flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotqun library prepared at Washington University Genome Sequencing Center." /organism="Brassica oleracea"
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Query Match Best Local Similarity

53.0%; Score 53; DB 8; Length 675; 75.6%; Pred. No. 7.6e-08;

ö 53 ceenaceanagereceresacnaentaresrecacreteasracaarerecrerearece 112 3 CGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCC Gaps ; 21; Indels 0; Mismatches 113 dcaradriradeccadececedadece 138 63 GCATAGTTAAGCCAGTATCTGCTCCC 88 65; Conservative Matches ò g ò . 염

Search completed: July 14, 2005, 23:22:58 Job time: 952.146 secs

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Compositi

BD009742

BD134374 Pepride 1
AR42894 Sequence
AX128181 Sequence
AX128181 Sequence
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AX128348 Sequence
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BX5625 Human semap
AX001326 Sequence

OM nucleic

Run on:

Sequence:

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Arsuziay 4291 bp DNA linear SYN 11-DEC-2001 Synthetic construct UOATP2 fusion protein gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGAGTCTAGAGGCCCGTTTAAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 185
                                                                                                                                                                                                                                                                                                                                                                                              Curtiss, R.I. and Kong, W.
Regulated bacterial lysis for gene vaccine vector delivery and antigen release Patent: WO 2004020643-A 117 11-MAR-2004;
WASHINGTON UNIVERSITY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTCGAGTCTAGAGGGCCCGTTTAAACCCGGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC
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1. .280
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32650"
/note="Description of Artificial Sequence: Multiple cloning site of pXA3650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 101; DB 6; Length 280; 100.0%; Pred. No. 2.6e-20;
                                                                                                                                                                                                                                                                                                             linear
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synthetic construct
other sequences; artificial sequences.
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                                           AX128345
AX128351
AX128367
AX128363
AX128364
AX128364
CQ788642
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AX128342
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CQ768745
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CQ788637.1 GI:45723394
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Best Local Similarity
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AF302189 Synthetic
                                                           July 14, 2005, 04:39:07; Search time 756.618 Seconds (without alignments) 6468.225 Million cell updates/sec
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                                                                                                                    1 ctcgagtctagagggcccgt......tcccccgtgccttccttgac 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
       version 5.1.6
- 2005 Compugen Ltd.
                                                                                                                                                                  4708233 segs, 24227607955 residues
                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                 US-09-482-682-44_COPY_3930_4030
101
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Maximum Match 100%
Listing first 45 summaries
                                          nucleic search, using sw model
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AF060226
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Gapop 10.0 , Gapext 1.0
      GenCore
Copyright (c) 1993
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score greater than or equal to
and is derived by analysis of
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Minimum DB Maximum DB

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Searched:

PAT 24-MAR-2004

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Gaps

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Result Š.

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Query Match
Best Local Similarity 100.0
Matches 101; Conservative
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BD085110
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                                                                                                                                           other sequences; artificial sequences.
1 (bases 1 to 4291)
Zullo,S.J., Parks,W.T., Chloupkova,M., Fenton,W.A., Merril,C.R. and
                                                                                                                                                                                                                             Eisenstadt,J.M.
Expression of oligomycin resistance (olir) in CHO cells following
transfer of the mitochondrial DNA-encoded olir ATPase 6 gene to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLMGLPIIILIIMPPPVIMTSSKRLVNNRFHTFQQWLIKLITKQMMAIHSPKGRTWSL
MLASLIIFISGSTULLGLLPHPFPPTTQLSMNLGMAIPPWAGAVLLGFRHKWKDSLAHF
LPQGTPIPLIPMLVIIKTISLPIQPMALAVRLTANITAGHLLMHLIGGATLVLTSISL
PTAMTPFIILIMLTILEFAVALIQAYVFTLLVSLYLHDYT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MLFNLRILLNNAAFRNGHNFMVRNFRCGOPLOMNENLFSSFITP"
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/note="contains Home sapiens ornithine transcarbamylase
/note="contains Home sapiens ornithine transcarbamylase
/note="contains Home sapiens ornithine transcarbamylase
/note: contains Home sapiens ornithine transcarbamylase
/contains taylas |
/protein_id="MAL40188.1"
/db_xref="G1:17483749"
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Bogaert, T.A. and Deraeymaeker, M.

Bogaert, T.A. and Deraeymaeker, M.

VERTEBRATE HOMOLOGUES OF UNC-53 PROTEIN OF C. ELEGANS

Patent: WO 9824810-A 10 11-JUN-1998;

BOGAERT THIERY ANDRE OLIVIER (BE); DERAEYMAEKER MARC (BE)

Location/Qualifiers
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    .5082
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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Sequence 10 from Patent WO9824810.
A91754
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/plasmid="puOATP2"
                              GI:17483748
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                                                                                                                                      2669 CTCGAGTCTAGAGGGCCCGTTTAAACCCGGTGATCAGCCTCGACTGTGCCTTCTAGTTGC 2728
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THIERRY ANDRE OLIVIER EDDY BOGAERT
C12N15/12,C12N5/10,C12N15/85,C07K14/435,C07K16/18,A61K38/17,
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                                                                                       CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
unclassified.
1 (bases 1 to 5082)
Platteeuw, C.J., Arjol, C.M.B., Deraeymaeker, M., Verhasselt, P.,
Plot, D.J., D., Maertens, J.S., Luyten, W., Geerts, H.,
Vandekerckhove, J.S., Geysen, J. and Bogaert, T.A.O.E.
Vertebrate homologues of UNC-53 protein of C elegans
Patent: JP 200152222-A 8 13-NOV-2001;
JANSSEN PHARMACEUTTA NV
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Strandedness: Double;
Topology: Circular
Vertebrate homologues of UNC-53 protein of C elegans FH
Location/Qualifiers
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JP 2001522222-A/8
13-NOV-2001
03-DEC-1997 JP 1998525231
04-DEC-1996 GB 9625283.8
CHRIST JULES PLATTEEUW, CARLOS MANUEL BUESA ARJOL, MARC
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JACQUES SIMON MAERTENS,
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  Length 5082;
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Vertebrate homologues of UNC-53 protein of C elegans.
BD085110
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100.0%; Pred. No. 2.5e-20;
ive 0; Mismatches 0;
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/organism="unidentified"
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JP 2001522222-A/8.
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985 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 1044
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The Scripps Research Institute (US); SYNGENTA AGRICULTURAL DISCOVERY, INC. (CA)
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Viruses; ssDNA viruses; Circoviridae; Circovirus.
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Patent: WO 0161024-A 2 23-AUG-2001;
Large Scale Biology Corporation (US)
Location/Qualifiers
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100.0%; Pred. No. 2.5e-20;
tive 0; Mismatches 0;
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/mol_type="unassigned DNA"
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/nofe="2C7-SID"
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/mol_type="unassigned DNA"
/db_xref="taxon:46221"
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Sequence 2 from Patent WO0161024.
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                  linear
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100.0%; Pred. No. 2.5e-20;
iive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
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                    DNA
                                                                                                                                                                           Screening assay of Abeta-peptide
Patent: JP 2002531141-A 2 24-SEP-2002;
AVENTIS PHARMA DEUTSCHLAND GMBH
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HOECHST MARION ROUSSEL DE GMBH (DE)
Location/Qualifiers
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JP 200231141-A/2
24-8EP-2002
27-NOV-1999 JP 2000586944
07-DEC-1998 DB 198 56 261.6
GISELA PERAUS
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Sequence 9 from Patent DE19856261.
                 BD234590
Screening assay of Abeta-peptide
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                                             BD234590
BD234590.1 GI:33044360
JP 2002531141-A/2.
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1905. 4443
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RETESAINGNPSWHLADSPANGATCHSSSLDAREVI PWAAYKQALREAGDBFELRYR
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VLVSRIASWWALYLIADHLEBWIQENGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGM
TVAGVVLLGSLFSRK"
circular SYN 14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                           Pirtskhalaishvili,G., Shurin,G.V., Gambotto,A., Esche,C., Wahl,M., Yurkovetsky,Z.R., Robbine,P.D. and Shurin,M.R. Transduction of dendritic cells with Bcl-xL increases their resistance to prostate cancer-induced apoptosis and antitumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF060226 S771 bp DNA circular SYN 14-AUG
Eukaryotic expression vector pCR3.1mBCL-XL, complete sequence.
AF060226
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Direct Submission
Submitted (17-APR-1998) Vector Core Facility, University of
Pittsburgh, 300 Technology Drive, Pittsburgh, PA 15219, USA
Location/Qualifiers
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                                                                             1761 CAGCCATCTGTTGTTTGCCCCTCCCCGGGCCTTCCTTGAC 1801
                                                                                                                                                                                                                                                                                  Bukaryotic expression vector pCR3.1mBCL-XL
Bukaryotic expression vector pCR3.1mBCL-XL
other sequences; artificial sequences; vectors.
( bases 1 to 5771)
                                                          CAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGAC 101
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note="pCR3.1 reverse priming site"
1827. .2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="T7; priming site also"
                                                                                                                                                                                                                                                                                                                                                                                                                                       effect in mice
J. Immunol. 165 (4), 1956-1964 (2000)
20384788
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protein_id="AAC15799.1"
db_xref="G1:3108233"
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/note="ColE1"
complement(3082. .3870)
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'note="BALB/c form"
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AF060226
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IELDINSGKIIESFRPERFPPMSTFKVILCGAVLSRIDAGGEGLGRRIHYSQNDLVB
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKEITAFLHNMGDHVTRL
DRWEPELNBAIPNDRDTTMEVAMATTIRKLLTGELLTLASRQQLIDWWEADKYAGPL
LIRSALPAGRAGTADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATWDERNRQIA
EIGASLIKHW
5313. 5769
/note="f1"
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Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
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|mol type="unassigned DNA"
|bxref="taxon:32690"
|noTe="commercial plasmid"
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Novel plasmid dna vectors
Patent: WO 0151626-A 10 19-JUL-2001;
ELIM BIOPHARMACEUTICALS, INC. (US)
Location/Qualifiers
1. 6650
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US 6512094.
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AR278592
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synthetic construct
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Best Local Similarity 100.
Matches 101; Conservative
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AR563971
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
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Unclassified.
Loases 1 to 6082)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Ranger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler, W.T. and Henderson, R.A. Compositions and methods for the therapy and diagnosis of
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Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 101; Conservative 0; Mismatches 0;
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Pred. No. 2.5e-20;
                         cancer
Patent: US 6512094-A 535 28-JAN-2003;
Location/Qualifiers
1. .6082
/organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent: US 6329505-A 535 11-DEC-2001;
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Sequence 535 from patent US 6620922.
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Sequence 535 from patent US 6329505.
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100.0%; Score 101; D
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 101; Conservative 0; Mismatches
                                                                                                /mol_type="genomic DNA"
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Unclassified.
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AR400324
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KEYWORDS
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
Hepler,W.T. and Henderson,R.A. Compositions and methods for the therapy and diagnosis of prostate
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                5988 CAGCCATCTGTTGTTTGCCCCTCCCCGGGCCTTCCTTGAC 6028
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CAGCCATCTGTTTGCCCCTCCCCGTGCCTTCCTTGAC 101
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                                                                                                                                                                                                                                       Query Match 100.0%; Score 101; DB 6; Best Local Similarity 100.0%; Pred. No. 2.5e-20; Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 101; DB 6;
100.0%; Pred. No. 2.5e-20;
iive 0; Mismatches 0;
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                                                                     Patent: US 6620922-A 535 16-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: US 6630305-A 535 07-OCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 535 from patent US 6759515.
AR563971
AR563971.1 GI:53979022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AR405591 6082 bp D
Sequence 535 from patent US 6630305.
                                                                                                                                                                 /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
                                                                                         Location/Qualifiers
1. 6082
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1. .6082
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                                                                                                                                           organism="unknown"
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AR405591.1 GI:40154428
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Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: US 6759515-A 535 06-UUL-2004;
Location/Qualifiers
1. 6082
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                     Query Match 100.0%; Score 101; DB 6; Length 6082; Best Local Similarity 100.0%; Pred. No. 2.5e-20; Matches 101; Conservative 0; Mismatches 0; Indels 0;
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5988 CAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCATGAC 6028
                                                                                                         source
                                                                    JOURNAL
FEATURES
                                    TITLE
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Search completed: July 14, 2005, 14:03:32 Job time : 758.618 secs

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July 14, 2005, 04:35:42; Search time 142.398 Seconds (without alignments) 4198.742 Million cell updates/sec
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                   nucleic search, using sw model
                      Copyright
                                                                                   OM nucleic
                                                                                                                                 Run on:
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US-09-482-682-44\_COPY\_3930\_4030

1 ctcgagtctagagggcccgt......tcccccgtgccttccttgac 101 score: Sequence:

4390206 seqs, 2959870667 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Searched:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesegn2004as:\* genesegn2004bs:\* geneseqn2003ds: geneseqn2003cs: geneseqn2001bs:\* geneseqn2003as:\* geneseqn2003bs:\* N\_Geneseq\_16Dec04: geneseqn1990s:\* geneseqn2001as: geneseqn2002as: geneseqn2000s:\* geneseqn1980s:\* geneseqn2002bs: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

									¥											
Description	Adm76942 Multiple	Ads74212 Interleuk	Acc62322 Human NOV	Adc26320 Human NOV	Adm35637 Novel hum	Ado42484 Human NOV	Acc62251 Human NOV	Acc62237 Human NOV	Ado42324 Human NOV	Adj94793 Novel NOV	Adj94791 Novel NOV	Adj94795 Novel NOV	Adm41037 Cytomegal	Acd19336 cDNA enco	Acd19334 cDNA enco	Ada05887 Human NOV	Adn63050 Human NOV	Ado42504 Human NOV	Ado42500 Human NOV	Ado42506 Human NOV
a	ADM76942	ADS74212	ACC62322	ADC26320	ADM35637	AD042484	ACC62251	ACC62237	AD042324	ADJ94793	ADJ94791	ADJ94795	ADM41037	ACD19336	ACD19334	ADA05887	ADN63050	AD042504	ADO42500	AD042506
DB	12	13	8	10	12	12	œ	œ	12	10	10	10	12	10	10	œ	12	12	12	12
* Query Match Length DB	278	880	1340	1353	1353	1353	1420	1461	1733	1770	1772	1772	1782	1822	1822	2017	2017	2017	2017	2022
* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101
Result No.	-	~	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20

Adhl1353 Vertebrat Adb33520 Plasmid p Aaa75084 Complete Adb33528 Expressio	Adhl1417 Plasmid p Aa289476 Transgeni Aah74866 Nucleotid		Aad10237 Commercia Aah93828 Human pro Aas63921 Human pro		ADISSIS numan FSI Aad56212 Human AB- Aad56211 Human AB-	Aad56210 Human AB- Acc95456 Prostate Adb13985 Human pro	Adg26401 Human pro Add56213 Human AB- Aad56215 Human PSM Aad56214 Human AB-
2 ADH11353 10 ADB33520 3 AAA75084 10 ADB33528	ADH11417 AAZ89476 AAH74866	a ABX94356 4 AAD11615 12 ADM97787	5 AAD10237 4 AAH93828 4 AAS63921	4 AAH85142 5 ACAS9729	ABL95292 AAD56212 AAD56211	3 AAD56210 3 ACC95456 10 ADB13985	10 ADG26401 8 AAD56213 8 AAD56215 8 AAD56214
3482 3972 4291 5015	5082 5432 5650	5650 5731 5821	6050 6082 6082	6082	6082 6082 6082	6082 6082 6082	6082 6085 6094 6097
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0 100.0 100.0
101	101	101	101	101	101	101	1011
23 23 24 24	25 27 27	30 78 30 8	32 132	9.8 4.8 5.0	337 337 347	39 41 14	4 4 4 2 6 4 4

#### ALIGNMENTS

RESULT 1

host-vector system; microorganism; vaccine; delivery; immunisation; poultry; coccidiosis; antibacterial; plasmid; vector; gene; ds. Multiple cloning site of pYA3650 DNA sequence. ADM76942 standard; DNA; 278 BP 29-AUG-2003; 2003WO-US026883. 01-SEP-2002; 2002US-0407522P. (first entry) WO2004020643-A2. 11-MAR-2004. 03-JUN-2004 Synthetic. ADM76942; ADM76942 

(UNIW ) UNIV WASHINGTON. WPI; 2004-239203/22. Kong W; Curtiss R,

useful New host-vector system comprising a host chromosome, and a vector, as a vaccine for immunizing a poultry, preferably chicken, against coccidiosis.

Example 13; Fig 39; 201pp; English.

The present invention describes a host-vector system comprising a host chromosome, and a vector. The host-vector system comprises: (a) a host chromosome comprising: (i) an activatible control sequence that is activatible by an inducer; (ii) a sequence that encodes a repressor, where the sequence is operably-linked to the activatible control sequence; and (iii) at least one essential gene that encodes a polypeptide that is necessary for synthesis of a rigid layer of a cell wall of a prokaryote, and where the essential gene is inactivated; and (b) a vector

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promoter sequence, a site for insertion of a gene encoding a desired gene product and a polyadenylation sequence; (ii) a prokaryotic activator—
product and a polyadenylation sequence; (ii) a prokaryotic activator—
promoter sequence; (iii) at least one origin of replication (ori); (iv) a regulatable prokaryotic promoter, which is repressible by the repressor; (v) at least one essential gene that is necessary for synthesis of a right layer of a cell wall of a prokaryote; (vi) at least one continuator sequence; and (vi) at least one CpG sequence motif that enhances immunogenicity. Also described: (1) a microorganism comprising the host vector system; (2) a vaccine comprising the comprising the host vector system; (2) a vaccine comprising the continuation a evidence of a cellivery of a nucleic acid vector and/or a desired gene product to a evidency of a nucleic acid vector and/or a minimizing a poultry against coccidiosis. The host vector system has immunising a poultry against coccidiosis. The present sequence represents a nucleotide sequence which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCGAGTCTAGAGGGCCCGTTTAAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-2-Fc epsilon-gamma receptor transmembrane domain fusion gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                     9
 comprising: (i) a eukaryotic expression cassette comprising a eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer; gene therapy; vaccine; human; interleukin-2; cytokine; Fc epsilon-gamma receptor; receptor; IL-2tm2; gene; ds.
                                                                                                                                                                                                                                                                                                                                                            Score 101; DB 12; Length 278; Pred. No. 8.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (pos: 662, ... 664, aa. Xaa)
(pos: 743, ... 745, aa. Xaa)
(pos: 764, ... 766, aa. Xaa)
(pos: 800, ... 802, aa. Xaa)
(pos: 845, ... 847, aa. Xaa)
(pos: 878, ... 880, aa. Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 CAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGAC 226
                                                                                                                                                                                                                                                                                                                            Sequence 278 BP; 60 A; 82 C; 65 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CAGCCATCTGTTTGCCCCTCCCCCGTGCCTTCCTTGAC 101
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/transl_except= (p
/transl_except= (p
/transl_except= (p
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transl_except=
                                                                                                                                                                                                                                                                                                                                                             100.0%;
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/*tag= a
/product= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             partial
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
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                                                                                                                                                                                                                                                                                                                                                               Query Match
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ADS7421
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or stop codon: Xaa= any amino acid"

07-MAR-2003; 2003US-0452989P. 08-MAR-2004; 2004WO-US007012.

WO2004080404-A2

23-SEP-2004

(UTAH ) UNIV UTAH RES FOUND

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The present is that of IL-2tm2, a fusion gene comprising a human interleukin-2 (IL-2) gene joined to DNA encoding the transmembrane domain of Fc epsilon-gamma. IL-2tm2 is an example of a novel fusion gene of the invention for use in cancer gene therapy that comprises a cytokine gene and a transmembrane domain gene. It is derived from IL-2tm ADS74208 by removal of a FLAG sequence and extraneous amino acids, and was expressed from vector poDNA3.1(+/-). The fusion protein is expressed as a membrane-bound cytokine which may be displayed on the surface of mammalian tumour cells. It is believed that by inducing expression of IL-2 on the surface of tumour cells, IL-2 will activate tumour-infiltrating lymphocytes in circase activation of antigen-specific T cells and hence to result in destruction of tumour cells expressing those antigens. Murine spinale cell skin cancer RD995 cells transfected with IL-2tm fusion gene or CMV2b (empty expression vector) were implanted subcutaneously into CHMSO Gene proximity to tumour growth compared with IL-2tm fusion gene or call fusion gene showed reduced tumour growth compared with controls.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anorectic; immunosuppressive; cytostatic; antidiabetic; antidiffertility; heucostatic; antidiabetic; antidiffertility; heucoptective; noctropic; antiasthmatic; anti-HIV; immunomodulator; neuroprotective; noctropic; antiasthmatic; anti-HIV; immunomodulator; gene therapy; cardiomyopath; atherosclerosis; hypertension; scleroderm; congenital heart defect; aortic stenosis; valve disease; transplantation; prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer; fertility; haemophilia; hypercoagulation; graft versus host disease; idiopathic thrombocycopenic purpura; AIDS; bronchial asthma; anorexia; crohn's disease; multiple sclerosis; infectious disease; cancer; cancer; anderes anderia; AlDS; bronchial asthma; anorexia; cancer; cancer-associated cachexia; AlDs; infectious disease; cancer; cancer; cancer; disease; multiple sclerosis; infectious disease; cancer; cancer; disease; disease; disease; disease; multiple sclerosis; disease; parkinson's disease; munume disorder; haematopoietic disorder; dyslipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
                                                                                                                                        New fusion protein comprising human interleukin-2 and a transmembrane domain of a protein and enhancing the activation of cytotoxic tumorinfiltrating lymphocytes within tumor, useful in preparing a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                               Claim 17; SEQ ID NO 15; 64pp; English.
                         Mcgregor J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolic syndrome X; gene; ss.
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Best Local Similarity 100.
Matches 101; Conservative
                      Samlowski W, Adams NB,
                                                                      WPI; 2004-668877/65.
                                                                                                                                                                                                                      for treating cancer
                                                                                               P-PSDB; ADS74209
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Claim 20; Page 236; 460pp; English
                                                       2001US-0322636P.
2001US-0322781P.
2001US-0322816P.
                                                                                 2001US-0323519P.
2001US-0323631P.
2001US-0323636P.
                                                                                                                 2001US-0324990P.
2001US-0341144P.
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2002US-0361663P.
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                                                                                                     2001US-0324969P
                                                                                                                                            2002US-0377908P
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                                                                                                                                                                      17-JUL-2002; 2002US-0396412P
13-AUG-2002; 2002US-0403517P
                         09-SEP-2002; 2002WO-US028538
                                                                                                                                                                                   06-SEP-2002; 2002US-00236417
                                                                                                                                                                                                                                                  Pena CEA, Rieger DK,
Spaderna SK, Spytek KZ
Zerhusen BD, Zhong M;
                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                             WPI; 2003-313241/30.
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WO2003023001-A2.
                                                                                                   25-SEP-2001;
25-SEP-2001;
26-SEP-2001;
26-DEC-2001;
                                                       17-SEP-2001; 2
17-SEP-2001; 2
17-SEP-2001; 2
17-SEP-2001; 2
                                                                                  19-SEP-2001; 2
20-SEP-2001; 2
20-SEP-2001; 2
                                                                                                                              26-FEB-2002;
05-MAR-2002;
                                                                                                                                                       29-MAY-2002;
                                                                                                                                            03-MAY-2002;
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The present invention describes isolated human NOVX proteins, where X is

1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
hypotensive, dermatological, anoretic, antiatherosclerotic, cardiant,
antidabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
antidathmatic, metabolic, immunomodulator, neuroprotective, nootropic,
antidathmatic, metabolic, immunomodulator, neuroprotective, nootropic,
antidathmatic, metabolic, immunomodulator, neuroprotective, nootropic,
antiparkinsonian and antilipaemic activities, and can be used in gene
therapy. NOVX proteins are useful for treating or preventing a pathology
associated with the human disease. NOVX nucleic acides, proteins and
antibodies can be used in the treatment and diagnosis of cardiamyopathy,
atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
antibodies can be used in the treatment and diagnosis of cardiamyopathy
atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
antibodies and hyperplasia, prostate cancer, diabetes, metabolic
disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
hypercoagulation, idiopathic thrombocytopenic purpura, graft versus host
infectious disease, anorexia, cancer, associated cachexia, cancer,
alsease, AlDS, bronchial asthma, Crohn's disease, multiple sclerosis,
infectious disease, anorexia, cancer-associated cachexia, cancer,
Alzheimer's disease, parkinson's disease, immune disorders,
haematopoietic disease, parkinson's disease, immune disorders,
haematopoietic discases anorexes and probes for human NOVX
sequences, which are used in examples from the present invention.
Agee ML, Alsobrook JP, Anderson DW, Berghs C, Boldog FL;
Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
Crabtree J, Dipippo WA, Edinger SR, Eisen AJ, Ellerman K;
Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
Kekuda R, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
Malyankar UM, Miller CE, Ooi CE, Ort T, Paddigaru M, Patturajan M;
Pena CEA, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA;
Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human proteins and nucleic acid encoding the proteins, useful for diagnosis, treatment and prevention of disorders involving the human protein or nucleic acid e.g. cardiac and neurological disorders.
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Casman SJ;

Burgess CE,

Boldog FL,

Anderson DW, Berghs C,

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ABRS4277 represents a human trypsinogen protein given in comparison with the human NOV35b protein in the exemplification of the present invention
                                                                                                        1 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                 circulatory; haemopoietic; wasting; cancer; gene therapy; vaccine;
transgenic; human; gene; ds.
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                                                  Ouery Match
Best Local Similarity 100.0%; Score 101; DB 8; Length 1340;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 101; Conservative 0; Mismatches 0; Indels 0
                                 Sequence 1340 BP; 286 A; 350 C; 332 G; 370 T; 0 U; 2 Other;
                                                                                                                                                                   1236 CAGCCATCTGTTTGCCCCTCCCCGTGCCTTCCTTGAC 1276
                                                                                                                                                     61 CAGCCATCTGTTTGCCCCTCCCCCGTGCCTTCCTTGAC 101
                                                                                                                                                                                                                                        ADC26320 standard; DNA; 1353 BP.
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2001US-0305262P.
2001US-0306085P.
2001US-0306085P.
2001US-0308238P.
2001US-030823P.
2001US-030823P.
2001US-0313328P.
2001US-03133380P.
2001US-03133380P.
2001US-0313380P.
2001US-0313380P.
2001US-0345038P.
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2002US-0360830P.
2002US-0361133P.
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2002US-0363637P.
2002US-0372326P.
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                                                                                                                                                                                                                                                                                       18-DEC-2003 (first entry)
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                                                                                                                                                                                                                                                                                                               Human NOV34d DNA.
                                                                                                                                                                                                                                                                                                                                                                                                          WO2003004687-A2
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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(CURA-) CURAGEN CORP
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                                             27-AUG-2002;
03-SEP-2002;
09-SEP-2002;
31-OCT-2002;
02-DEC-2002;
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07-DEC-2001;
07-DEC-2001;
             23-AUG-2002;
26-AUG-2002;
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  23-AUG-2002;
                                    27-AUG-2002;
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                                                                                                                                         Berghs
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ADO42484
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                                                                                                                                                                                                                                                                                                                                                                            CTCGAGTCTAGAGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 1246
                                                                                                                                                                      The invention relates to a novel isolated NOV polypeptide. The polypeptide of the invention demonstrates cytostatic activity and may be used for determining the presence of, or predisposition to a disease associated with altered levels of expression of the polypeptide, including metabolic disorders, immune disorders, neurodegenerative disorders, circulatory diseases, haemopoietic disorders, wasting diseases and cancer. The polypeptide may also be utilised during gene therapy procedures, vaccine development and transgenic animal production. The current sequence is that of the human NOV DNA of the invention.
                                                                                                  New isolated NOVX polypeptide, useful for determining the presence of, or predisposition to a disease associated with altered levels of expression of the polypeptide, and for treating or preventing cancer.
                                                                                                                                                                                                                                                                                                                                                               1 CTCGAGTCTAGAGGGCCCGTTTAAACCCGGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 60
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                                                                                                                                                                                                                                                                                                                                         Gaps
  Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; gene; antidiabetic; anorectic; screening; insulin resistance;
Catterton E, Edinger S, Eisen AJ, Ellerman K, Gerlach V, Gc
Guo X, Jeffers M, Kekuda R, Li L, Malyankar UM, Miller CE;
Padigaru M, Patturajan M, Pena CEA, Rastelli L, Shenoy S;
Shimkets RA, Spaderna SK, Spytek KA, Stone DJ, Taupier RJ;
Vernet CAM, Voes EZ, Zhong M;
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                                                                                                                                                                                                                                                                                                                100.0%; Score 101; DB 10; Length 1353; 100.0%; Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                            Sequence 1353 BP; 324 A; 354 C; 356 G; 319 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       1247 CAGCCATCTGTTGTTTGCCCCTCCCCGGGCCTTCCTTGAC 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human NOVX gene for treating diabetes and obesity.
                                                                                                                                                                                                                                                                                                                                                                                                             CAGCCATCTGTTTGCCCCTCCCCGTGCCTTCCTTGAC 101
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                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                   Claim 20; SEQ ID NO 145; 478pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM35637 standard; DNA; 1353 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002US-0401315P.
2002US-0401316P.
2002US-0401627P.
2002US-0401788P.
2002US-0403620P.
2002US-0404649P.
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2002US-0405400P.
2002US-0405684P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 101, Conservative
                                                                    WPI; 2003-221607/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obesity; diabetes.
                                                                               P-PSDB; ADC26321
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20-AUG-2002;
20-AUG-2002;
22-AUG-2002;
22-AUG-2002;
23-AUG-2002;
23-AUG-2002;
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06-AUG-2002;
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07-AUG-2002;
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CTCGAGTCTAGAGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel isolated human nucleic acid molecules and their encoded proteins designated NOVX proteins. The nucleic acids and encoded polypeptides are useful in screening for compounds useful for treating conditions such as insulin resistance, obesity or diabetes. This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating conditions such as insulin resistance, obesity and diabetes
                                                                                                                                                                                                                                                                                                                                                                      Vernet CAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New NOVX nucleic acids and polypeptides, useful in identifying
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                                                                                                                                                                                                                                                                                                                                                                      Rieger DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence corresponds to one of the genes of the invention.
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100.0%; Pred. No. 1.3e-23;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      Ort I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 71; 325pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO42484 standard; cDNA; 1353 BP
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                                                                                                                                                                                                                                                                                                                                                                      Gno X,
; 2002US-0405687P.
; 2002US-0406538P.
; 2002US-0406130P.
; 2002US-04061310P.
; 2002US-0407919P.
; 2002US-0403466P.
; 2002US-0403466P.
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2001US-0336820P.
2001US-0338285P.
2001US-0338318P.
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Matches 101; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                      C, Ellerman K,
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2001US-0340981P.
2001US-0341346P.
2001US-0340390P.
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2002US-0360924P.
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2002US-0361028P.
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2002US-0361264P.
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2002US-0364181P.
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2002US-0373288P.
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2002US-0381004P.
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28-MAY-2002; 2002US-0383534P.
28-MAY-2002; 2002US-0383744P.
29-MAY-2002; 2002US-0383829P.
                                                                                                                                                                                                                                                                                                                                                                    29-MAY-2002; 2002US-0384024P.
02-JUL-2002; 2002US-0393332P.
06-AUG-2002; 2002US-0401315P.
07-AUG-2002; 2002US-0401788P.
                                        2001US-0339611P
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2001US-0341540P.
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2002US-0364978P.
                                                                                                                                   2001US-0342592P
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ELLERMAN K.
GANGOLLI E A.
GERLACH V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BERGHS C.
BOLDOG F L.
BURGESS C E.
CATTERTON E.
DIPIPPO V A.
EDINGER S R.
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                      11-DEC-2001;
11-DEC-2001;
11-DEC-2001;
12-DEC-2001;
14-DEC-2001;
14-DEC-2001;
14-DEC-2001;
14-DEC-2001;
14-DEC-2001;
14-DEC-2001;
14-DEC-2001;
14-DEC-2001;
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01-FEB-2002; 2
01-FEB-2002; 2
26-FEB-2002; 2
26-FEB-2002; 2
27-FEB-2002; 2
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13-MAR-2002; 2
13-MAR-2002; 2
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                                                                                                         17-DEC-2001;
17-DEC-2001;
18-DEC-2001;
20-DEC-2001;
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28-FEB-2002;
28-FEB-2002;
28-FEB-2002;
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(EDIN/)
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(GANG/)
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The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The invention also relates to antibodies specific to the NOVX polypeptides. The polypeptides, polynucleotides and antibodies are useful for manufacturing a medicament for treating a syndrome associated with a human disease, such as a pathology associated with the NOVX polypeptide. The sequences are useful for diagnosing, treating or preventing a NOVX-associated disorder, e.g., cancer, atheroscierosis, diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host disease, scleroderma, hypertension, haemophilia, idiopathic thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia, obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated cachexia, multiple sclerosis or fertility. The nucleic acids may be used as hybridisation probes, in chromosome mapping, in tissue typing, in preventive medicine or in pharmacogenomics. This sequence represents a human NOVX polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1187 CTCGAGTCTAGAGGGCCCGTTTAAACCGGCTGATCAGCCTCGACTGTGCCTTTGTAGTTGC 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human NOVX polypeptides and nucleic acid molecules, useful for diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
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B, Dipippo VA, Edinger SK, Eisen A;

EA, Gerlach V, Gorman L, Rothberg BG, Guo
en Y, Ji W, Kekuda R, Khramtsov NV;

Y DM, Li L, Macdougall JR, Miller CE, Ort T
an M, Pena CEA, Peyman JA, Rieger DK;

Y SG, Smithson G, Spaderna SK, Spytek KA;

Vernet CAM, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 101; DB 12; Length 1353; 100.0%; Pred. No. 1.3e-23; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1353 BP; 324 A; 355 C; 356 G; 318 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CAGCCATCTGTTTGCCCCTCCCCCGTGCCTTCCTTGAC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 333; 610pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Burgess CE, Catterton E, Dij
Ellerman K, Gangolli EA, Ge-
Herrmann JL, Halvorsen Y, J.
Laromenn Lepley DM, L.
Padigaru M, Patturajan M, Pr
Rothenberg ME, Shenoy SG, SY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                                                            ROTHENBERG M. E. SHENOY S. G. SMITHSON G. SPADERNA S. K. SPYTEK K. A. STONE D. J. TAUFIER R. J. TAUFIER R. J. VERNET C. A. M. VOSS E. Z. ZHONG M.
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                               LAROCHELLE W J.
LEPLEY D M.
                                                                  LI L.
MACDOUGALL J R.
MILLER C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taupier RJ,
               KHRAMTSOV N V.
                                                                                                                              PADIGARU M.
PATTURAJAN M.
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P-PSDB; ADO42485.
                                                                                                                                                               PENA C E A.
PEYMAN J A.
RIEGER D K.
 KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scleroderma.
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(VERN/)
(VOSS/)
(ZHON/)
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                                             (LEPL/)
(LILL/)
(MACD/)
(MILL/)
                                                                                                                              (PADI/)
(PATT/)
(PENA/)
(PEYM/)
(RIEG/)
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(SHEN/)
(SMIT/)
(SPAD/)
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(STON/)
                                 LARO/)
셤
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1247 CAGCCATCTGTTGTTTTGCCCCTCCCCCGTGCCTTCCTTGAC 1287

ROTHBERG B G. GUO X S. HERRMANN J L. HALVORSEN Y.

GERL/) GORM/) (HERR/) (HALV/) (JIWW/)

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Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological; anorectic; immunosuppressive; cytostatic; antidabetic; antiinfertility; haemostatic; antiinflammatory; antiasthmatic; anti-HIV; immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic; gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma; congenital heart defect; aortic stenosis; bypertension; scleroderma; tuberous sclerosis; obesity; congenital adrenal hyperplasis; diabetes; prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer; fertility; haemobolytopenic purpura; AIDS; bronchial asthma; anorexia; diopathic thrombocytopenic purpura; AIDS; bronchial asthma; anorexia; cancer associated cacheria; infectious disease; cancer; cancer; haematopoletic disorder; disease; parkinson's disease; immune disorder; haematopoletic disorder; dyslipidaemia; metabolic syndrome X; gene; ss.
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Burgess CE, Casman SJ, Catterton E, Chant JS, Chaudhuri A;
Crabtree J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K;
Gangolli EA, Gerlach VL, Giot L, Gorman L, Guo X, Gusev VY, Ji W;
Kekuda R, Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
Malyankar UM, Miller CE, Ooi CE, Ort T, Padigaru M, Patturajan M;
Pena CEA, Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA;
Spaderna SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ
Zerhusen BD, Zhong M;
                                                                                                                                    Human NOV3h encoding cDNA SEQ ID NO:31
                                 ACC62251 standard; cDNA; 1420 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-2001; 2001US-0322781P.
17-SEP-2001; 2001US-0322816P.
17-SEP-2001; 2001US-0322817P.
19-SEP-2001; 2001US-0323519P.
20-SEP-2001; 2001US-0323631P.
25-SEP-2001; 2001US-032365P.
25-SEP-2001; 2001US-032469P.
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14-DEC-2001; 2001US-0341144P.
26-FEB-2002; 2002US-0359599P.
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2002US-0383863P.
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                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003023001-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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17-SEP-2001;
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                                                                   ACC62251;
RESULT 7
                 ACC62251
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The present invention describes isolated human NOVX proteins, where X is

1 to 42. ACC62236 to ACC62345 encode the human NOVX proteins given in
ARS42167 to ABEA4276. NOVX sequences have antiatheroscelerotic, cardiant,
hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
antidiabetic, metabolic, immunomodulator, neuroprotective, notropic,
antidathisonian and antilipaemic activities, and can be used in gene
therapy. NOVX proteins are useful for treating or preventing a pathology
associated with the human disease. NOVX nucleic acids, proteins and
antibodies can be used in the treatment and diagnosis of cardiomyopathy,
atherosclerosis, hypertension, congenital heart defects, aortic stenosis,
congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
congenital adrenal hyperplasia, prostate cancer, fertility, haemophilia,
congenital ion, idiopathic thrombocytopenic purpura, graft versus host
disease, AlDS, bronchial asthma, crohn's disease, multiple sclerosis,
infectious disease, anorexia, cancer-associated cachexia, cancer,
congenier's disease, Parkinson's disease, immune disorders,
conferences, which are used in examples from the present invention.

Alzheimer's disease, Parkinson's disease, immune disorders,
conferences, which are used in examples from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; NOVX; antiatherosclerotic; hypotensive; cardiant; dermatological; anorectic; immunosuppressive; cytostatic; antidiabetic; antinfertility; haemostatic; antinflammatory; antiasthmatic; anti-HIV; immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic; antilipaemic; gene therapy; cardiomyopathy; atherosclerosis; hypertension; scleroderma; congenital heart defect; aortic stenosis; valve disease; transplantation; tuberous sclerosis; openital adrenal hyperplasis; diabetes; prostate cancer; metabolic disorder; neoplasm; lymphoma; uterus cancer; fertility; haemophilia; hypercoagulation; graft versus host disease; fidiopathic thrombocycopenic purpura; AIDS; bronchial asthma; anorexia; crohn's disease; multiple sclerosis; infectious disease; cancer; cancer; haematopoietic disorder; disease; parkinson's disease; multiple sclerosis; infectious disease; cancer; and the propositio disorder; dyslipidaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARE 4277 represents a human trypsinogen protein given in comparison with
the human NOV35b protein in the exemplification of the present invention
Novel human proteins and nucleic acid encoding the proteins, useful for diagnosis, treatment and prevention of disorders involving the human protein or nucleic acid e.g. cardiac and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1420 BP; 326 A; 392 C; 338 G; 364 T; 0 U; 0 Other;
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                                                                                                          Claim 20; Page 111-112; 460pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NOV1b encoding cDNA SEQ ID NO:3.
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Matches 101; Conservative
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Voss EZ;

WPI; 2003-313241/30. P-PSDB; ABR54182.

Gusev VY, Ji W;

9

Gaps

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Indels

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Score 101; DB 8; Pred. No. 1.3e-23; 0; Mismatches 0;

.08;

Length 1461;

us-09-482-682-44\_copy\_3930\_4030.rng

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CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 1348
  ABRS4277 represents a human trypsinogen protein given in comparison with
the human NOV35b protein in the exemplification of the present invention
                                                                                                                                                                                                  CTCGAGTCTAGAGGGCCCGGTTTAAACCCGGTGATCAGCCTCGACTGTGCCTTCTAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; NOVX; gene; 88; cancer; atherosclerosis; diabetes;
Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scleroderma; hypertension; haemophilia;
idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia;
                                                                  Sequence 1461 BP; 325 A; 448 C; 386 G; 302 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer-associated cachexia; multiple sclerosis; fertility.
                                                                                                                                                                                                                                                                                                             1349 CAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGAC 1389
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2001US-0338989P.
2001US-0339022P.
2001US-0339314P.
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2001US-0339517P.
2001US-0339611P.
2001US-0340981P.
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2001US-0342592P.
2001US-0344903P.
                                                                                                                                  100.0%;
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2001US-0341477P.
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2002US-0353288P.
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2002US-0360924P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2004 (first entry)
                                                                                                           Query Match
Best Local Similarity 100.
Matches 101; Conservative
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10-DEC-2001;
11-DEC-2001;
11-DEC-2001;
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27-FEB-2002;
28-FEB-2002;
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L-DEC-2001;
2-DEC-2001;
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1 to 42. ACG62236 to ACC62345 encode the human NOVX proteins given in
ABR54167 to ABR54276. NOVX sequences have antiatherosclerotic, cardiant,
hypotensive, dermatological, anorectic, immunosuppressive, cytostatic,
antidiabetic, antiinfertility, haemostatic, antiinflammatory, anti-HIV,
antisathmatic, metabolic, immunomodulator, neuroprotective, nootropic,
antipatkinsonian and antilipaemic activities, and can be used in gene
therapy. NOVX proteins are useful for treating or preventing a pathology
associated with the human disease. NOVX nucleic acids, proteins and
antibodies can be used in the treatment and diagnosis of cardiomyopathy,
athorocalerosis, hypertension, congenital heart defects, aortic stenosis,
valve disease, tuberous sclerosis, scleroderma, obesity, transplantation,
congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic
disorders, neoplasm, lymphoma, uterus cancer, fertility, haemophilia,
hyperparion, idiopathic thrombocytopenic purpura, graft versus host
disease, AlDS, bronchial asthma, crohw's disease, multiple sclerosis,
infectious disease, anorexia, cancer-associated cachexia, cancer,
Alzehimer's disease, Parkinson's disease, immune disorders,
harmonicalienticalison's disease, immune disorders,
harmonicalienticalison's disease, immune disorders,
harmonicalienticalisorders, dyslipidaemias, and probes for human NOVX
sequences, which are used in examples from the present invention.
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E, Caman SJ, Catterton E, Chant JS, Chaudhuri A;
J, Dipippo VA, Edinger SR, Eisen AJ, Ellerman K,
KA, Gerlach VL, Giot L, Gorman L, Guo K, Gusev VY, Ji W;
Khramtsov NV, Leach MD, Lepley DM, Li L, Liu X;
VM, Miller CE, Ooi CE, Ort T, Padigaru M, Patturajan M;
Rieger DK, Rochenberg ME, Shenoy SG, Shimkets RA;
SK, Spytek KA, Taupier RJ, Twomlow N, Vernet CAM, Voss EZ,
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diagnosis, treatment and prevention of disorders involving the human
protein or nucleic acid e.g. cardiac and neurological disorders.
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2001US-0323636P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-313241/30.
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WO2003023001-A2
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Malyankar UM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burgess CE, C
Crabtree J, D
Gangolli EA,
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26-SEP-2001;
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05-MAR-2002;
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                                           20-MAR-2003
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Pena CEA,

Agee ML,

Guo XS

Ort T;

cancer,

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The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The invention also relates to antibodies specific to the encoding them. The polypeptides, polynucleotides and antibodies are useful for manufacturing a medicament for treating a syndrome associated with a human disease, such as a pathology associated with the NOVX polypeptide. The sequences are useful for diagnosing, treating or preventing a NOVX-associated disorder, e.g., cancer, atheroscierosis, diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host disorder, an hypertenaton, hemophilia, idiopathic thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia, obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated cachexia, multiple sclerosis or fertility. The nucleic acids may be used a hybridisation probes, in chromosome mapping, in tissue typing, in preventive medicine or in pharmacogenomics. This sequence represents a human NOVX polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1580 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 60
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                                                                                                                                                           New human NOVX polypeptides and nucleic acid molecules, useful for diagnosing, preventing or treating NOVX-associated disorder, e.g. cance atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
Jerlach V, Gorman L, Rothberg L.
Ji W, Kekuda R, Khramtsov NV;
Li L, Macdougall JR, Miller CE, Ort
Pena CEA, Peyman JA, Rieger DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 101; DB 12; Length 1733; 100.0%; Pred. No. 1.4e-23; tive 0; Mismatches 0; Indels 0;
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                                                        M, Pena CEA, Peyman JA, Riege
SG, Smithson G, Spaderna SK, S
Vernet CAM, Voss EZ, Zhong M;
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                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 173; 610pp; English.
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                Ellerman K, Gangolli EA, G
Herrmann UL, Halvorsen Y,
Larochelle WJ, Lepley DM,
Padigaru M, Patturajan M,
Rothenberg ME, Shenoy SG,
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Best Local Similarity 100.0
Matches 101; Conservative
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                                                                                                                   WPI; 2004-268786/25.
P-PSDB; ADO42325.
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Edinger SR, Eisen A;
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3, Catterton E, Dipippo VA,
                                                     28-FEB-2002; 2002US-0361254P.
05-MAR-2002; 2002US-0361264P.
05-MAR-2002; 2002US-0361210P.
05-MAR-2002; 2002US-0364181P.
13-MAR-2002; 2002US-0364238P.
15-MAR-2002; 2002US-0364978P.
15-MAR-2002; 2002US-036998P.
17-APR-2002; 2002US-036998P.
17-APR-2002; 2002US-036998P.
16-MAY-2002; 2002US-036998P.
16-MAY-2002; 2002US-036998P.
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29-MAY-2002, 2002US-0384829P.
02-MAY-2002, 2002US-0384024P.
02-MG-2002, 2002US-038432P.
07-MG-2002, 2002US-0401315P.
07-AUG-2002, 2002US-0401315P.
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2002US-0405400P.
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28-MAY-2002; 2002US-0383744P.
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SHENOY S G.
SMITHSON G.
SPADERNA S K.
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KHRAMTSOV N V.
LAROCHELLE W J.
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MACDOUGALL J R.
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ELLERMAN K.
GANGOLLI E A.
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HERRMANN J L.
HALVORSEN Y.
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PADIGARU M.
PATTURAJAN M.
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BOLDOG F L.
BURGESS C E.
CATTERTON E.
DIPIPPO V A.
EDINGER S R.
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PEYMAN J A.
RIEGER D K.
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GORMAN L.
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TAUPIER R J.
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23-AUG-2002;
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Burgess CE,
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(ALSO/)
(ANDE/)
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(BOLD/)
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(SPYT/)
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Gaps

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WO2003040325-A2.

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Agee ML, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chant Us; Chaudhuri A, Dipippo VA, Edinger SR, Eisen A, Ellerman K; Chaudhuri BA, Gorman L, Gerlach VL, Ji W, Kekuda K, Khramtsov NV; ii L. Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I; ii L. Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I;
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2001US-0348283P
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                             05-NOV-2002;
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29-NOV-2001;
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04-DEC-2001;
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28-MAY-2002;
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                                                  06-NOV-2001;
              15-MAY-2003
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New isolated NOVX polypeptides and polynucleotides, useful for

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The invention relates to novel isolated polypeptides, mature forms of these, or a sequence that is at least 95 % identical to, or having one or more conservative amino acid substitutions in the polypeptides. The material acid molecules and antibodies are useful in the polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a manufacture of a medicament for treating a syndrome associated with a manufacture of a medicament for treating a syndrome associated with a molecules, polypeptides and antibodies are useful for treating.

CC preventing or diagnosing diseases such metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodespenerative disorders, Alzheimer's disease, configuration of disorders, inflammatory skin disorders, asthma, and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. meurogenesis, cell differentiation, cell proliferation, cell proliferation, cell proliferation, cententiation of antibodies that bind immunospecifically to NoVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. This sequence typing, preventive medicine, and pharmacogenomics. This sequence corresponds to the gene encoing one of the NoVX polypeptides of the
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preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1770 BP; 486 A; 427 C; 425 G; 432 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1665 CAGCCATCTGTTGTTTTGCCCCTCCCCCGTGCCTTCCTTGAC 1705
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                                                                                                 Claim 20; SEQ ID NO 21; 800pp; English.
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Matches 101, Conservative
                      osteoarthritis, obesit asthma, or infections.
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2001US-0331641P
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2001US-0334526P.
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# (CURA-) CURAGEN CORP.

Agee ML, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chant JS; Chaudhuri A, Dipippo VA, Edinger SR, Eisen A, Elleman K, Gangolli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NV; Li L, Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I; Ooi CE, Ort T, Padigaru M, Patturajan M, Rastelli L, Rieger DK; Rothenberg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupler RJ; Vernet CAM, Zerhusen BD, Zhong M;

### WPI; 2003-441551/41. P-PSDB; ADJ94792.

New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.

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The invention relates to novel isolated polypeptides, mature forms of these, or a sequence that is at least 95 % identical to, or having one or more conservative amino acid substitutions in the polypeptides. The more conservative amino acid substitutions in the polypeptides. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a conservative preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders (osteoarthritis), hematopoietic disorders, inflammatory skin disorders, asthma, and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, call differentiation, call proliferation, call proliferation, call proliferation, changing and angiogenesis, in gene therapy, in the corresponds to the plant probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The nucleic acids are trither used as hybridization probes, in chromosome mapping, tissue corresponds to the gene encoing one of the NOVX polypeptides of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTCGAGTCTAGAGGGCCCGGTTTAAACCCGGTGATCAGCCTCGACTGTGCCTTCTAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds, gene, antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, virucide, antibacterial, fungicide, protozoacide, nostropic, neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, antiarthritic, antialfammatory; metabolic disorder, diabetes, obesity; infectious disease; anorexia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1772 BP; 486 A; 428 C; 427 G; 431 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1666 CAGCCATCTGTTTGCCCCTCCCCGGGCCTTCCTTGAC 1706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 101; DB 10;
; Pred. No. 1.4e-23;
0; Mismatches 0;
                 Claim 20; SEQ ID NO 19; 800pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ94795;
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invention relates to novel isolated polypeptides, mature forms of

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39008P
                                                                                                  2002US-0354393P.
                                                                                                      :002US-0354409P.
                                                                                                               2002US-0360148P.
                                                                                                                                           2002US-0364181P.
                                                                                                                                                                             2002US-0401594P
                                                                                                                                                                                                                  2002US-00287226
                                                                                          :002US-03
                                                                                              :002US-03
                       20-NOV-2001;
21-NOV-2001;
27-NOV-2001;
                                                                        10-DEC-2001;
10-DEC-2001;
                   20-NOV-2001;
                                    28-NOV-2001;
                                        28-NOV-2001;
                                            29-NOV-2001;
                                                     NOV-2001;
                                                        04-DEC-2001;
04-DEC-2001;
                                                                 07-DEC-2001;
                                                                                 11-DEC-2001;
                                                                                     01-FEB-2002;
01-FEB-2002;
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                                                                                                          -FEB-2002;
                                                                                                                                           13-MAR-2002;
                                                                                                                                                                             07-AUG-2002;
       09-NOV-2001;
                                                30-NOV-2001;
                                                                                              04-FEB-2002;
                                                                                                              27-FEB-2002;
                                                                                                                           05-MAR-2002;
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# (CURA-) CURAGEN CORP.

Agee ML, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chant JS; Chaudhuri A, Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khramtsov NV; Li L, Malyankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I; Ooi CE, Ort T, Padigaru M, Patturajan M, Rastelli L, Rieger DK; Rothenberg ME, Shenoy SG, Spaderna SK, Spytek KA, Taupier RJ; Vernet CAM, Zerhusen BD, Zhong M;

WPI; 2003-441551/41.

P-PSDB; ADJ94796.

New isolated NOVX polypeptides and polymucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections

Claim 20; SEQ ID NO 23; 800pp; English

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these, or a sequence that is at least 95 % identical to, or having one or more conservative amino acid substitutions in the polypeptides. The polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a manufacture of a medicament for treating a syndrome associated with a molecules, polypeptides and antibodies are useful for treating, the manufacture of identication and iseases, preferably a NOVX-associated disorders, diabetes, preventing or diagnosing diseases such metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders (osteoarthritis), hematopoietic disorders, inflammatory skin disorders, asshma, and various dyslipidemias. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or calcinate or calcinate or calcinate or thibit e.g. neurogenesis, calcinate and anglogenesis, in gene therapy, in the corresponds to the gene encoing one of the NOVX polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1606 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTCGAGTCTAGAGGGCCCGTTTAAACCCGGTGATCAGCCTCGACTGTGCCTTCTAGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1772 BP; 486 A; 428 C; 427 G; 431 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caeccarcretristrisccccrcccccrgccrrccrrgac 1706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 10;
100.0%; Pred. No. 1.4e-23;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytomegalovirus nucleotide sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thompson SC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-2002; 2002US-0411790P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
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ACD19334;
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                                                                                                                                                                                                                                                                                                                      1486 CICGAGICTAGAGGCCCGITITAAACCCGCIGAICAGCCTCGACIGIGCCTICIAGIIGC 1545
                                  replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metabolism-related disease, obserity, central nervous system disorder; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; schizophrenia; depression; autoimmune disorder; inflammatory disorder; psoriasis, allergy; lupus erythematosus; asthma; concer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; brain cancer; melanoma; liver disease; inver cirrhosis; stroke; infection; gene; ss.
                                                                                                                                                                                                                                                                                             1 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTTCTAGTTGC 60
                                                                                                                                                                 sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                     Gaps
                         The present invention describes a method for engrafting foreign
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                                                                                                                                                                                                                                           Score 101; DB 12; Length 1782; Pred. No. 1.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; NOV; gene therapy; endocrine related disease; diabetes;
                                                                                                                                                                                                                   Sequence 1782 BP; 458 A; 399 C; 451 G; 474 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                             1546 CAGCCATCTGTTGTTTGCCCCTCCCCGTGCCTTCCTTGAC 1586
                                                                                                                                                                                                                                                                                                                                               61 CAGCCATCTGTTGTTTGCCCCTCCCCGTGCCTTCCTTGAC 101
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                                                                                                                                                                                                                                                                    0; Mismatches
Disclosure; SEQ ID NO 5; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding novel human protein #16.
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2001US-0318430P.
2001US-0322636P.
2001US-0322781P.
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2001US-0323636P.
2001US-0324969P.
2001US-0325091P.
                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACD19336 standard; cDNA; 1822
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2001US-0323519P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-2002; 2002WO-US028539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                    Matches 101; Conservative
                                                                                                                                                                                                                                                         Local Similarity
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25-SEP-2001;
25-SEP-2001;
                                                                                                                                                                                           specification
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17-SEP-2001;
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19-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACD19336;
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
ACD19336
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The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, polypeptide, nucleic acid and antibody are useful as theraticularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polymucleotide is useful for treating endocrine/ metabolism-related disease (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, cepilepsy, multiple sclerosis, schizophrenia or depression), autoimmune asthma, inflammatory bowel disease, rheumatoid arthritis or asthma, inflammatory bowel disease, rheumatoid arthritis or or torstate or brain cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers (e.g. colon, lung, liver, breast, ovarian, cirrhosis), lung diseases (emphyema or obstructive pulmonary disease), haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional applications, and for monitoring the effects of drugs during clinical applications, and for monitoring the effects of drugs during clinical trials. This sequence encodes a novel human NOV protein
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                                                                                                                                                                                                                                                       , Gorman L, Li L, Anderson DW, Zhong M;
Ellerman K, Bergis C, Rothenberg ME, Guo X;
Catterton E, Kekuda R, Ji W, Miller CE;
Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
Burgess CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX) and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding novel human protein #14.
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26-SEP-2001; 2001US-0324990P.
17-APR-2002; 2002US-0373212P.
                                                                                       06-SEP-2002; 2002US-00236177
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                                                                                                                                                                                                                                                                Patturajan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                       Vernet CAM,
                                                                                                                                                                                                                                                                                                                                      Shimkets RA, Leach MD,
Rieger DK, Taupier RJ,
Lepley DM, Edinger SR,
                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-313242/30.
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inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; breast cancer; ovarian cancer; prostate cancer; breast cancer; breast cancer; broatn cancer; mean cancer; m
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Zhong M; , Gorman L, Li L, Anderson DW, Zhong M; Bllerman K, Berghs C, Rothenberg ME, Guo X Catterton E, Kekuda R, Ji W, Miller CE; Shency SG, Liu X, Padigaru M, Alsobrook JP; Burgess CE;

New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX) and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.

## Claim 20; Page 118-119; 586pp; English

The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polymucleotide is useful for treating endocrine/ metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. posriasis, allergy, lupus erythematosus, asthma inflammatory bowel disease, rheumatoid arthritis or stemmatory bowel disease, rheumatoid arthritis or osteoarthrilis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (emphysema or obstructive pulmonary disease), these are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications, and for monitoring the effects of funge during clinical analysis of warming contains them as a contains and associated to the contains and associated to the contains and associated to the contains and contains the con This sequence encodes a novel human NOV protein

Sequence 1822 BP; 415 A; 552 C; 500 G; 355 T; 0 U; 0 Other;

100.0%; Score 101; DB 10; Length 1822; 100.0%; Pred. No. 1.4e-23;

17-SEP-2001; 2001US-0322817P. 19-SEP-2001; 2001US-0323519P. 20-SEP-2001; 2001US-0323631P. 20-SEP-2001; 2001US-0323636P. 17-SEP-2001; 2001US-0322781P 25-SEP-2001; 2001US-0324969P. 25-SEP-2001; 2001US-0325091P. 26-SEP-2001; 2001US-0324990P. 2002US-0373212P 06-SEP-2002; 2002US-00236177 Spytek KA, Patturajam..., Gerlach VL, Vernet CAM, F Shimkets RA, Leach MD, C Rieger DK, Taupier RJ, S (CURA-) CURAGEN CORP. WPI; 2003-313242/30. Query Match Best Local Similarity P-PSDB; ABO14641. 

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pgn2c.pk001.h10.f Chicken Lymphoid cDNa library (pgn2c) Gallus gallus cDNA clone pgn2c.pk001.h10.f 3'end of pat.pk0008.d125',
                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

(bases 1 to 400)
Flinin, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De Koeyer, D., Audy, P., Goyer, C., Li, X.-O., Wang-Pruski, G. and Regan, S. Generation of ESTs from stolon tissues of potato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI; Site_2: XhoI; supplier: Developmental series. Plants from pathogen-free Solanum tuberosum var. Shepody, clone 1756, nuclear stok were grown in a screenhouse under natural conditions. RNA was isolated from stolon tissue."
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Morgan, R.W. and Burnside, J.
Chicken ESTB from lymphoid tissue- 3'
Unpublished (2004)
Contact: Robin W. Morgan
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/mol_type="mRNA"
                                                                                                                                                                                                                                                           Contact: Barry Flinn
The Canadian Potato Genome Project
921 College Hill Rd, Fredericton,
Email: bflinn@bioatlantech.nb.ca
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Tel: 302-831-1341
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Location/Qualifiers
                        Solanum tuberosum (potato)
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/clone_lib="Swollablescript II SK(+) XR; Site_1: EcoRI;
/note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; supplier: Developmental series. Plants from pathogen-free Solanum tuberosum var. Shepody, clone 1756, nuclear stock were grown in a screenhouse under natural conditions. RNA was isolated from swollen stolon issue, 3-10mm in length, which was cut from the tip, to the base
                                                                     86 CTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGC 145
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterias, lamidas, Solanales, Solanaceae, Solanum.
1 (bases 1 to 605)
Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M.,
DeKoeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and
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19817 Swollen Stolon Solanum tuberosum cDNA, mRNA sequence
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The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 629, CANADA
Email: bflinn@bloatlantech.nb.ca
Clones can be requested from BioAtlantech via
bflinn@bloatlantech.nb.ca
Seq primer: T3
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                                                                                                                                            61 CAGCCATCTGTTGTTTGCCCCTCCCCGTGCCTTCCTTGAC 101
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Shepody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Solanum tuberosum (potato)
                                                                                                                                                                                                                                                                                                                                                                                    CK719567.1 GI:42511281
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  101; Conservative
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REFERENCE AUTHORS

KEYWORDS SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to S21, Wirtz, M.K., Samples, Xu, H., Severson, T. and Acott, T.S. Expression Profile and Genome Location of cDNA Clones from an
                                                                                                                                                                                                                                                BM887817 521 bp mRNA linear EST 08-MAR-
TM553 Human Trabecular Meshwork cDNA library Homo sapiens cDNA
clone 122060 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: wirtzm@ohsu.edu
Seg primer: T7 Reverse
High quality sequence scop: 350.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="122060"
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Best Local Similarity 9
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BM887817
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Wirtz,M.K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.
Wirtz,M.K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.
Infant Human Trabecular Meshwork Library
Unpublished (2002)
                                                                                     /tissue_type="thymus, bursa, spleen, PBL, bone marrow"
/lab host="B.coli EMDH108"
/clone lib="Chicken Lymphoid cDNA library (pgn2c)"
/note="Vector: pCMVSPORT 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TM108 Human Trabecular Meshwork cDNA library Homo sapiens cDNA clone 104447 5', mRNA sequence.
BM888450
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Cell_type="trabecular meshwork"
dev_stage="2 week to 2 year old infants"
lab_host=="70P10F" "
/clone_lib="Human Trabecular Meshwork cDNA library"
                           /clone="pgn2c.pk001.h10.f 3'end of pat.pk0008.d12"
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wirtz MK
Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-4698
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                                                                                                                                                                                                                                                               Length 295;
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                                                                                                                                                                                                                                                            74.3%; Score 75; DB 7; Length 295
94.0%; Pred. No. 6.8e-13;
ive 0; Mismatches 5; Indels
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94.0%; Pred. No. 7.5e-13;
ive 0; Mismatches 5; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 bp
   /db xref="taxon:9031"
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Seg primer: T7 Reverse.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="104447"
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                                                                                                                                                                                                                                                                                                                         78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .519
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Best Local Similarity
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Best Local Simi
Matches 78;
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                                                                                                                                                                                                                                                                                                                      Matches
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TITLE
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BM888450
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/clone lib="Human Trabecular Meshwork cDNA library"
/note="Wector: pcDNA3; Site 1: EcoRI; Site 2: EcoRI; Human cdNA library made from mRNA isolated from rabecular meshwork cells established fom eyes from 6 individuals, ages 2 weeks to 2 years. Cells were harvested at passages 3 through 6. Invitrogen made a unidirectional cDNA library from the mRNA from the frozen cells using a pcDNA3 vector and TPO10F'' host cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                             Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-6875
Fax: 503-494-6875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="eye"
| coll_type="trabecular meshwork"
|dev_stage="trabecular meshwork"
|dev_stage="trapecular meshwork"
|lab_host="Toplu6""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.3%; Score 75; DB 5; Length 521 larity 94.0%; Pred. No. 7.5e-13; Conservative 0; Mismatches 5; Indels
Infant Human Trabecular Meshwork Library Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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CR154962.1 GI:49933807
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78

Gaps

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CR074510 132 bp DNA linear GSS 05-JUL-2004 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP255d22, genomic survey sequence.
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OST350781 Mus musculus 1295v/Ev Mus musculus cDNA clone OST350781,
ages 2 weeks to 2 years. Cells were harvested at passages 2 through 6. Invitrogen made a unidirectional cDNA library from the mRNA from the frozen cells using a pcDNA3 vector and TPO10P'' host cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (baese I to 132) Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A. Davies, M. Hinxton, Cambridgeshire, Direct Submission Content (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 329)
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                                                                                                                               Length 534;
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                                                                                                                                                                       Indels
                                                                                                                               72.7%; Score 73.4; DB 5;
92.8%; Pred. No. 2.4e-12;
live 0; Mismatches 6;
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Pred. No. 2.2e-12;
0; Mismatches 8;
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GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="MHPP255d22"
/clone_lib="MHPP"
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Mus musculus (house mouse)
Mus musculus
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90.7%;
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Best Local Similarity 90.77
Best Local Similarity 70.77
                                                                                                                                                   Best Local Similarity 92.8
Matches 77; Conservative
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E 1 (Dasses 1 to 534)

S I (Dasses 1 to 534)

Wirtz,M.K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.

Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library

L Unpublished (2002)

Contact: Wirtz MK

Glaucoma Genetics Lab

Oregon Health Sciences University

3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA

Tel: 503-494-4698

Fax: 503-494-6875

Email: wirtzmedohau.
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/cell type="trabecular meshwork"
/dev_stage="2 week to 2 year old infants"
/lab host="roblor"
/clone_lib="Human Trabecular Meshwork cDNA library"
/clone_lib="Human Trabecular Meshwork cDNA library"
/clone_lib="trapecular Meshwork cDNA library"
cdNA library made from mRNA isolated from trabecular
meshwork cells established fom eyes from 6 individuals,
                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Rogers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Dibmitted (20-FBB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM887701 534 bp mRNA linear EST 08-MAR-2002
TM304 Human Trabecular Meshwork cDNA library Homo sapiens cDNA
clone 107917 5', mRNA sequence.
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Pred. No. 1.3e-12;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="genomic DNA"
/db xref="taxon:10090"
/clone="MHPP182j09"
/clone lib="MHPP"
      genome survey sequence; MICER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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/db_xref="taxon:9606"
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Location/Qualifiers
                          Mus musculus (house mouse)
Mus musculus
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Best Local Similarity 88.9%;
Matches 80; Conservative (
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/organism="Mus musculus"
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Best Local Similarity
Matches 78; Conserv
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Mammalia; Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
1 (bases 1 to 286)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J., and Bradley, A.
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                                                                                                                                                                                                                                                                                      RACE from mouse ES cells as
1998 Apr 9;392(6676):608-11)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qlan, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Why I kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-FBB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers
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                                                                                                                                                                                                                         Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES
described in Zambrowicz et al (Nature. 1998 Apr 9;392(667
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Pred. No. 5.1e-12;
0; Mismatches 8; Indels (
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Pred. No. 2.5e-12;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
Calone="0831360/181"
Cell type="embryonic stem cell"
/clone_lib="Mus musculus 1298v/Ev'
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GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
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    .286
    /organism="Mus musculus"

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/db_xref="taxon:10090"
/clone="MHPP263n05"
/clone_lib="MHPP"
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                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="129Sv/Ev"
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96.2%;
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90.6%;
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Best Local Similarity 90.6
Matches 77; Conservative
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Les 75; Conserv
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CR083191/c
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.
1 (bases I to 130)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Direct Submission
Submitted (10-FBB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 18A, UK. http://www.sanger.ac.uk/MICER
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                                                                                                                                                                                                                                                                                                BX988352 130 bp DNA linear GSS 05-JUL-200 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP120m07, genomic survey sequence.
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71
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                                                 120 accacccarccaraccaracarroaccrccacrererererarrocarecarecar
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Pred. No. 1.2e-11;
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Mus musculus
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
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/clone="MHPP120m07"
/clone_lib="MHPP"
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                                                                                                        TGTTTGCCCCTCCCCGTGCCTTCC 96
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  BX988352.1 GI:49719810
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86.7%;
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/clone lib="Numan Trabecular Meshwork cDNA library"
/note="Vector: pcDNA3; Site 1: EcoR1; Site 2: EcoR1; Human
cdNA library made from mRNA isolated from rabecular
meshwork cells established fom eyes from 6 individuals,
ages 2 weeks to 2 years. Cells were harvested at passages
3 through 6. Invitrogen made a unidirectional cDNA library
from the mRNA from the frozen cells using a pcDNA3 vector
and TPO10F'' host cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 bp mRNA linear EST 08-MAR-2002
TM397 Human Trabecular Meshwork cDNA library Homo sapiens cDNA
Elone 119752 5', mRNA sequence.
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1 (bases 1 to 600)
Witz, M.K., Samples, J.R., Xu, H., Severson, T. and Acott, T.S.
Witz, M. Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library
Unpublished (2002)
                                                                                                                                                                                                                                  87
                                                                                                                                                                                                                                                       74 CGCTGATCAGCCTCGACTGTGCCTTATAGTTGCCAGCCATTTGTTGTTTGCCCCTCCCCC 15
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Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Fax: 503-494-4698
Email: wirtzm@ohsu.edu
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                                                                                                                                      Length 75;
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/tissue_type="eye"
/coll_type="trabecular meshwork"
/dev_stage="2 week to 2 year old infants"
/lab_host="TOP10F'"
                                                                                                                                                                                2; Indels
                                                                                                                                    69.1%; Score 69.8; DB 9;
97.3%; Pred. No. 2.3e-11;
iive 0; Mismatches 2;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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High quality sequence stop: 400.
Location/Qualifiers
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BM887768.1 GI:19271512
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Homo sapiens
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Matches 71; Conservative
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516 GCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTNTAGTTGCCAGCCATCTGTTGGTTGC 575

19 GITIAAACCCGCTGAICAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGC

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CR092687

Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP224h16, genomic survey sequence.
                                                                                                                                                                                                                                                   Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 166)

1 (bases I to 166)

Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.

Biggs, P.J., Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
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Pred. No. 4.1e-11;
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GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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/clone="WHPP2.4h16"
/clone_lib="WHPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: July 14, 2005, 23:23:04 Job time: 967.667 secs
                   CCCTCCCCCGTGCCTTNCTTG 596
CCCICCCCCGIGCCIICCIIG 88
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85.6%;
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AJ224121 Canis fam AY5369493 Escherich AY538700 Serratia AY538701 Serratia AX538702 Serratia AX538702 Serratia AX538699 Serratia AX538699 Serratia AX538699 Serratia AX538699 Serratia AX538699 Serratia AJ30555 Escherich AX10542 Escherich AF104441 Klebsiell AF104442 Escherich AF28199 Escherich AK28199 Escherich AX628199 Escherich AX628199 Escherich AX628195 Escherich AX628195 Escherich AX628195 Escherich AX628195 Escherich AX628195 Escherich AX729027 Proteus m X54606 Pseudomonas X54607 Pseudomonas X54607 Pseudomonas X54607 Pseudomonas X54609 Pseudomonas X54607 Pseudomonas

Sequence:

Run on:

Searched:

Database

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1 (bases 1 to 142)
Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
Rosen, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus polynucleotides and sequences
Patent: US 6593114-A 2608 15-JUL-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 101; DB 6;
100.0%; Pred. No. 8.7e-20;
ive 0; Mismatches 0;
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6737248.
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                                                                                                                                                                                                                                                                                            Sequence 2608 from patent US 6593114.
AR356490.1 GI:33762574
                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
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                                                            AY394610
ECO308558
                                                                                                                                                                                                       PATN2PN1B
PATN3PN1A
        AY589493
AY538698
AY538700
                                 AY538701
AY538702
AY538699
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AX195443
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AF104441
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AY101764
                                                                                                                                                                                      AY729027
PATN1PN2
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Sequence 2608 from patent US
AR538046
AR538046.1 GI:53929263
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BD195256 Nucleotid
BO0892 Synthetic D
E01156 DNA fragmen
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AX260190 BAQuence
AX260190 Sequence
AX560150 Sequence
A43586 Sequence
A43585 Sequence
A4559171 Pseudomon
X97254 S. marcescen
Z92776 Caenorhabdi
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M10199 Plasmid pMM
E00018 DNA coding
I01644 Sequence 1
                                                        July 14, 2005, 04:39:07; Search time 756.618 Seconds (without alignments) 6468.225 Million cell updates/sec
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AR538046 Sequence
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                                                                                                                l agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                            4708233 segs, 24227607955 residues
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                               US-09-482-682-44_COPY_7860_7960
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101644
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Maximum Match 100%
Listing first 45 summaries
                                          - nucleic search, using sw model
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AY559171
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seq length: 200000000
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Enterobacteriacae; Escherichia.
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1 (bases 1 to 142)

Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAAATG 48
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                       100.0%; Score 101; DB 6; Length 142; 100.0%; Pred. No. 8.7e-20; ive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210. .>228
/product='B.coli penicilinase'.
Location/Qualifiers
                                                                                             Rosen, C.A.
Staphylococcus aureus polynucleotides and sequences
Patent: US 6737248-A 2608 18-MAY-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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DNA coding for Escherichia coli penicillinase.
E00019
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    .228
    organism="Escherichia coli"

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/db_xref="taxon:562"
                                                                                                                                                                                                1. 142
/organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                      Location/Qualifiers
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Escherichia coli
Escherichia coli
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Best Local Similarity 100.
Matches 101; Conservative
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AUTHORS
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TITLE
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E00019/c
LOCUS
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KEYWORDS
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BCT 26-APR-1993
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                                                                                                                                                                                                                                                                                                                                                   other sequences; plasmids.

1 (bases 1 to 240)

Remper, B., Jensch, F., von Depka-Prondzynski, M., Fritz, H.J.,

Borgmeyer, U. and Mizuuchi, K.

Resolution of Holliday structures by endonuclease VII as observed
in interactions with cruciform DNA

Cold Spring Harb. Symp. Quant. Biol. 49, 815-825 (1984)

85153063
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Enterobacteriaceae, Escherichia.
                                                                                                                                                    PMMOENDO 240 bp DNA linear BCT 26-APR-1
Plasmid pWM110 region of endo VII cleavage sites near cruciform
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Uorutaa,G. and Karen,T.
SYNTHESIS OF SELECTIVE AGED PROTEIN OR POLYPEPTIDE IN BACTERIA
Patent: JP 1981154999-A 1 30-NOV-1981;
UNIY HARVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGCTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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JP 198115499-A/1
30-NOV-1981
09-APR-1981 JP 1981052488
11-APR-1980 US 80 139225
11-APR-1980 US ARRN TARUMATSUJI
UORUTAA GIRUBAATO, KARRN TARUMATSUJI
C12P21/00,C07H21/00,C12N1/00,C12N1/19; CC
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GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 75
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DNA coding for Escherichia coli penicillinase.
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PN JP 198115499-A/1
PP 30-NOV-1981
PP 30-NOV-1981 JP 1981052488
PR 11-APR-1980 US 80 139225
PC C12P21/00,C07H21/00,C12N1/00,C12N15/00
strandedness: Double;
CC topology: Linear;
CC anti-sense: No;
CC anti-sense: No;
CC fragment_type: N-Terminal Fragment;
CC *source: Clone=pKT241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source text: Plasmid pMM110 DNA.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:2599"
/plasmid="Plasmid pMM110"
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JP 1981154999-A/1.
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Escherichia coli
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Annealing: 60C 10sec
Extension: 72C 20sec
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primer_bind
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                                                                                                                                                                                                                                                             175 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 116
                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 344)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: US 4338397-A 1 06-JUL-1982;
President and Fellows of Harvard College; Cambridge, MA
                                               /product='E.coli penicilinase' FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 251;
                                                                                                                                                                                Length 251;
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Human chromosome 8 STS UT5345, sequence tagged site.
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llarity 100.0%; Pred. No. 8.7e-20;
Conservative 0; Mismatches 0;
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    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 101644 251 bp ss-DNA
Sequence 1 from Patent US 4338397.
                                                                                                      /organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
/mol_type="unassigned DNA"
                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
1 (bases 1 to 251)
Gilbert, W. and Talmadge, K.
Mature protein synthesis
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FH Key
FH CDS
FT CDS
TATA_signal
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Best Local Similarity
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PD 08-MAY-2002
PD 08-MAY-2002
PP 21-NOV-1997 JP 1998523916
PR 22-NOV-1996 US 60/031626,14-OCT-1997 US 60/061953 PI
PATRICK J DILLON,GIL H CHOI,RODNEY A WELCH
PC C12M15/11,C12M15/63,C07K16/12,G01N33/569,G06F17/30,G11B7/00 CC
Strandedness: Double;
CC Topology: Linear;
CC Nucleotide sequence of Escherichia coli pathogenicity islands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ballard, L., Melis, R., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Rodriguez, P., Albertson, H., Lalouel, J.-M. and White, R. Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome tompublished (1933).
Ontobalished (1933).
Original source text: Home sapiens DNA.
Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
1160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112.
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1 (bases 1 to 400)

Dillon, P.J., Choi, G.H. and Welch, R.A.

Nucleotide sequence of Escherichia coli pathogenicity islands
Patent: JP 2002513277-A 43 08-MAY-2002;

HUMAN GENOME SCIENCES INC, WISCONSIN ALUMNI RESEARCH FOUNDATION
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Nucleotide sequence of Escherichia coli pathogenicity islands.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mg++: 2mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
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/standard_name="STS UT5345"
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                                                                                                                                                                                                                                                                                                                 Primer A: GAGCAAAAACAGGAAGGCAAAATGC
Primer B: TTCGGGGAAATGTGCGGGGACC
32P-label: B Primer
PCR Profile:
Initial Denaturation: 94C 3008ec
PCR Cycles: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="8"
                                                                                                                                                                                                                                                                                            e-mail: sts@corona.med.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36. .60 complement (202. .224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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BD195256.1 GI:33005021
JP 2002513277-A/43.
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61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
/db_xref="taxon:32630"
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hypothetical: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E01156.1 GI:2169415
JP 1987083890-A/1.
synthetic construct
synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Artificial gene
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mat_peptide
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VERSION
KEYWORDS
SOURCE
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E01156/c
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AUTHORS
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...TOR, MICROORGANISM
...YPEPTIDE WITH MICROORGANI.
...Sol149089-A/1
...JUL-1986;
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1 (bases 1 to 456)
Okai, H., Momota, Y., Kumakura, T., Tochifusa, N., Kitazawa, T.,
Ojida, K. and Matunshiro, A.
POLYPEPTIDE SECRETION DEVELOPMENT VECTOR, MICROORGANISM TRANSFORMED
WITH SAME, AND PRODUCTION OF POLYPEPTIDE WITH MICROORGANISM
PATENT: JP 1986149089-A 1 07-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F
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                                                                                                                                                                                                                                                                                                                                              /product='signal peptide of beta-lactonase'
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                                                                                                                                                                                                                                                                                                                  1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E00892 456 bp DNA linear PAT Synthetic DNA encoding fused polypeptide between E coli beta-lactamase and human beta-urogastrone.
                                                                                                                                                                                                                         100.0%; Score 101; DB 6; Length 400;
larity 100.0%; Pred. No. 8.7e-20;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                   . .400
organism='Unidentified'
Location/Qualifiers

    456
    /organism="synthetic construct"
/mol_type="genomic DNA"

                                                                                           1. .400
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/db_xref="taxon:32644"
                                                               Location/Qualifiers
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JP 1986149089-A/1.
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synthetic construct
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  Key
source
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les 101; Conserv
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FT
표되답
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KEYWORDS
SOURCE
ORGANISM
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Matches
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E00892/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
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OKAI HIDEO
C12N15/00,C12N1/20,C12P21/00,(C12N1/20,C12R1:19),(C12N1/20, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      other sequences; artificial sequences.

1 (bases 1 to 456)
Yoshikawa,K., Momota,Y., Kajifusa,N., Koide,T. and Okai,H.
POLYPEPTIDE SECRETION EXPRESSION VECTOR, MICROORGANISM TRANSFORMED
BY SAID VECTOR AND PRODUCTION OF POLYPEPTIDE USING SAID
PATENT: JP 1987083890-A 1 17-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                     1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
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    Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125. .170
/note='beta lactamase promoter'
                                                                                                                                                                                                                                                                                                                      linear
                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product='beta urogastrone'
209. .277
                                                                                                                                                                   DNA fragment which secrets beta urogastrone.
Query Match 100.0%; Score 101; DB 6; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 101; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .456
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Artificial sequence; Genes. JP 1987083890-A/1
                                                                                                                                                                                                                                                                                                                      456 bp
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09-OCT-1985 JP 1985225393
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C12N15/00, C07H21/04, C12N1/00, C12P21/02, (C12N1/00, C12R1:19), PC
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                                                                                                                                                                                                             14-FEB-1986 JP 1986031415
OKAI HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, KOIDE TAKAO,
MOMOTA YUTAKA
                                                 Okai, H., Kumakura, T., Kawamoto, S., Koide, T. and Momota, Y. POLYPEPTIDE-EXPRESSION VECTOR, HOST TRANSFORMED WITH SAID VECTOR WND PRODUCTION OF POLYPEPTIDE USING SAID HOST PAtent: JP 1987190083-A 1 20-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product='human beta-urogastrone'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product='human beta-urogastrone'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 101; DB 6; Length 456; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 101; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 456
/organism="synthetic construct"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                  other sequences; artificial sequences.
1 (bases 1 to 456)
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Patent: WO 0172774-A 60 04-OCT-2001;
Cyclacel Limited (GB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 bp
Sequence 60 from Patent WO0172774.
AXZ60098
                                                                                                                               Artificial gene
Artificial sequence; Genes.
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200. .203
209. .277
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strandedness: Double;
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                                                                                                                                                             Homo sapiens
JP 1987190083-A/1
                                                                                                                                                                                                                                                                                                                         topology: Linear;
hypothetical: No;
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        synthetic construct
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mat_peptide
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31-JAM-1986 JP 1986021032
OKAI HIDBO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, ADACHI SHOJI, MATSUBARA AKIMASA, OJIDA KAZUHIDE, YANO MAKI, MIHARA SHIGERU, MATSUSHIRO AIZO, YANAHARA NOBORU CI2P21/00,CI2R1:91);
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PATENT: JP 1987179398-A 1 06-AUG-1987;
EARTH CHEM CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E01302 456 bp DNA linear PAT 29-5 DNA encoding human beta-urogastrone fused with DNA encoding promoter and signal peptide of beta-lactamase.
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/product='beta-urogastron'
113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                            other sequences; artificial sequences.
1 (bases 1 to 456)
                                                                                                                                                                                                                                                                                                                                      Artificial gene
Artificial sequence, Genes.
Homo sapiens
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200. .203
209. .277
278. .436
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hypothetical: No;
anti-sense: No;
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E01302.1 GI:2169561
JP 1987190083-A/1.
synthetic construct
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JP 1987179398-A/1.
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synthetic construct
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mat_peptide
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E01274/c
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PAT 26-OCT-2001

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Cuphea lanceolata

Bukaryota, Viridlantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids, Myrtales, Lythraceae; Cuphea.

1 (Dases I to 693)

1 (Daser, R., Bautor, J., Bothmann, H., Filsak, E.,
Hoericke-Grandpierre, C., Klein, B., Martini, N., Mueller, A.,
Schulte, W., Voetz, M., Walek, J. and Schell, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location Qualifiers
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100.0%; Pred. No. 8.7e-20;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deak, P., Glover, D.M. and Midgley, C. Cell cycle progression proteins Patent: WO 0172774-A 112 04-OCT-2001; Cyclacel Limited (GB)
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MAX PLANCK GESELLSCHAFT (DE)
Other publication CA 2169093 950316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Sequence 112 from Patent WO0172774.
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Sequence 11 from Patent W09507357.
A43586
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                                                              al Similarity 100.
101; Conservative
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A43586
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Other publication AU 7615494 950327.
Location/Qualifiers
Location/Qualifiers
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                                                                                                                                                                                                                                                                     0; Mismatches
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Matches 101; Conservative
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version 5.1.6
- 2005 Compugen Ltd.
 GenCore
Copyright (c) 1993
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July 14, 2005, 04:35:42; Search time 142.398 Seconds (without alignments) 4198.742 Million cell updates/sec Run on:

US-09-482-682-44\_COPY\_7860\_7960 101 Perfect score:

1 agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101 Sequence:

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

4390206 segs, 2959870667 residues Searched: 8780412

length: 0 length: 2000000000 seq Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04: Database :

geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn1980s:\* geneseqn1990s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs: geneseqn2004as

## SUMMARIES

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Result No.	Score	Query, Match	Query, Match Length DB	DB	ID	Description
0 1	101	100.0	142	2	AAV76919	Aav76919 Staphyloc
0	101	100.0	228	Н	AAN10032	Aan10032 Sequence
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Ω	101	100.0	400	~	AAV31229	Aav31229 E. coli J
C 5	101	100.0	456	Н	AAN60624	Aan60624 Plasmid p
9	101	100.0	456	-	AAN71080	Aan71080 Sequence
0 7	101	100.0	456	ч	AAN70833 .	Aan70833 Beta-uroq
<b>8</b>	101	100.0	456	ч	AAN81765	Aan81765 Sequence
o U	101	100.0	466	9	ABA90413	Aba90413 Drosophil
c 10	101	100.0	487	~	AAX21173	Aax21173 Polynucle
c 11	. 101	100.0	535	0	AAX21149	Aax21149 Polynucle
c 12	101	100.0	573	9	ABA90456	Aba90456 Drosophil
13	101	100.0	605	12	ADH58311	Adh58311 Electroph
c 14	101	100.0	176	4	AAS30560	Aas30560 DNA encod
c 15	101	100.0	116	4	AAS27819	Aas2781,9 DNA encod
c 16	101	100.0	776	4	ABK42984	Abk42984 Genomic s
c 17	101	100.0	776	4	AAL07344	Aal07344 Human rep
c 18	101	100.0	776	4	AAL03229	Aal03229 Human rep
c 19	101	100.0	176	4	AAL06588	Aal06588 Human rep
c 20	101	100.0	776	4	AAL07340	Aal07340 Human rep

Aba14573 Human ner	Aas34681 Human DNA	Ada41574 Human sec	Acc50905 Human sec	Abz71508 Secreted	Adb91869 Human sec	Adb61140 Connectiv	Adb94622 Novel hum	Adc74663 Human sec	Adas7709 BAC fragm	Adn41551 Novel hum	Aas30559 DNA encod	Aas27818 DNA encod	Abk42983 Genomic s	Aas41807 Genomic s	Aas41855 Genomic s	Aak85485 Human imm	Aak85434 Human imm	Aal07343 Human rep	Aal06587 Human rep	Aal07339 Human rep	Aal03228 Human rep	Abal4572 Human ner	Aas34680 Human DNA	Adb61139 Connectiv
ABA14573	AAS34681	ADA41574	ACC50905	ABZ71508	ADB91869	ADB61140	ADB94622	DC74663	DA57709	ADN41551	AAS30559	AAS27818	ABK42983	AAS41807	AAS41855	AAK85485	AAK85434	AAL07343	AAL06587	AAL07339	AAL03228	ABA14572	AAS34680	ADB61139
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101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	.101	101
c 21	c 22	c 23	c 24	c 25	c 26	c 27	c 28	c 29	c 30	c 31	c 32	c 33	c 34	c 35	c 36	c 37	c 38	c 39	c 40	c 41	c 42	c 43	C 44	c 45

## ALIGNMENTS

AAV76919 standard; DNA; 142 (first entry) 16-MAR-1999 AAV76919; AAV76919/c RESULT 1 

BP.

Staphylococcus aureus contig SEQ ID #2608

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

Staphylococcus aureus

EP786519-A2.

30-JUL-1997

97EP-00100117. 07-JAN-1997; 96US-0009861P. 05-JAN-1996; (HUMA-) HUMAN GENOME SCI INC

Fannon MR, Rosen CA; Dillon PJ, Barash SC, Choi GH, WPI; 1997-374922/35. Kunsch CA,

Polynucleotide(s) and proteins derived from Staphylococcus aureus -stored on computer readable medium and used in the production of anti-S.aureus vaccines.

Claim 1; Page 2287; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or

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industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. sureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used (or recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                                                                                readable medium
         88888888888888888
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ö 9 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 48 **AGGGTTATTGTCTCATGAGCGGATACATATTTTGAATGTATTTTAGAAAAATAAACAAATAG** Gaps .; 0 Length 142; 0; Indels Sequence 142 BP; 45 A; 25 C; 26 G; 45 T; 0 U; 1 Other; GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101 GGGTTCCGCGCACATTCCCCCGAAAGTGCCACCTGACGTC 7 Score 101; DB 2; Pred. No. 2.1e-21; 0; Mismatches 0; 100.0%; Query Match
Best Local Similarity 100. 107 61 47 g

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032/c AAN10032 standard; DNA; 228 AAN10032/ RESULT

(first entry) 13-AUG-1992

AAN10032;

Sequence of the pKT218 EcoRI-PstI penicillinase gene fragment.

Cloning vehicle; bacterial vector; transformed host; penicillinase; insulin; ds

Escherichia coli

Location/Qualifiers /\*tag= b /label= sticky end /\*tag= a /label= sticky end 225. .228 \*tag= misc\_feature misc\_feature 

EP38182-A

21-OCT-1981

81EP-00301561 09-APR-1981; 80US-00139225. 11-APR-1980;

(HARD ) HARVARD COLLEGE

Gilbert W, Talmadge K;

WPI; 1981-80125D/44. P-PSDB; AAP10039. Synthesis of mature protein or polypeptide - by using bacterial host transformed by cloned vehicle contg. DNA fragment etc.

Example; Fig 3; 34pp; English.

The closest identifiable promoter for the penicilinase gene in pKT241 (AAN10031) is located in the region 14 to 20 nucleotides before its

20 9 translational start signal. In the examples, the 3' end of pKT241 was attached to the signal DNA sequence of the DNA fragment (19) for rat preproingulin (see AAN10033). The closest identifiable promoter for the penicillinase gene in pKT218 (AAN10032) is located in the region 14 to 2 mucleotides before its translational start signal. In the examples, the 3' end of pKT218 was attached to the signal DNA sequence of the DNA fragment (CB6) for rat preproingulin (see AAN10034) The closest identifiable promoter for the penicilinase gene in pKT241 (AAN10031) is located in the region 14 to 20 nucleotides before its translational start signal. In the examples, the 3' end of pKT241 attached to the signal DNA sequence of the DNA fragment (19) for rat preproinsulin (see AAN10033). The closest identifiable promoter for the penicillinase gene in pKT218 (AAN10032) is a located in the region 14 to 2 nucleotides before its translational start signal. In the examples, the by using bacterial host ragment etc. Cloning vehicle; bacterial vector; transformed host; penicillinase; ó; Sequence of the pKT241 EcoRI-PstI penicillinase gene fragment 100.0%; Score 101; DB 1; Length 228; 100.0%; Pred. No. 2.3e-21; Indels 61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101 Sequence 228 BP; 72 A; 37 C; 46 G; 73 T; 0 U; 0 Other; GGTTCCGCCCACATTTCCCCGAAAAGTGCCACCTGACGTC 75 Synthesis of mature protein or polypeptide - by us transformed by cloned vehicle contg. DNA fragment 0; Mismatches Location/Qualifiers /\*tag= b /label= sticky /\*tag= a /label= sticky BP. Example; Fig 2; 34pp; English. 81EP-00301561 80US-00139225 AAN10031/c ID AAN10031 standard; DNA; 251 (first entry) 248. .251 Best Local Similarity 100. Matches 101; Conservative (HARD ) HARVARD COLLEGE Talmadge K; WPI; 1981-80125D/44. P-PSDB; AAP10038. Escherichia coli. feature misc feature 39-APR-1981; 11-APR-1980; 13-AUG-1992 21-OCT-1981 Gilbert W, EP38182-A. 115 AAN10031; insulin; Query Match misc RESULT 3 8×33333333 셤 Š 셤 ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a B. coli strain J96 contig containing pathogenicity island (PAI) sequences, and represents a nucleic acid molecule of the invention. PAIS are large fragments of DNA which comprise pathogenicity determinants. The sequences of the invention are taken from PAI IV and PAI IV. PAI IV is located at approximately 64 min (near pheV) approximately 94 min (at pheR) on the B. coli chromosome and is greater than IVO kb. PAI V is located at approximately 94 min (at pheR) on the B. coli chromosome and is approximately 160 kb in size. Antibodies specific to the proteins encoded by the PAI open reading frames of the invention can be used in kits to detect uropathogenic B. coli. The proteins are used in vaccines to elicit a protective immune response in an animal to the uropathogenic B. coli
                                                                                                                       PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; vaccine; protective immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to elicit an immune response to pathogenic E. coli.
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                                                                                                         1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                   Gaps
3' end of pKT218 was attached to the signal DNA sequence of the DNA fragment (CB6) for rat preproinsulin (see AAN10034)
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                                                           Length 251;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 400 BP; 106 A; 77 C; 91 G; 126 T; 0 U; 0 Other;
                                                                                                                                                        GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                    Sequence 251 BP; 74 A; 45 C; 50 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                      GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 75
                                                                                   ;
0
                                                          Query Match
100.0%; Score 101; DB 1;
Best Local Similarity 100.0%; Pred. No. 2.3e-21;
Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                 E. coli J96 pathogenicity island contig #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; Page 140-141; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon PJ, Choi GH, Welch RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US021347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0031626P.
97US-0061953P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC. (UYWI-) UNIV WISCONSIN.
                                                                                                                                                                                                                                          AAV31229 standard; DNA; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-312461/27.
                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1997;
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14-OCT-1997;
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Gaps

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Indels

100.0%; Score 101; DB 2; 100.0%; Pred. No. 2.5e-21; ive 0; Mismatches 0;

Query Match 100.
Best Local Similarity 100.
Matches 101; Conservative

Length 400;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant vector for polypeptide secretion - contains signal peptide sequence directly bonded to peptide-coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oshiden K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The plasmid produces secreted beta-urogastrone in a transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kitazawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                   GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= d
/label= Beta-lactamase signal peptide
278. .436
                                                                                                                         105 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 65
                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pUG201 sequence encoding beta-urogastrone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kajifusa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-lactamase signal peptide; pGH54; pGH55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= e
/label= Beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Table 4; 79pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuwakura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84JP-00271206
                                                                                                                                                                                                                    AAN60624/c
ID AAN60624 standard; DNA; 456
                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
209. .439
/*tag= c
209. .277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1986-182911/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAP60678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1984;
                                                                                                                                                                                                                                                                                                                           25-MAR-2003
29-OCT-1991
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BP.

ds.

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Detection of DNA and/or RNA - by converting to single strand form and using probe contg. labelled inosine deriv.
                                                                                                                                                                                                       cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SEKI ) SEKISUI CHEM IND CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                            86JP-00087368.
                                                                                                                                                                                                                                                                                                                                                                                                   86JP-00087368
AAN70833/c
ID AAN70833 standard; DNA; 456
                                                                                                                                                  Tumour; inosine; DNA probe;
                                                                 (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                        /*tag= a
209. .277
/*tag= d
                                                                                                                        Beta-urogastrone sequence
                                                                                                                                                                                                                                  /*tag=
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                                                                                                                                                                                                                                                                           209.
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P-PSDB; AAP70505.
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                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1986;
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                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                              JP62244398-A
                                                                 25-MAR-2003
10-MAR-2003
                                                                                             18-JAN-1991
                                                                                                                                                                                                                                                                                                     sig_peptide
                                                                                                                                                                                                                                                                                                                                                                         24-OCT-1987
                                       AAN70833;
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promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 114
               Sequence encodes beta-urogastrone under the control of a tac promoter. The peptide may be expressed from plasmid pUGT 150s in a transformed E.coli host. The plasmid may carry several separately expressing sequences comprising a tac promoter, SD site, signal peptide, and coding sequence, to produce beta-UG in high yield. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression vector contg. multiple information units is used to transform host all for increased prodn. of polypeptides.
1 AGGGTTATTGTCTCATGAGCGGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                      GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= b
'transl_except= (pos:434. .436,aa:Arg)
                                                                    113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 553; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                           cocation/Qualifiers
                                                                                                                                                                                                                                                             Sequence encoding beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86JP-00031415
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                                                                                                                                    AAN71080/c
ID AAN71080 standard; DNA; 456
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   .439
                                                                                                                                                                                                                                                                                                                                                                         125. .170
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EART ) EARTH SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                       *tag=
                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                        pUGT 150s; beta-UG; ds
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                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-1986;
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13-MAY-1991
                                                                                                                                                                                                        25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-1987.
                                                                                                                                                                             AAN71080;
                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                                                                                                                                                                                                                         promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                       RESULT
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An example of a sequence detected by a probe consisting of polyinosine, polydeoxyinosine, oligoinosine and/or oligodeoxyinosine is labeled. The seDNA and probe are hybridized and the existence of DNA in the product is detected. It can be used to detect the presence of malignant tumour. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAAAAAATAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAACAAATAG
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                                                                                                                                                                                                                                                                                Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
Disclosure; Page 11; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
AAN81765/c
LD AAN81765 standard; DNA; 456 BP.
XX
AC AAN81765;
XX
DT 25-MAR-2003 (revised)
DT 13-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                                                                     to correct PA field.)
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RESULT

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280 AGGCTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 221
                                                                                                                                                                                                                                                                                                                                                             The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90366-ABA90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting the cell division cycle, or capable of inhibiting a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autofimmune disorders such as (glomeralonephritis and rheumatoid arthritis), dermatological disorders (such as psoriasis), antiinflammatory, antifungal and antiparasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG
                                                                                                                                                                                                                                                                Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide sequence from the genome of Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 466 BP; 135 A; 87 C; 93 G; 150 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 101; DB 6;
; Pred. No. 2.6e-21;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                          Claim 1; Page 99; 213pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
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                                                                                                                                                                                       Glover DM, Midgley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                          23-MAR-2001; 2001WO-GB001297
                                                                                                               24-MAR-2000; 2000GB-00007268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX21173 standard; DNA; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders (such as malaria)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                                                                              WPI; 2002-055132/07
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                                                                                                                                                   (CYCL-) CYCLACEL
WO200172774-A2
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                                      04-OCT-2001
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                                                                                                                                                                                         Deak P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The deriv. has various biological activities such as gastric acid secretion inhibiting action, or cell proliferation promoting action. The deriv. has the same biological or pharmacological activities as betaurogastrone. It is not susceptible to denaturation by oxidn. and is chemically stable. Deriv. has resistance to proteolytic enzymes such as protease. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of HB101 (pGH201) encoding new beta-urogastrone deriv. Met(21),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New beta-urogastrone deriv. - has gastric acid secretion inhibition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 101; DB 1; Length 456; 100.0%; Pred. No. 2.6e-21; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                        secretion; cell proliferation; hormone; ds
                                                                                                                                                                                                                                                    "New beta-urogastrone deriv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 685; 76pp; Japanese.
                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferation promotion activity.
                                                                                                                                                                                                                                                                                                                                                                                                         86JP-00153783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAP81349
                                                                        Gastric acid
                                                                                                                                                                                                                                                                                      JP63012298-A
                                                                                                                                                                                                                                                                                                                                                                   30-JUN-1986;
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                                                                                                          Synthetic
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antiinflammatory; antipsoriatic; dermatological; antifungal; mitosis; antiparasitic; antimalarial; antirheumatic; antiarthritic; cell division; cell cycle progression protein; tumour; proliferative disorder; cardiovascular; autoimmune; dermatological disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABM90366-ABM90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting mitosis and/or melosis. They can also be used in a method for treating a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as (glomerulonephritis and rheumatoid arthritis), dermatological disorders
                                                                                                                                                         AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antiproliferative; cytostatic; cardiant; immunosuppressive; meiosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory, antifungal and antiparasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila cell cycle progression protein coding sequence #91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 573 BP; 154 A; 118 C; 116 G; 184 T; 0 U; 1 Other;
                                                                                                                                                                                                        61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC
                     ; Score 101; DB 2;
; Pred. No. 2.7e-21;
0; Mismatches 0;
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                       100.0%;
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                Query Match
Best Local Similarity 100.'
Matches 101, Conservative
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Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CXCL-)
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                                          New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
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                                                                                                                                                                                                      diagnosis,
                                                                                                                                                                       AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosi characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                       Length 487;
                                                                                                                                                                                                                                                                                                                                            Sequence 487 BP; 125 A; 127 C; 113 G; 121 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 101; DB 2;
100.0%; Pred. No. 2.6e-21;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                               biosynthetic products such as enzymes
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                                                                                                                                      Claim 1; Page 1106; 1150pp; English.
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WPI; 1999-081273/07
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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RESULT 11

Query Match

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Sequence 535 BP; 145 A; 108 C; 122 G; 155 T; 0 U; 5 Other;

AAS30560 standard; DNA; 776

AAS30560/

AAS30560;

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This invention relates to a novel method for the optimisation of primer libraries. Specifically, it refers to increasing the affinity of short boilgonucleocide primers also known as extendable oligos (EOs), for their template sequences. The present invention describes improved methods for sequencing and the linear and exponential amplification of DNA that can be useful for PCR, RT-PCR, ligation chain reaction (LCR), rolling circle amplification. Accordingly, these extendable oligos with improved specificity and affinity are particularly important in fields ranging from biotechnology and agriculture to medical research. This polynucleotide sequence is the electropherogram of a DNA sequencing reaction that used the pUCI9 plasmid and E154/T422 oligos, used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                           ds; primer library; extendable oligos; EO; ligation chain reaction; LCR; rolling circle amplification; strand displacement amplification; isothermal DNA amplification; biotechnology; agriculture; medical research; pUCI9 plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Increasing the affinity of an extendable oligonucleotide (EQ) for a target nucleic acid, for providing primers having improved specificity, comprises hybridization of the EO to a template oligonucleotide (TQ) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGGCTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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                                                                                                                                                                                                                                        Electropherogram of a DNA sequencing reaction using E154 & T422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGTTCCGCGCACATTCCCCCGAAAGTGCCACCTGACGTC 359
                       295 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
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                                                                                                                             ADH58311 standard; DNA; 605 BP
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Best Local Similarity
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Escherichia coli.
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antianaemic; dermatological; immunosuppressive; antiinflammatory; antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic; osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative; ds.
                                                                         Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
                                                   DNA encoding novel prostate gland antigen, Seq ID No 418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0224518P.
2000US-0224519P.
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                             21-NOV-2001 (first entry)
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                                                                                                                                                                                                         Homo sapiens.
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            2000US-0231243P.
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08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-0249207P.
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17-NOV-2000;
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The invention relates to novel isolated prostate gland related nucleic acids (1) and polypeptides (II). (1) and (II) are useful for diagnosis, prognosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, prostatodystonia, prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic compressions, granulomatous prostatitis, malacoplakia, benign prostatic compactatophy or hyperplasia, and prostatitis, malacoplakia, benign prostatic dadenocarcinomas, transitional cell carcinomas, ductal carcinomas, and adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and caquamous cell carcinomas. (1), (II) and antibody to (II) are useful for altanging reproductive system disorders (Paget's disease), cuthinis), blood-related disorders (sickle cell anaemia), archinish, blood-related disorders (sickle cell anaemia), hyperproliferative disorders, urinary system disorders

(glomerulonephritis), cardiovascular disorders (arrhythmias), respiratory disorders, musculoskeletal system disorders, neural activity and cutorine disorders (Alzheimer's disease and Parkinson's disease), confocrine disorders (Addison's disease and Parkinson's disease), conformine disorders (alsorders (biliary liver cirrhosis), concreatic and gall bladder disorders (biliary liver cirrhosis), concreatic and maintented disorders (diseases at the cellular level, and wound healing and epithelial cell proliferation. (I) or (II) and organs before transplantation, and as food additive or preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
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             2000US-0249245P.
2000US-0249264P.
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2000US-0249300P.
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AAS27819/c ID AAS27819 standard; DNA; 776 BP.

RESULT 15

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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid archritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality, Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; ds; acquired immune deficiency syndrome.
                                                    DNA encoding novel signal transduction pathway protein, Seq ID 1479.
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2000US-0186350P.
2000US-0189874P.
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19-MAY-2000;
07-JUN-2000;
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24-FEB-2000;
02-MAR-2000;
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The invention relates to novel isolated polypeptides (I), and

C polynucleotides (II). (I) and the antibody to (I) are useful for

C diagnosting, preventing and treating diseases including immune system

C disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

C disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ

C (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and

C charblood-related disorders (sickle cell anaemia), myeloproliferative

C disorders, primary haematopoietic disorders, hyperproliferative disorders

C disorders, primary haematopoietic disorders, chromosomal abnormalities

CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities

CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities

CC Alzheimer's disease, parkinson's disease), chromosomal abnormalities

CC Alzheimer's disease, parkinson's (e.g. stroke), renal disorders (e.g.

C plomerulorephritis), cardiovascular disorders (e.g. Arrythmia),

C respiratory disorders, dermatological disorders (e.g. Addison's

C disease), reproductive system disorders, in wound healing,

C disease), reproductive system disorders (cirrhosis), as stimulators of

C inflammatory disorders), liver disorders (cirrhosis), as stimulators of

C higher affinity antibodies, and as a means to induce tumour proliferation

C in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-

C AAS27850 represent novel signal transduction pathway protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1479; 880pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM;
                                                           01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025103P.
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Best Local Similarity 100.
Matches 101; Conservative
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                                          17-NOV-2000;
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Run on:

Sequence:

Searched:

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Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Cortinariaceae; Hebeloma.

(bases 1 to 300)

Wipf, D., Benjdia, M., Tegeder, M. and Frommer, W.B.

Construction of a functional cDNA library from the ectomycorrhizal fungus Hebeloma cylindrosporum

Unpublished (2001)
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ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
Fax: 49 7071 293287
Email: daniel.wipf@zmbp.uni-tuebingen.de
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/mol_type="mRNA"
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/tissue_type="Mycelia"
/lab_host="E. coli XL1-Blue"
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High quality sequence stop: 300
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                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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92b_est4:3

92b_est6:3

92b_gss1:3

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92b_gss1:3

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92b_gs
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Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Homobasidiomycetes,
Agaricales, Cortinariaceae, Hebeloma.

1 (bases 1 to 300)
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Hebeloma cylindrosporum
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
suppression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and Frommer, W.B.
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ZMBP - Center for Molecular Biology of Plants
Line for Molecular Biology of Plants
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
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                                                                                                61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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/tissue_type="Mycelia"
/lab_host="E. coli_XL1-Blue"
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/strain="H1"
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Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y.,
Williams, G. and Brenner, S.
Direct Submission
Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
Centre Hintston, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
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F.rubripes GSS sequence, clone 010H20aC4, genomic survey sequence.
                                                                                                                                         A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis
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Agaricales; Cortinariaceae; Hebeloma.
1 (bases 1 to 300)
Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and Frommer, W.B.
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/lab_host="E. coli XL1-Blue"
/clone lib="Hebeloma cylindrosporum functional cDNA
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Best Local Similarity 100.0%; Pred. No. 8.1e-19;
Matches 101; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       Unpulsahed (2002)
Unpulsahed (2002)
Contact: Wipf D
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
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Tel: 49 7071 2976160
Fax: 49 7071 293287
Email: daniel.wipf@zmbp.uni-tuebingen.de
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/organism="Hebeloma cylindrosporum"
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Genome Res. 9 (10), 960-971 (1999)
99455097
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SSS, genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
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Class: plasmid ends
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84112, US
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemannGdkfz- heidelberg de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 bp mRNA linear EST 04-SEP-2003 nonym: hlcc2) Homo sapiens cDNA clone
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I (bases 1 to 391)
Koehrer, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S.
EST (Koehrer, K. Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="313 (synonym: hlcc2)"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone (DKEZD31371611) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualiflers
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                                                                                                                                                                                                                                      100.0%; Score 101; DB 9; Length 309; 100.0%; Pred. No. 8.2e-19;
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                                                                                        1. .309
/organism="Takifugu rubripes"
                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                          /mol_type="genomic DNA"
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/clone="010H20aC4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKFZp313J1611 rl 313 (synonym: h
DKFZp313J1611 5', mRNA sequence.
                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL597149.1 GI:15154845
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PRIMER: KS
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AL597149
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1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60

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/lab host="UserJourners | / Lab host="UserJourners | / Lab host="E. Coli strain XL10-Gold, T1-resistant, F-" / Clone lib="Oxytricha plasmid UUGCIO library" / Alone lib="Oxytricha plasmid UUGCIO library" / Alone Oxytricha trifallax was blunt end-repaired with DNA from Oxytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pwW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Bukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida, Oxytrichidae; Sterkiella.
1 (bases 1 to 414)
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100005D19R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100005D19 R, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
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                                                                                                                                            288 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 328
                                                                                                     61 GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 101
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Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
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                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei; Cichlidae; Haplochromis.

1 (bases 1 to 417)

8 Watanabe,M., Kobayashi,N., Shin-i,T., Kohara,Y. and Okada,N. Orf sequences of cichlid in Lake Victoria are essentially same Unpublished (2004)

Concact: Tadasus Shin-i Center For Genetic Resource Information
National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                    BJ684174 BJ684174 HCEST library Haplochromis chilotes cDNA clone no90c12,
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Sterkiella histriomuscorum
Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichida;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (Dases 1 to 491)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Haplochromis chilotes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 101; DB 4;
100.0%; Pred. No. 8.3e-19;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="varied"
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/clone="no90c12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="jaw"
                                                                          BJ684174
BJ684174.1 GI:46527295
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                                                                                                                                      Haplochromis chilotes
                                                                                                                                                      Haplochromis chilotes
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Matches 101; Conservative
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                                                          mRNA sequence.
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/done="Urdacountry years"
/done="Urdacountry years"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone lib="Movyricha plasmid UUGC10 library:
/note="Vector: PWMAD4nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWM42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enrhartoideae; Oryzae; Oryza;

1 (bases 1 to 495)

Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X.,

Wu, H.F., Jiang, Y.X., Yu, P.C., Gao, O.K. and Lou, Y.C.

Unpublished (2001)
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Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86882051
Fax: 0086-571-86961525
Bmail: webmastereestarray.org, URL: http://www.estarray.org
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                                                                                                                                                                                                                                                                                      /organism="Sterkiella histriomuscorum"
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                                                           Plate: 0006 row: J column: 13
Seq primer: CACACAGAAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 491.
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/clone="S035A01"
                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:94289"
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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392 AGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sterkiella histriomuscorum
Bukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichida
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 996)
                                                                                                                      CC818523 496 bp DNA linear GSS 17-JUI 100004L13R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC100004L13 R, genomic survey
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Paired end reads from plasmid inserts of Oxytricha trifallax
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                                                                                                                                                                                                                                         61 GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                            332 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
                            Pred. No. 8.4e-19;
                                                         Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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100.08; Pre-
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Unpublished (2003)
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                                                         Matches 101; Conservative
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Fax: 801 585 7177
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                            Best Local Similarity
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CC818523/c
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100004B07R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100004B07 R, genomic survey .
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Stichotrichida, Oxytrichidae, Sterkiella.
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                                                   /dev_stage="3-5 leaf stage"
/clone_lib="Stem library from Oryza sativa (3-5 leaf
stage)"
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Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2002)
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                                                                                                                                                                                                                                         Length 495;
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                                                                                                                                                                                                                                  100.0%; Score 101; DB 4;
llarity 100.0%; Pred. No. 8.4e-19;
Conservative 0; Mismatches 0;
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Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
                                                                                                                                               /note="Vector: pSport2"
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'db_xref="taxon:94289"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                         /tissue_type="Stem"
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CC818374/c
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/done lib="Oxytricha plasmid UUGCIO library"
/clone lib="Oxytricha plasmid UUGCIO library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi[4732114]gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:94289"
/clone="UUGC100004L13"
/lab_host="E. Coli strain XL10-Gold, T1-resistant,
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                                                                                                                               organism="Sterkiella histriomuscorum"
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High quality sequence stop: 496.
Location/Qualifiers
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Length 495;

DB 9;

100.0%; Score 101;

Query Match

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histriomuscorum genomic clone UUGC100003C16 R, genomic survey
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GSS.
                                                                       CC817752.1 GI:32897039
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Fax: 801 585 7177
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Best Local Similarity
Matches 101; Conserv
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84112, USA
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CC817128/c
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/clone_lib-"Oxytricha plasmid UUGC1O library"
/note="Vector: PMD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
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Sterkiella histriomuscorum
Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 503)
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                                                                                                                                                                                                                                                                                                                                                                                                      Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
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331 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 291
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|db_xref="taxon:94289"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tell: 801 585 5606
Fax: 801 585 7177
Email: ddunmogenetics.utah.edu
Plate: 0006 row: N column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 503.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                      macronuclear chromosomes
                                                                                                                                                                                                                                              CC819854.1 GI:32900533
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Best Local Similarity
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                                                                                           RESULT 12
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/Mol type=genomic DNA"
// Ab Arzef="Laxon:94289"
// Clone=wudgcloo003C16"
// Lab host="E. Col; strain XL10-Gold, T1-resistant, F-"
// Lone lib="Coytricha plasmid UUGC10 library"
// Actione lib="Coytricha plasmid Tab blunt end-repaired with DNA from Oxytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pWM92 (gi|4733114|gp|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. Coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Sterkiella histriomuscorum
Eukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
                                                               Eukaryota, Alveolata; Ciliophora; Spirotrichea; Stichotrichia; Stichotrichida; Oxytrichidae; Sterkiella.

1 (bases 1 to 515)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes
Unpublished (2003)
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100002D21R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC100002D21 R, genomic survey
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Sterkiella histriomuscorum (Oxytricha trifallax)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Plate: 0003 row: C column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                       Sterkiella histriomuscorum
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Search completed: July 14, 2005, 23:23:05
Job time: 962.667 secs
          University of Utah
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                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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/note="Vector: PMD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
TH DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed fro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Eukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella.
1 (bases 1 to 519)
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100002J19R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100002J19 R, genomic survey
Stichotrichida, Oxytrichidae, Sterkiella.
1 (bases 1 to 518)
Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
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Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes
Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Sterkiella histriomuscorum"
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Class: plasmid ends
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="UUGC100002D21"
                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                            macronuclear chromosomes
Unpublished (2003)
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CC817162.1 GI:32896449
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Matches 101; Conservative
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molar excess. Vector DNA was prepared from a derivative of pwD42 (gi[4732114]gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector INA, and transformed into chemically-competent E. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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  Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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100.0%; Pred. No. 8.4e-19;
7ative 0; Mismatches 0; Indels C
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                                                  rel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@enetics.utah.edu
Plate: 0002 row: J column: 19
Seq priner: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 519.
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Best Local Similarity
  Rm. 308, B:
84112, USA
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Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database :

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AX31127 Squence
AX31282 Sequence
AX34365 Sequence
156772 Sequence
3 155540 Sequence
3 155540 Sequence
AX02478 Sequence
AX02478 Sequence
AX673107 Sequence
AX68674 Sequence
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AX6842488 Sequence
AX6842488 Sequence
AX342685 Sequence
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U89673 Cloning vec BD234590 Screening AX026821 Sequence AX319694 Sequence A44171 Sequence 1
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AX211281 Sequence
AX349365 Sequence
BD232461 Recombina
                                                                                          AR116416 Sequence
AR222266 Sequence
AR411127 Sequence
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 5 13-JUN-2000;
Location/Qualifiers
1.3853
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AR098190
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AY437643
AX211282
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195540
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AR098192 Sequence
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(c) 1993 - 2005 Compugen Ltd.
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N JP 2001503638-A/3

PN JP 2001503638-A/3

PD 21-MAR-2091

PP 13-NOV-1997 JP 1998522958

PR 15-NOV-1996 US 08/751517,14-FEB-1997 US 08/801092 PI

DOUGLARA ANTELMAN RICHARD J GREGORY, KENNETH N WILLS PC

COT121/04,CO7K5/00,A6K1X38/00,A6K1X35/12

CC Strandedness: Single;

CC Topology: Linear;

PH Key 2009 862.
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Tissue specific expression of retinoblastoma protein.
BD009729
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(bases 1 to 3853)
Antelman, D. Gregory, R.J. and Wills, K.N.
Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 3 21-MAR-2001;
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             1 (bases 1 to 3853)
Antelman,D., Gregory,R.J. and Wills,K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 5 30-APR-2002;
Location/Qualifiers
                                                                                                                     /mol_type="unassigned DNA"
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/mol_type="genomic DNA"
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cloning vector; expression vector; multiple cloning site; Plasmid. synthetic construct synthetic construct
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                                                                                                       Peters,H., Hundhausen,T., Kroenke,M. and Marget,M.
A new small sized high-level eukaryotic expression vector
Unpublished
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Peters, H.
Direct Submission
Submitted (07-AUG-1995) H. Peters, Inst. f. Immunologie, Michaelisetr.5, D- 24105 Kiel, FRG
Related sequences: M21295 and K03104.
Location/Qualifiers
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/note="multiple cloning site (MCS)"
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0; Mismatches 0;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 19 13-JUN-2000;
Location/Qualifiers
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Sequence 19 from patent US 6074850.
AR098191.1 GI:12807448
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/wol_type="unassigned DNA"
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/mol_type="other DNA"
/db_xref="taxon:32630"
/plasmid="pcDNA3ZEO"
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Query Match 100.0%; Score 100; DB 6; Best Local Similarity 100.0%; Pred. No. 9.3e-24; Matches 100; Conservative 0; Mismatches 0;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 33 30-APR-2002;
Location/Qualifiers
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Sequence 33 from patent US 6379927.
AR207834
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AR098192
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Tissue specific expression of retinoblastoma protein.
BD009730
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Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 4 21-MAR-2001;
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100.0%; Score 100; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.3e-24;
Matches 100; Conservative 0; Mismatches 0;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 19 30-APR-2002;
Location/Qualifiers
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Sequence 19 from patent US 6379927.
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AR207833.1 GI:21507689
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/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2001503638-A/4.
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Materials and methods relating to immune responses to fusion
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Hyaluronic acid microspheres for sustained gene transfer
Patent: WO 0078358-A 3 28-DEC-2000;
The Collaborative Group, Ltd. (US)
The Collaboration/Qualifiers
1. .4597
                                                                                                                              Length 4341;
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; Pred. No. 9.3e-24;
0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/noTe="Vector pVAC1"
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Cancer Research Ventures Limited (GB)
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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unclassified.
unclassified.

I (bases 1 to 4341)

Hawkins, R.E., Russell, S.J., Stevenson, F.K. and Winter, G.P.
Hawkins, R.E., Russell, S.J., Stevenson, F.K. and Winter, G.P.
IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
REDICAL: WO 9408008-A 58 14-APR-1994;
REDICAL: WO 9408008-A 58 14-APR-1994;
Cher publication AU 4832493 940436
Other publication AU 4832493 940436
Other publication JP 8501699T 960227.

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OS Unidentified
PN UP 2001503638-A/5
PD 21-MAR-2001
PF 13-NOV-1997 UP 1998522958
PR 15-NOV-1996 US 08/751517,14-FEB-1997 US 08/6
PR 15-NOV-1996 US 08/751517,14-FEB-1997 US 08/6
PR 15-NOV-1996 US 08/751517,14-FEB-1997 US COTH21/04 (20785)0. AGIK38/10. AGIK38/12
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source /organism='Unidentified'.
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Tissue specific expression of retinoblastoma protein.
BD009731
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1 (bases 1 to 4249)
Antelman, D. Gregory, R. J. and Wills, K. N.
Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 5 21-MAR-2001;
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100.0%; Pred. No. 9.3e-24;
tive 0; Mismatches 0;
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JP 2001503638-A/5.
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established comm ercially available vectors that are cited
with their vendor within the patent applicatio"
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Patent: JP 2002520000-A 18 09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other sequences; artificial sequences.
1 (bases 1 to 5053)
Fikes,J.D., Hermanson,G.G., Sette,A., Ishioka,G.Y., Livingston,B. and Chesnut,R.W.
                                                                                                                                                             1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="pCDNA3.1/GS vector by Invitrogen Corporation"
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Patent: WO 0119853-A 1 22-MAR-2001;
THE UNIVERSITY OF SHEFFIELD (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 100; DB 6; Best Local Similarity 100.0%; Pred. No. 9.2e-24; Matches 100; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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JP 2002520000-A/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
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OS Artificial Sequence
PN JP 2002520000-A/18
PD 09-UUL-2002
PF 13-MAY-1999 UP 200548449
PR 13-MAY-1999 US 60/085751 PI
JOHN D FIKES, GARX G HERMANSON, ALESSANDRO
SETTE, GLENN Y ISHIORA,
PC CIZNIS/09, A61K31/711, A61K39/00, A61K39/12, A61K39/21, A61R39/29,
PC A61P31/16, A61P31/20, A61R31/10, A61P37/02, C12N15/00
CC vector PEP2 Location/Qualifiers
FH Key Location/Qualifiers
FT source //organism='Artificial Sequence'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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0
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                                                                                                                                                                                                                                                                                                                            ce 1. .5053
/organism='Artificial Sequence'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               1. .5053
/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 100; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                        nucleic search, using sw model
                                                                                      OM nucleic
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July 14, 2005, 04:35:42 ; Search time 140.988 Seconds Run on:

(without alignments)
4198.742 Million cell updates/sec

US-09-482-682-47\_COPY\_1\_100

Title: Perfect score:

1 gacggatcgggagatctccc......ctgctccctgcttgtgtgtt 100 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003ds:\* geneseqn2004as:\* geneseqn2004bs:\* geneseqn2003cs: geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\* N\_Geneseq\_16Dec04:\* geneseqn2002as:\* geneseqn1990s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score 1 100 2 100 3 100 4 100	00000000000000000000000000000000000000	Query Match 100.0 100.0 100.0	Match Length DB Match 1506 12 100.0 1506 12 100.0 1600 2 100.0 2241 1100.0 2294 1100.0 3853 2 100.0 4026 2 2		1D ADM41035	Description
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W 44 70	00000	100.0	1782 2241 2294 3853 4026	12	AUGIT 1343	Adh11349 Vertebrat
4.2	0000	100.0	2241 2294 3853 4026	13	ADM41037	Adm41037 Cytomegal
5	000	100.0	2294 3853 4026	7	ADM41034	Adm41034 Human nuc
	007	100	3853 4026	12	ADM41036	Adm41036 Cytomegal
9	0		4026	0	AAV40006	Aav40006 Plasmid p
7 1	2	100.0		7	AAV40007	Aav40007 Plasmid p
89	007	100.0	4249	7	AAV63466	Aav63466 Plasmid p
9	001	100.0	4341	7	AAQ62391	Aaq62391 Vector pv
10	001	100.0	4341	9	AAS17704	Aas17704 Vector pV
11	001	100.0	4341	ø	ABN83143	Abn83143 Plasmid p
12	001	100.0	4597	4	AAF24901	Aaf24901 Nucleotid
13 1	100	100.0	4639	9	AAD39652	Aad39652 Human sma
14 1	100	100.0	4840	4	AAF83146	Aaf83146 Complete
15	100	100.0	5015	10	ADB33528	Adb33528 Expressio
16 1	100	100.0	5053	е	AAZ38633	Aaz38633 pEP2 expr
17 1	001	100.0	5070	4	AAS12839	Aas12839 DNA seque
18	001	100.0	5082	7	ADH11417	Adh11417 Plasmid p
19 1	001	100.0	5162	10	ADF10526	Adf10526 Plasmid p
20	001	100.0	5162	10	ACC44637	Acc44637 Murine rD

Ada75099 Plasmid p Acc44692 Plasmid p Abv77540 Plasmid p Abv77538 Plasmid p	Abv77549 Plasmid p Ad334681 Nucleotid Abv77539 Plasmid p Adh11233 Vertebrat	Abn86685 Nucleotid Ade21866 Plasmid v Ado5277 pcDNA3 pl Aaz89476 Transgeni	Aas18619 Renilla l Abl53540 Vector pc Adn36314 Plasmid p Abl58494 Recombina Abl58494 Recombina	ADIO953 RCCOMDING ADK88868 TOPOISOME Ade83791 Plasmid p Ado06720 Recombina ADI58489 Recombina	
ADS75099 ACC44692 ABV77540 ABV77538	ABV77549 ADI34681 ABV77539 ADH11233	ABN86685 ADE21866 ADO05277 AAZ89476	AAS18619 ABL53540 ADN36314 ABL58494	ABK88868 ADE83791 ADO06720 ABL58489	ABL58490 AAQ88310 AAI66195 ABK40237
13	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	9 17 3	9 2 7 9 9	175	0 N N O
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23 23 24	25 26 27 28	31 31 35 35	8 8 8 8 6 8 4 6 6 6	0 W W 44 4	. 4. 4. 4. 1. 6. 4. 7.

## ALIGNMENTS

ВЪ. ADM41035 standard; DNA; 1506 (first entry) 17-JUN-2004 ADM41035; RESULT 1 ADM41035 

Fungus nucleotide sequence SEQ ID NO:3.

engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; fungus; gene; ds.

Unidentified

WO2004027029-A2.

01-APR-2004.

17-SEP-2003; 2003WO-US029251.

19-SEP-2002; 2002US-0411790P.

(XIME-) XIMEREX INC.

Thompson SC; Beschorner WE, Sosa CE,

WPI; 2004-295402/27.

Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.

Disclosure; SEQ ID NO 3; 48pp; English.

The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replacement cells so the tissue of the fetal non-human mammal host.

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                                                                                                                                                                                                                                                                                           GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                     1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNC-53 vertebrate protein homologue, UNC-53; Caenorhabditis elegans; cell shape regulator; cell motility regulator; cell migration, cell behaviour regulator; phenotype; signal transduction pathway; signal transducing protein; signal integrator protein; neuronal regeneration; revaculatisation; wound healing; chronic neurodegeneration; disease; acute traumatic injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoting neuronal regeneration, treating chronic neuro-degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Verhasselt P;
Vandekerckhove JS;
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                                                                                                                                                                                            DB 12; Length 1506;
                                                                                                                                                       Seguence 1506 BP; 454 A; 277 C; 361 G; 414 T; 0 U; 0 Other;
                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                               4e-26;
                                                                                                                                                                                        100.0%; Score 100; I
100.0%; Pred. No. 4e-
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases or acute traumatic injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH11349 standard; DNA; 1600 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibrotic disease; gene; ds.
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                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ADH11350
                                                                                                                    specification
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a compound identified as an enhancer or inhibitor of the regulation of cell shape, motility, or the direction of cell migration for use as a therapeutic; (7) a method for determination of whether a protein is an inhibitor or enhancer of regulation of cell behaviour, growth, shape or contility or the direction of migration by contacting a host cell expressing a homologue of UNC-53 and determining a change of phenotype; (8) a method for identification of vertebrate homologues of C. elegans unc-53 gene by hybridising a probe of 15-50 bp of the unc-53 sequence to conclude in the signal transduction pathway of a cell of which a vertebrate homologue of UNC-53 is a component comprising; (i) contacting an extract of a cell with an antibody to the UNC-53 homologue; (ii) identifying an antibody/homologue complex, and (iii) analysing such a complex to dentify any non-antibody protein bound to the complex. UNC-53 is a signal transducing or signal integrator protein involved in controlling directionality of cell migration and cell shape in C. elegans. Vertebrate complexes of UNC-53 can be used to promote neuronal regeneration, revascularisation or wound healing, to treat chronic neurodegenerative diseases or acute traumatic injuries or fiberotic diseases. The present constitution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 100; DB 2; Length 1600; Pred. No. 4.1e-26; 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1600 BP; 397 A; 409 C; 398 G; 396 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
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Best Local Similarity 100.7
Matches 100; Conservative
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mammalian host, and for producing chimeric mammals that can be used

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replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; human; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                           1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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                                                                                                                                                                                                                                                                                     Sequence 1782 BP; 458 A; 399 C; 451 G; 474 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                                                                                                                                                                            100.0%; Score 100; DB 12; 100.0%; Pred. No. 4.2e-26;
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                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human nucleotide sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM41034 standard; DNA; 2241 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-SEP-2002; 2002US-0411790P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-2003; 2003WO-US029251
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                                                                                                                                                                                                                                                                                                                                                                 Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-295402/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (XIME-) XIMEREX INC
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                  specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-2004
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                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
ADM41034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells in the cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to
                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                     1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                 develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.
                                                                                                                                                                                                                                                 1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                           ;
0
                                                                                                                                 Sequence 2241 BP; 498 A; 630 C; 609 G; 504 T; 0 U; 0 Other;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                             CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                 CCGCATAGITAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                     Score 100; DB 12;
Pred. No. 4.5e-26;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-295402/27.
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                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004027029-A2
                                                                                           specification
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Best Local Simi
Matches 100;
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mastadenovirus.
unidentified bacteriophage; T7.
unidentified bacteriophage; SP6
Macaca mulatta; polyoma virus.
                                    Example 1; Fig 4; 91pp; English
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                                                                                                                                                                                                                                                                                                                                     100.0%;
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/note= "SP6 ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc feature
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15-FEB-1999
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                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter
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                                                                                                                             GACGGATCGGGAGATCTCCCCTATGGTCGACTCTCAGTACATCTGCTCGATG 60
                                                                                                       1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fusion polypeptide of, e.g. transcription factor - used to treat,
                                                                       Gaps
                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        E2F; transcription factor; human; retinoblastoma protein RB; bladder cancer; restenosis; angioplasty; diabetic retinopathy; thyroid hyperplasia; Grave's disease; psoriasis; benign prostatic hypertrophy; Li-Fraumeni syndrome; peripheral vascular disease; therapy; plasmid pCTM; ss.
                                100.0%; Score 100, DB 12; Length 2294; 100.0%; Pred. No. 4.5e-26; cive 0; Mismatches 0; Indels 0;
Sequence 2294 BP; 466 A; 680 C; 641 G; 507 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function= "tripartite leader sequence"
                                                                                                                                                                         CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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/note= "pUC19 backbone H3 to AatII"
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/note= "CMV promoter"
907. .1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wills KN;
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/note= "AMP-ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified bacteriophage; T7.
unidentified bacteriophage; SP6.
Macaca mulatta; polyoma virus.
Bos taurus.
                                                                                                                                                                                                                                                                                                   AAV40006 standard; DNA; 3853 BP.
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                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytomegalovirus.
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                                                  Local Similarity
les 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CANJ-) CANJI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pCTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2003
15-FEB-1999
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                                                                                                                                                                                                                                                                                                                                     AAV40006;
                                                                                                                                                                           61
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric
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                                                                     Matches
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This is the nucleotide sequence of pCTM, a plasmid which contains a CMV promoter, a tripartite adenovirus leader flanked by T7 and SP6 promoters, and a multiple cloning site with a bovine growth hormone polyA site and downstream SV40 polyA site. It has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastcoma protein (BP, see AAW62465) and BZF transcription factor (see AAW62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to traat hyperproliferative conditions, specifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the BZF promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
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e.g. hyper-proliferative disease such as cancer and restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3853 BP; 936 A; 986 C; 942 G; 989 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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/note= "pUC19 backbone H3 to AatII"
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; Pred. No. 5.2e-26;
0; Mismatches 0;
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/note= "CMV promoter"
907. .1074
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Macaca mulatta; polyoma virus.
                                                                                misc_feature
                                                                                                                                                                                                                                            misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1998
              Bos taurus.
                       Chimeric.
                                                    promoter
                                                                                                                                                                                enhancer
                                                                                                                                                                                                               enhancer
                                                                                                                                                                                                                                                                                                             promoter
                                                                                                                  intron
                                                                                                                                                                                                                                                                              intron
                                                                                                                                                mRNA
                                            Key
                                                                                                                                                                                                                                                                                                                                                                          CDS
 This is the nucleotide sequence of pCTMI, a plasmid that was constructed from pCTM (see AAV40006) by digesting pCTM with XhoI and NotI and subcloning a 180 bp intron XhoI-NoII fragment from a pCMW-beta-gal vector. Plasmid pCTMI has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastoma protein (BP, see AAW62465) and E2F transcription factor (see AAW62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, specifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the E2F promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct os field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                 New fusion polypeptide of, e.g. transcription factor - used to e.g. hyper-proliferative disease such as cancer and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E2F; transcription factor; human; retinoblastoma protein RB; bladder cancer; restenceis; angioplasty; diabetic retinopathy; thyroid hyperplasia; Garave's disease; pscriasis; benign prostatic hypertrophy; Li-Fraumeni syndrome; peripheral vascular disease; therapy; plasmid pCTMIE; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4026;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4026 BP; 978 A; 1021 C; 982 G; 1045 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 100; DB 2;
100.0%; Pred. No. 5.3e-26;
iive 0; Mismatches 0;
 complement (3032, .3890)
                                                                                                                                                         Wills KN;
            /*tag= f
/note= "AMP-ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mastadenovirus.
unidentified bacteriophage; T7.
unidentified bacteriophage; SP6.
                                                                                                                                                                                                                                 Example 1; Fig 6; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV63466 standard; DNA; 4249 BP
                                                                                 97WO-US021821
                                                                                                    96US-00751517.
97US-00801092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                         Gregory RJ,
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                              WPI; 1998-297858/26
                                                                                                                                    (CANJ-) CANJI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pCTMIE.
                                                                                                    15-NOV-1996;
14-FEB-1997;
                                       WO9821228-A1
                                                                                13-NOV-1997;
                                                           22-MAY-1998.
                                                                                                                                                         Antelman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2003
15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV63466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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This is the nucleotide sequence of pCTMIE, a plasmid that was constructed by amplifying the SY40 enhancer from SY40 viral DNA by PCK, digesting the amplified product with BglII and inserting into BamHI-digested plasmid pCMTI (see AA40007). Plasmid pCTMIE has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastcoma protein (BP, see AA4062465) and E2F transcription factor (see AAM62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to trath hyperproliferative conditions, specifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the E2F promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion polypeptide of, e.g. transcription factor - used to treat, e.g. hyper-proliferative disease such as cancer and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4249 BP; 1020 A; 1074 C; 1048 G; 1107 T; 0 U; 0 Other;
                                                                                                                                        "tripartite leader sequence"
                                                                                                                                                                                                                                                                                                                                                              bp tandem repeat enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "72 bp tandem repeat enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to AatII"
                                                                                                                                                                                      *tag= c
note= "hybrid SV40 late intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "hybrid SV40 late intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
"T antigen binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "pUC19 backbone H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (3255. .4113)
                                        *tag= a
/note= "CMV promoter"
907. .1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            = "SP6 promoter"
.4249
                                                                                                                                                                                                                                                                *tag= d
note= "early mRNA"
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antelman D, Gregory RJ, Wills KN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "AMP-ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 8; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US021821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-00751517.
97US-00801092.
                                                                                                                                                               081. .1145
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                                                                                                                                                                                                                                         .1366
                                                                                                                                                                                                                                                                                                                .1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1545
                                                                                                                                                                                                                                                                                                                                            "72
                                                                                                                                        function=
                    .864
                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                            *tag=
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                                                                                                                                                                                                                                           164.
                                                                                                                                                                                                                                                                                                                261.
                                                                                                                                                                                                                                                                                                                                                                                          333.
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                                                                                                                   9
                                                                                                                                                            1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector, pVAC1; pRc/RSV; leader sequence; termination signal; fusion protein; pSfi/Not.Tag1; pelB leader; human; immunoglobulin; VH1; single chain; Fv; murine antibody; retroviral; envelope; plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the vector pVAC1. This vector is based on the
                                                                                                                 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating immune response to a disease marker - by administering a vector which expresses the disease marker to interact with the immune
                                                                        Gaps
                                                                     .;
0
                        Length 4249;
                                                                   Indels
                                                                                                                                                                                                          61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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                     ; Score 100; DB 2;
; Pred. No. 5.4e-26;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (1. .775)
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/note= "Claim 8"
606. .716
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'note= "Claim 9"
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/note= "Claim 7"
                                                                                                                                                                                                                                                                                                                                                                       AAQ62391 standard; DNA; 4341 BP
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                        100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
         Query Match
Best Local Similarity 100.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9408008-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector pVAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hawkins RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ62391;
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                                                                                                                                                                                                                                                                                                                            RESULT 9
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The invention relates to a nucleic acid construct for delivery into living cells in vivo, to induce an immune response to a disease peptide antigen, where the construct directs expression of a fusion protein comprising the peptide antigen and the first domain of Frc. Also included are a nucleic acid vector comprising the above construct or vector and a method of producing a nucleic acid construct for vector and a method of producing a nucleic acid construct for inducing an immune response. The method comprises identifying a nucleic acid sequence encoding a disease peptide comprises dentifying a pricipes characteristic of the disease cloning the nucleic acid sequence, introducing the cloned nucleic acid into a vector which allows the antigen to be expressed as a fusion with a first domain Frc from tetanus toxin, and optionally isolating the construct from the vector. The construct for vector is used as a vaccine to induce an immune response, particularly to tumour antigene. The present sequence is vector
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                                                                                                                                                                                                                                                1 GACGGATCGGGAGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTCGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTL; PCR primer; pVAC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            including cancer, expresses the first domain of tetanus toxin FrC fused to a disease peptide antigen to provide a vaccine.
antibody/retroviral envelope fusion protein can be used as a plasmid vaccine and it induces a strong humoral response to the antibody moiety in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                       1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid construct, useful to immunize against various diseases
                                                                                          Sequence 4341 BP; 1032 A; 1099 C; 1091 G; 1119 T; 0 U; 0 Other;
                                                                                                                                                                            ;
0
                                                                                                                                   DB 2; Length 4341;
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                             61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                                                                                                                                                                                                                                                                                                                      CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                                                                                                                 Query Match 100.0%; Score 100; DB 2; Best Local Similarity 100.0%; Pred. No. 5.4e-26; Matches 100; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vector pVAC1 encoding a DNA vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS17704 standard; DNA; 4341 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2000; 2000GB-00009470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stevenson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-066370/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium tetani.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2001
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GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide is administered to the patient. The construct is also useful in medical treatment, and in the preparation of a vaccine for treating or preventing a disease state associated with the antigen. The sequence shows the complete sequence of vector pVAC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immune response; plant viral coat protein; pVAC1; cytostatic; virucide; cancer; B cell malignancy; ds.
                                                                                                                                    1 GACGGATCGGGAGATCTCCCCAATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                             1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid construct for delivery into living cells as a vaccine, useful for treating e.g. cancer, directs the expression of a fusion protein comprising an antigen and an adjuvant sequence derived from a
                                                                             Gaps
Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
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0
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                                       Length 4341;
                                                                           0; Indels
                                                                                                                                                                                        CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                                                            CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                   100.0%; Score 100; DB 6;
100.0%; Pred. No. 5.4e-26;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pVAC1 complete sequence.
                                                                                                                                                                                                                                                                                                                         ABN83143 standard; DNA; 4341 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2001; 2001WO-GB005142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Savelyeva N, Stevenson F;
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                     al Similarity 100.
100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant viral coat protein.
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                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                               ABN83143;
                                   Query Match
                                                       Best Local
                                                                         Matches
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The specification describes a microsphere comprising dihydrazide derivatised hyaluronic acid crosslinked to a nucleic acid (NA). The microspheres cause reduced inflammatory responses, and have increased safety and biodegradability. The microspheres are useful for transfecting a cell of a subject and for treating a subject having myocardial ischemia, by increasing cardiac anglogenesis. They are also useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hyaluronic acid micro spheres for use in gene therapy of myocardial ischemia and hemophilia, comprising dihydrazide derivatized hyaluronic acids crosslinked to nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating haemophilia. The present sequence represents the plasmid pCDNA3.1/GS, into which is inserted a polymucleotide sequence which is crosslinked to hyaluronic acid. The polymucleotide sequence encodes a vascular endothelial growth factor (VBGF)
1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGGATCGGGAGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                           Microsphere, dihydrazide, hyaluronic acid, inflammatory response, myocardial ischemia, cardiac angiogenesis, haemophilia, vascular endothelial growth factor, VEGF, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4597 BP; 1062 A; 1214 C; 1206 G; 1115 T; 0 U; 0 Other;
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                                                                61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                          CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CCCCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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                                                                                                                                                                                                                                                                          Nucleotide sequence of the plasmid pCDNA3.1/GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 36-38; 38pp; English.
                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COLL-) COLLABORATIVE GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2000; 2000WO-US016837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0%;
Matches 100; Conservative 0
                                                                                                                                                                AAF24901 standard; DNA; 4597
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-071363/08.
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200078358-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999;
                                                                                                                                                                                                                                       20-APR-2001
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                                                                                                                                                                                                    AAF24901;
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                                                                                                                             RESULT 12
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RESULT 13 AAD39652

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Gaps

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100.0%; Score 100; DB 6; Length 4341; 100.0%; Pred. No. 5.4e-26; ive 0; Mismatches 0; Indels 0;

Query Match 100. Best Local Similarity 100. Matches 100; Conservative

AAD39652

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The invention provides a nucleic acid molecule (I) comprising at least the functional part of blasticidin resistance (BS) gene, or its homolog, linked through a recognition sequence to at least one selected gene. (I) is useful in treatment comprising:(I) providing cells/tissues transfected with (I); (2) surgical administration of the cells/tissues to the patient to be treated; and optionally (3) monitoring the status of the cells/tissues by the patient. Therapeutic compositions comprising cells/tissues transformed with (I) is useful in identifying the role of genes in healthy and diseased tissue, in tissue engineering and in cosmetic surgery. Tissue engineering can be used to treat arthritis, joint replacement, skin grafts for burn victims, and replacement coronary arteries. Cosmetic tissue surgery includes rhinoplasty. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion protein; amyloid precursor protein; APP; transcription factor;
nootropic; neuroprotective; APP inhibitor;
amyloid precursor protein inhibitor; Alzheimer's disease; beta-secretase;
                                                                                                                                                                                                                                                                                  Novel nucleic acid molecule useful for therapeutic and cosmetic tissue engineering, comprising at least a functional part of blasticidin resistance gene linked through a recognition sequence, to a selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4840 BP; 1154 A; 1227 C; 1236 G; 1223 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 100; DB 4; Length 4840; 100.0%; Pred. No. 5.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression vector nucleotide sequence SEQ ID NO:27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                               Kafienah W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma-secretase; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig C; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB33528 standard; DNA; 5015
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                                                              11-SEP-2000; 2000WO-GB003462
                                                                                                         99GB-00021418
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                                                                                                                                                                                               Hollander AP, Barker MD,
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                                                                                                                                                   (UYSH-) UNIV SHEFFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       containing the BS gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003072041-A2
                                                                                                       11-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2003
                  22-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a recombinant vector which comprises DNA, consisting of an insertion cassette contained between at least two insertion sites, that encodes a small nuclear (sn) RNA. The invention is used to identify snRNA modifications that inhibit expression of transcription products (and the identified snRNA are used to suppress expression) for delivering antisense sequences to the nucleus and to create transgenic animals. The present DNA sequence is human snRNA, UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant vector containing sequence for small nuclear RNA, useful e.g. for identifying variant snRNA that suppresses expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blasticidin resistance, BS gene, gene therapy, tissue engineering, cosmetic surgery, arthritis, joint replacement, skin graft, rhinoplasty,
                                                                                                                                                              Human; recombinant vector; insertion cassette; small nuclear RNA; snRNA; transgenic animal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4639;
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100.0%; Pred. No. 5.5e-26;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete sequence of vector pIRES/BS.
                                                                                                                              Human small nuclear RNA (snRNA) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВР
AAD39652 standard; DNA; 4639 BP
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                                                                                                                                                                                                                                                                                                                                                                           12-MAR-2001; 2001US-00804481
                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-2000; 2000US-0188304P
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                                                                                     (first entry)
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Best Local Similarity 100.
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lander ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-499510/53.
                                                                                                                                                                                                                                                                                      US2002058287-A1
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                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                16-MAY-2002.
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                                                                                  22-OCT-2002
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RESULT 14 AAF83146

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27-FEB-2002; 2002US-0360274P.
              Espeseth AS, Ferrer M,
Miller MD, Register B,
        (MERI ) MERCK & CO INC
                      WPI; 2003-689968/65.
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Flores OA, Hazuda DJ, Inglese J; Shi X, Simon AJ, Zuck PD;

DNA encoding a fusion protein of amyloid precursor protein, useful in screening for anti-Alzheimer agents, comprises a fused transcription factor.

Disclosure; Fig 32B-F; 193pp; English.

The present introduction describes a sum miscense of amyloid precursor protein (FP) comprising: (i) an amino acid sequence of amyloid precursor protein (APP), either the wild type, Swedish or NFEV versions; and (ii) a cranscription factor (TP), fused in frame to the C-terminus of (i). Also described: (1) an expression vector containing (1); (2) a cukaryotic cell cinhibite processing of APP, using the cells of (2). (i) has nootropic and neuroprotective activities. (i) can be used to produce cukaryotic cells that express FP and are useful in screening for agents that inhibit the express FP and are useful in screening for agents that inhibit correction of Alzheimer's disease. Cells that express FP can screen for inhibitors of: (a) beta- and gamma-secretases; and (b) cytoplasmic/extracellular APP signaling in a single assay. Cell-based assays may be free of interference from alpha-secretase activity and are homogeneous (no chromatography, immunoprecipitation or washing required) so well suited to high-throughput screening. The present sequence The present invention describes a DNA molecule (I) that encodes a fusion represents a plasmid nucleotide sequence from the present invention.

Sequence 5015 BP; 1167 A; 1297 C; 1279 G; 1272 T; 0 U; 0 Other;

Gaps . 0 100.0%; Score 100; DB 10; Length 5015; 100.0%; Pred. No. 5.6e-26; tive 0; Mismatches 0; Indels 0; Query Match
Best Local Similarity 100.
Matches 100; Conservative

1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60 1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG

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61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100

Search completed: July 14, 2005, 07:01:42 Job time : 141.038 secs

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100004F18 100003C08

BZ050047

100003117 100004J13 100004E20 100005001 100002J14

100002K13 100006M24

100003A09

CC818492 CC817661 CC818511 CC818574 CC819049 CC817069 CC817069 CC817762 CC817762 CC817762 CC817762 CC817762 CC817762 CC817763 CC817763 CC8177763 CC8177763 CC8177763 CC8177763 CC8177763 CC8177763 CC8177777

100003G07 100003B21

nucleic

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Run on:

Sequence:

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/organism="Cryptosporidium parvum"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="texon:5807"
/db xref="texon:5807"
/db b xref="texon:5807"
/done lib="CpiOWAgDNA2"
/note="Vector: PCR-Script Amp SK+; Site 1: SrfI; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared coproduce fragments having a tight, size distribution between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center
                                                                                                                                                                                                                                                                                                                                            CpG0047A CpIOWAgDNA2 Cryptosporidium parvum genomic, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted sequence has been edited to remove vector sequences 5' the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Alveolata; Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 602)
Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 602.
Location/Qualifiers
1. .602
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                                                      CC818511
CC818574
CC819049
CC817069
                                                                                                  CC817074
CC820036
CC817652
CC817682
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CC819240
                                                                                                                                                                                     CC817834
                                                                                                                                                                                                            CC819820
                                                                                                                                                                           CC818384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: malaria@itsa.ucsf.edu
                                                                                                                                                                                                                                                                                                                                                                                                         Cryptosporidium parvum
Cryptosporidium parvum
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B67169.1 GI:2642750
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Seg primer: T7
Class: shotgun
Francisco
sequence.
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B67169
LOCUS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
 B67169 CpG0047A Cp
BZ052929 jnr13903.
BZ050328 jnr42c12.
BZ054067 jnr38b09.
AW409112 sall0h5 S
AL715724 AL715724
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BZ051815 jnr57d03.
BZ052857 jnr13g03.
BZ050646 jnr66f08.
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nbeb0022E
CIT-HSP-2
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212009.p1
207j04.p1
209p08.p1
ISB1-118J
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jnq98d01.
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                                                                           July 14, 2005, 05:15:57; Search time 952.146 Seconds (without alignments) 3997.736 Million cell updates/sec
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                                                                                                                                                   gacggatcgggagatctcc......ctgctccctgcttgtgtgtt 100
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CK119397 2
CK120360 2
CK117844 2
CK1141237 I
CL140877 I
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BZ049113
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                                                                                                                                                                                                                                     68479088
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                              34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                         US-09-482-682-47_COPY_1_100
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                                                       nucleic search, using sw model
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AW409112
AL715724
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CK119397
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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92b_est2:;

93b_est43:;

93b_est6:;

93b_gs81:;

95b_gs81:;
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1009
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Perfect score:
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GSS 12-MAY-2000

linear

California, San

100003A24 100003M12 100006H09 100004J10

100003F16

Minimum DB 8 Maximum DB 6

Database

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Result Š

Searched:

100005D19 100004C11

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264 GCATAGTTAAGCCAGCCCCGACACCC 239
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Matches 67; Conserv
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BZ054067/c
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KEYWORDS
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                                                                 RESULT 3
BZ050328
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(http://sequence-www.stanford.edu/group/techdev/shear.htm)
The randomly sheared gDNA was chromatographed on sephacry1 5-400 to remove any small fragments and DNA eluting in the void volume was blunt-ended with T4 DNA Polymerase, treated with alkaline phosphatase to prevent the ligation of multiple fragments, ligated to Srf I-digested pCR-Script Amp (SK+) vector and transformed into E. coli strain XIIO Gold. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 primers."
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jnr13g03.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
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//clone lib="B.Oleracea001"
//note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the Shotgun library prepared at Washington University Genome Sequencing Center."
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Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
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                                                                                                                                                                                                                                                     Length 602;
                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                   Score 60; DB 8; Le
Pred. No. 2.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Sequencing Center
Washington University School of Medicine
Baall: submissions@watson.wustl.edu
Plate: jnr13 row: g column: 03
Seq primer: -28RPpOT reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Brassica oleracea"
                                                                                                                                                                                                                                    60.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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/db xref="taxon:3712"
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High quality sequence start: 32
High quality sequence stop: 551.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Richard K. Wilson
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Best Local Similarity
Matches 67; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
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Best Local S
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1...696
/organism="Brassica oleracea"
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db xref="taxon:312"
/clone_lib="B.oleracea001"
/note="Yector: pOTval; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
B2050328 GSS 09-OCT-2002
jnr42c12,b1 B.oleracea001 Brassica oleracea genomic, genomic survey
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jnr38b09.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
tosida; eurosida II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 717)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
                                                                                                                                                                                                                         Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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Delebaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
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High quality sequence stop: 180.
Location/Qualifiers
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Seg primer: -21UPpOT forward
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BZ050328.1 GI:23649718
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Brassica oleracea
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Gaps

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70

EST 18-APR-2002 CDNA Danio

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AL/14571 All 345 bp mRNA .linear EST 18-APR-2002 AL714571 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA clone BN0AA007ZC02 5', mRNA sequence.
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1 (bases 1 to 343)
Coimbra, K., Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J. P., Weissenbach, J. and Perit, C. A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio (zebrafish)
Danio rerio
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
         Length 348;
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                                                                   15; Indels
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84.5%; Pred. No. 4.8e-08;
iive 0; Mismatches 11;
Score 53.6; DB 2;
Pred. No. 4.1e-08;
0; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="inner ear"
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/db_xref="taxon:7955"
/clone="BNOAA018ZF12"
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AL715724.1 GI:20180327
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ilarity 80.5%;
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AW409112.1 GI:11999687
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A high density transcript map between markers D8S550 and D8S1759 on 9p22-23, using cDNA direct selection Unpublished (2000)
Contact: Ramsay M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Boleracea001"
/rione_lib="Boleracea001"
/note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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P.O.Box 1038, Johannesburg, Gauteng, 2000, South Africa
Fax: 2711 489 9226
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   Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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Washington University School of Medicine
Baail: submissions@watson.wustl.edu
Plate: jnr38 row: b column: 09
Seq primer: -28RPpOT reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Brassica oleracea"
mol_type="genomic DNA"
db_xref="taxon:3712"
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Class: shotgun
High quality sequence start: 87
High quality sequence stop: 543.
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                                                                                             Contact: Richard K. Wilson
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/mol_type="mRNA"
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Matches 60; Conservative
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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/clone="BNOAA0072C02"
/tlssue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                      Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 314)

1 (bases 1 to 314)

Loimbra, R., Weil, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J.P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio) Unpublished (2002)
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Peilner, T., Immink, R.G.H., Cahill, D.J. and Kersten, B. Generation of a cDNA expression library from Arabidopsis inflorescence meristem
Unpublished (2003)
Contact: Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ihnestr. 73, D-14195 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             th 53.4%; Score 53.4; DB 1; Length 345; Similarity 84.5%; Pred. No. 4.8e-08; 60; Conservative 0; Mismatches 11; Indels C
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Insert Length: 761 Std Error: 0.00
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/ecotype="Columbia"
/db_xref="GABI:954234"
/db_xref="taxon:3702"
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                                                                                                                                                                           Contact: Genoscope
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/tissue_type="inflorescence meristem"
/dev stage="about one week after bolting"
/lab_host="E. coli SCS-1/pSB111"
/clone_lib="Abut lab" | SCS-1/pSB111"
/clone_lib="Abut lab" | SCS-1/pSB111"
/note="Vector: pQE-30NAST-attB (AY386205); Site_1: SalI; Site_2: NotI; About lawek after bolting, cDNA synthesis laing SuperscriptTM-system (Invitrogen) with an oligo(dT)-primer containing NotI restriction site and a SalI adapter. The main library (plate numbers begin with lof 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209908.pl AtMl Arabidopsis thaliana cDNA clone MPMGp2011P08209
5-PRINE, mRNA sequence.
Site 2: Not1; About 1 week after bolting, cDNA synthesis using SuperscriptTM-system (Invitrogen) with an oligo(dT)-primer containing Not1 restriction site and a SalI adapter. The main library (plate numbers begin with (plate numbers begin with 201) containing 5,000 putative expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) containing to the rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GMBI-LARP; data are also accessible at https://gabi.rzpd.de"
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             679 TTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 620
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Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Innestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
Fax: +49(0)30/84131128
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Insert Length: 788 Std Error: 0.00
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/ecotype="Columbia"
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/db_xref="taxon:3702"
/clone="MPMGp2011P08209"
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Best Local Similarity
Matches 60; Conserv
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COMMENT

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CL141237 898 bp DNA linear GSS 05-JAN-2004 ISB1-118J17_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-118J17,
expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at
                                                                                                                                                                                                                                                               514 TTCACACCCCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 455
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
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1 (bases 1 to 898)
Kremirzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
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                                                                                                                                                                                             11; Indels
                                                                                                                                                  53.4%; Score 53.4; DB 7;
llarity 84.5%; Pred. No. 5.7e-08;
Conservative 0; Mismatches 11;
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Email: submissions@watson.wustl.edu
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/mol_type="genomic DNA"
/db_xref="taxon:8364"
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High quality sequence stop: 742.
Location/Qualifiers
                                                                                     https://gabi.rzpd.de"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence.
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RESULT 12 CL140877/c

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  Class: BAC ends
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CL140877 899 bp DNA linear GSS 05-JAN-2004 ISB1-118B12_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-118B12,
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Xenopus tropicalis

Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1009)

Kremitzki,C., Carrer,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)
                                                                                                                                          Xenopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Barrachia; Amura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
I (Dases I to 899)
I (Asemitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
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/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
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                                                                                                                                                                                                                                                                                                                                           Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wateson.wustl.edu
Inseri_Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAAGG
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Washington University School of Medicine
mail: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTATAAGG
                                                                                                                      Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Xenopus tropicalis"
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/db_xref="taxon:8364"
/clone="ISB1-118B12"
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High quality sequence stop: 681.
Location/Qualifiers
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                                      genomic survey sequence.
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CL123953.1 GI:40617588
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High quality sequence start: 167

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1. Location/Qualifiers

1. Location
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Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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Query Match

53.2%; Score 53.2; DB 8; Length 814;

Best Local Similarity 78.0%; Pred. No. 6.7e-08;

Matches 64; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 7 TCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCAT 66

Db 279 TGGGCGGATTTTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCAT 338

Qy 67 AGTTAAGCCAGTATCTGCTCCC 88

ORIGIN

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica. Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K. Whole genome shotgun reads from Brassica oleracea Unpublished (2002) Contact: Richard K. Wilson Genome Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu Plate: jnr57 row: d column: 03 Seq primer: -21UPpOT forward High quality sequence start: 29 High quality sequence stop: 94. Location/Qualifiers BZ051815 BZ051815.1 GI:23652690 (bases 1 to 675) Brassica oleracea Brassica oleracea 1. .675 Class: shotgun sequence. VERSION KEYWORDS SOURCE ORGANISM source REFERENCE AUTHORS ACCESSION JOURNAL FEATURES TITLE COMMENT

igh quality sequence stop: 94.

Location/Qualifiers

1. 675
/organism="Brassica oleracea"
//mol type="genomic DNA"
//db\_xref="taxon:3712"
//clone=lib="8.oleracea001"
//note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center.

Score 53; DB 8; Length 675; Pred. No. 7.6e-08;

53.0%; 75.6%;

Query Match Best Local Similarity

ORIGIN

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| Matches 65; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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Search completed: July 14, 2005, 23:23:05 Job time : 952.146 secs THIS PAGE BLANK (USPTO)

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Run on:

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A91754 Sequence 10
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BD234590 Screening
AX026821 Sequence
AX202478 Sequence
AX202478 Sequence
AX202478 Sequence
AX302478 Sequence
AR367288 Sequence
AR40324 Sequence
AX6591 Sequence
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AX213182 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Lu,X., Sun,L. and Zhang,Y.
Novel plasmid dna vectors
Patent: WO 0151626-A 10 19-JUL-2001;
ELIM BIOPHARMACEUTICALS, INC. (US)
Location/Qualifiers
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/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="commercial plasmid"
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                                                           AX202478
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                                                                     July 14, 2005, 04:39:07; Search time 756.618 Seconds
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BD268252 A
CQ788637 S
          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                       4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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9b_pr: *

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Minimum DB Maximum DB

Database

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PAT 28-AUG-2001

3887

Result

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Gaps

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PAT 06-AUG-2001

source

FEATURES

JOURNAL AUTHORS

TITLE

ORGANISM

KEYWORDS

REFERENCE

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2243 AAGGGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCT 2302
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                                                                            Barbas, C.F., Kadan, M. and Beerli, R.
Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 12 03-MAY-2001;
Novartis AG (CRI), The Scripps Research Institute (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon.32630"
/noTe="Construct E2CLBDBS"
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Patent: WO 0146694-A 6 28-JUN-2001;
Biosignal Packard Inc. (CA)
Location/Qualifiers
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Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 11 03-MAY-2001;
Novartis AG (CH); The Scripps Research Institute (US)
Location/Qualifiers
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Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 6 03-MAY-2001;
Novartis AG (CH); The Scripps Research Institute (US)
Location/Qualifiers
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tive 0; Mismatches 0;
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Sequence 12 from Patent W00130843.
AX128351 AX128351.1 GI:14134864
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Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 8 03-MAY-2001;
Novartis AG (CRI); The Scripps Research Institute (US)
Location/Qualifiers
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Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 14 03-MAY-2001;
Novartis AG (CH); The Scripps Research Institute (US)
Location/Qualifiers
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                                                                                                                                     1. .6695
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Sequence 15 from Patent WO0130843.
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Barbas, C.F., Kadan, M. and Beerli, R.
Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 15 03-MAY-2001;
Novartis AG (CRI); The Scripps Research Institute (US)
Location/Qualifiers
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Ligand activated transcriptional regulator proteins
Patent: WO 0130843A 5 03-MAY-2001.
Novartis AG (CH) ; The Scripps Research Institute (US)
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iive 0; Mismatches 0;
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                                            Ligand activated transcriptional regulator proteins Patent: WO 0130843-A 7 03-MAY-2001; Novartis AG (CR); The Scripps Research Institute (US) Location/Qualifiers
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Sequence 1 from Patent W00130843.
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Barbas, C.F., Kadan, M. and Beerli, R.
Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 10 03-MAY-2001;
Novartis AG (CH); The Scripps Research Institute (US)
Locarion Qualifiers
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Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 2 03-MAY-2001;
Novartis AG (CR); The Scripps Research Institute (US)
Location/Qualifiers
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Sequence 2 from Patent WO0130843.
AX128341 GI:14134854
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Sequence 9 from Patent W00130843.
AX128348
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Matches 101; Conservative
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Barbas, C.F., Kadan, M. and Beerli, R.
Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 9 03-MAY-2001;
Novartis AG (CH); The Scripps Research Institute (US)
Location/Qualifiers
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Ligand activated transcriptional regulator proteins
Patent: WO 0130843-A 3 03-MAY-2001;
Novartis AG (CH); The Scripps Research Institute (US)
Location/Qualifiers
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2702 TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC 2742 Search completed: July 14, 2005, 14:03:32 Job time : 756.618 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries

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## ALIGNMENTS

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss. Human NOV55b encoding cDNA SEQ ID NO:247. Location/Qualifiers ADA05887 standard; cDNA; 2017 BP. (first entry) Homo sapiens 06-NOV-2003 ADA05887; Key RESULT 1 ADA05887 

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16-MAY-2002; 2002US-0378077P.
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01-OCT-2002; 2002US-00262511.
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Patturajan M, Spytek KA,
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The present invention describes NOVX proceins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) at kit comportising in one or more described above and a carrier; (2) at the composition described above; (3) an isolated mucleic acid molecule which encodes a NOVX protein of the invention; (4) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) a cell comprising the mucleic acid molecule described above; (6) a cell comprising the mucleic acid molecule of presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (6) a disease associated with altered levels of expression of the above adsease associated with altered levels of expression of the above; (10) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for medulator of activity or of latency or predisposition to a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of such a pathology that the polypeptide; (12) a method for modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method of mammal; and (14) a method for producing the above polypeptide in a method for producing the above polypeptide is useful in method for producing the above polypeptide or the nucleic and antilipaemic activities, and can be used above; (13) method or procein continue may be used to diagnose, treat or prevent metabolic and molecule may be used to diagnose, treat or prevent metabolic diagnose, immune disorders such as Alzheimer's disease or Parkinson's disease undmand adabetes and various metabolic, the present invention mapping, itsue typing, preventive medicine and processer, inchronsome mapping, itsue typing, preventive medicine and processer, in chronsome mapping, itsue typ thson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; turajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B; A, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; A, Mikets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; en AJ, Gangolli EA, Rieger DK, Spaderna SK; New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or Claim 20; Page 316-317; 586pp; English.

(/ננחנ)

Sequence 2017 BP; 345 A; 613 C; 617 G; 442 T; 0 U; 0 Other;

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1839 AAGCGGCCGCTCGAGTCTAGAGGCCCCGTTTAAACCCCGCTGATCAGCCTCGACTGTGCCT 1898
                                           9
                                                                                                                                                                                                                                                     infectious disease; anorexia; cancer, cancer-associated cachexia;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia;
                       Gaps
                    .
0
                                                                                                                                                                                                                                            gene; human; NOVX; metabolic disorder; diabetes; obesity;
 Length 2017;
                     Indels
                                                                                            1899 TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC 1939
                                                                                   61 TCTAGTTGCCAGCCATCTGTTTGCCCCCCCCCCGTGCC 101
                       ö
  Score 101; DB 8;
Pred. No. 2.4e-24;
                     0; Mismatches
                                                                                                                                                                                                                                                                                     metabolic syndrome X; wasting disorder.
                                                                                                                                                          ADN63050 standard; DNA; 2017 BP
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2001US - 0346357P.
2002US - 0373815P.
2002US - 0373815P.
2002US - 0373817P.
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2001US-0328044P.
2001US-0328056F.
2001US-0328849F.
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2001US-0330142P.
2001US-0330309P.
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2001US-0339266P.
2001US-0343629P.
  100.0%;
100.0%;
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2001US-0327449P.
2001US-0327917P.
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2002US-0374977P
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2002US-0381042P.
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Query Match
Best Local Similarity 100.0
Matches 101; Conservative
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MILLET I.
PEYMAN J A.
KEKUDA R.
JU J.
                                                                                                                                                                                                                        Human NOV55b DNA.
                                                                                                                                                                                                                                                                                                                            US2004038223-A1.
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09-OCT-2001;
09-OCT-2001;
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18-OCT-2001;
22-OCT-2001;
24-OCT-2001;
24-OCT-2001;
                                                                                                                                                                                                                                                                                                          Homo sapiens
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17-APR-2002;
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expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides may also be used as DNA production of antibodies and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (semilar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators and integonists of the expression and activity of NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypeptide antibodies agonists may also be used as antibodies and polymucleotide may be used in this way to prevent, diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, norexia, cancer, cancer-associated with obsity, the metabolic syndrome X and wasting disorders associated with obsity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shenoy SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peyman JA, Kekuda R, Ju J, Li L, Guo X
, Edinger SR, Ellerman K, Malyankar UM;
sen BD, Anderson DW, Zhong M, Catterton
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Smithson G, Millet I, Peyman.
Patturajan M, Spytek KA, Edinger Sk, ...
Ort T, Gorman L, Zerhusen BD, Anderson DW, ZHUNG, Ji W, Miller CE, Rastelli, Stone DJ, Pena CEA, Sheno, Ji W, Miller CE, Rastelli, L, Stone DJ, Pena CEA, Sheno, Ji RA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 247; 395pp; English.
                                                                                              MALYANKAR U M.
                                                                                                                              GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                 SPYTEK K A.
EDINGER S R.
ELLERMAN K.
                                                                                                                                                                                                                                                                                                     SHIMKETS R A. ROTHENBERG M 1
                                                                                                                                                                                                                                                                                                                                                                                                                         EISEN A.
GANGOLLI E A.
                                 PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                          DIPIPPO V A.
                                                                                                                                                                                                 CATTERTON E.
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                                                                                                                                                                                                                                                                                                                                                       LEACH M D.
                                                                                                                                                                                                                                                                      STONE D J.
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BERGHS C.
                                                                                                                                                                                                                                  MILLER C | RASTELLI |
                                                                                                                                                                                   ZHONG M.
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(MALY/)
(ORTT/)
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(MILL/)
(RAST/)
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(SPAD/)
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                                                   SPYT/)
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1839 AAGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCGGTGATCAGCCTCGACTGTGCCT 1898
                                                                   9
                                                                  1 AAGCGCCCCCTCCAGTCTAGAGGCCCCCTTTAAACCCCCCTCGATCAGCCTCGACTGTGCCT
                                              Gaps
                                                                                                                                                                                                                                                                                           Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes;
Alzheimer's disease; Parkinson's disease; graft-versus-host disease;
                                                                                                                                                                                                                                                                                                                 scleroderma; hypertension; haemophilia;
idiopathic thrombocytopenic purpura; immunodeficiency; AIDS;
dyslipidemia; obesity; crohn's disease; bronchial asthma; anorexia;
cancer-associated cachexia; multiple sclerosis; fertility
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                     Length 2017;
Sequence 2017 BP; 351 A; 625 C; 599 G; 441 T; 0 U; 1 Other;
                                              Indels
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                                                                                                               TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCGTGCC 101
                       DB 12;
                    Query Match 100.0%; Score 101; DB 12; Best Local Similarity 100.0%; Pred. No. 2.4e-24; Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                    Human NOVX polynucleotide #177.
                                                                                                                                                                                               ADO42504 standard; cDNA; 2017
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2001US-0339516P.
2001US-0339517P.
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2001US-0341768P.
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                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                      AD042504;
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The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The invention also relates to antibodies specific to the NOVX polypeptides. The polypeptides, polynucleotides and antibodies are useful for manufacturing a medicament for treating a syndrome associated with a human disease, such as a pathology associated with the NOVX polypeptide. The sequences are useful for diagnosing, treating or preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host disorder, bypertension, haemophilia, idiopathic thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia, obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated cachaxia, multiple sclerosis or fertility. The nucleic acids may be used a hybridisation probes, in chromosomics. This sequence represents a human NOVX polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1839 AAGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCT 1898
                                                                                                                                                                                                New human NOVX polypeptides and nucleic acid molecules, useful for diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCGGCTGATCAGCCTCGACTGTGCCT
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DM, Li L, Macdougall JR, Miller CE,
M, Pena CEA, Peyman JA, Rieger DK;
SG, Smithson G, Spaderna SK, Spytek
Vernet CAM, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 2017 BP; 345 A; 613 C; 617 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 12;
100.0%; Pred. No. 2.4e-24;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 353; 610pp; English.
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05-DEC-2001; 2001US-0336820P.
Larochelle WJ, Lepley DM,
Padigaru M, Patturajan M,
Rothenberg ME, Shenoy SG,
Stone DJ, Taupier RJ, Ve
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Matches 101; Conservative
                                                                                                                            WPI; 2004-268786/25
                                                                                                                                                    P-PSDB; ADO42505
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                                                                                                                                                                                                                                                                              scleroderma.
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                                                              05-MAR-2002; 200203-036230F)
13-MAR-2002; 200203-0364230F)
13-MAR-2002; 200203-0364230F)
15-MAR-2002; 200203-036430RP)
15-MAR-2002; 200203-036430RP)
15-MAY-2002; 200203-0369081P,
15-MAY-2002; 200203-038081P,
15-MAY-2002; 200203-0380381P,
16-MAY-2002; 200203-038034P,
28-MAY-2002; 200203-038034P,
28-MAY-2002; 200203-0380324P,
29-MAY-2002; 200203-0380332P,
07-AUG-2002; 2002U3-0404676P,
23-AUG-2002; 2002U3-0405684P,
23-AUG-2002; 2002U3-0405684P,
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26-AUG-2002; 2002US-0406353P
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LAROCHELLE W J.
LEPLEY D M.
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MILLER C E.
ORT T.
PADIGARU M.
PATTURAJAN M.
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SMITHSON G.
SPADERNA S K.
SPYTEK K A.
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ELLERMAN K.
GANGOLLI E A.
GERLACH V.
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PEYMAN J A.
RIEGER D K.
ROTHENBERG M E
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ALSOBROOK J P.
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TAUPIER R J.
VERNET C A M.
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HERRMANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANDERSON D W.
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BOLDOG F L.
BURGESS C E.
CATTERTON E.
DIPIPPO V A.
EDINGER S R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GORMAN L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burgess CE, C
Ellerman K, G
Herrmann JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGEE)
(ALSO/)
(BERG/)
(BERG/)
(BUDD/)
(BUDD/)
(CATT/)
(EISE/)
(EISE/)
(GORM/)
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(TAUP/)
(VERN/)
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9

ROTHENBERG M E. SHENOY S G. SMITHSON G. SPADERNA S K.

SHEN/ (SPAD/)

(SMIT/)

(SPYT/) (STON/)

(TAUP/

PADIGARU M.
PATTURAJAN M.
PENA C E A.
PEYMAN J A.
RIEGER D K.

(PENA/) (PEYM/) (RIEG/) (ROTH/)

LAROCHELLE W J.

LEPLEY D M.

(LARO/) (LEPL/) (LILL/) (MACD/)

KHRAMTSOV N V.

KHRA/

HALVORSEN Y.

MACDOUGALL J R.

MILLER C E.

(MILL/) (ORTT/)

(PADI/

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2001US-0340608P.
2001US-0341144P.
2001US-0341440P.
2001US-0341540P.
2001US-0341568P.
2001US-0353286P.
2002US-0353286P.
2002US-0353288P.
2002US-03595P.
2002US-03596P.
2002US-03596P.
2002US-03596P.
2002US-03596P.
2002US-03596P.
                           2001US-0339114P.
2001US-0339514P.
2001US-0339516P.
2001US-0339511P.
2001US-0340981P.
2001US-0340390P.
2001US-0340440P.
2001US-0340565P.
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2002US-0361028P.
2002US-0361256P.
2002US-0361264P.
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2002US-0362230P.
2002US-0364181P.
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2002US-0393332P.
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                                                                                                                                                                                                                                                                                                                                                                                                            AGEE M L.
ALSOBROOK J P.
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BOLDOG F L.
BURGESS C E.
CATTERTON E.
DIPIPPO V A.
EDINGER S R.
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GANGOLLI E A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERLACH V.
GORMAN L.
                                                                                                                                    31-DEC-2001;
01-FEB-2002;
01-FEB-2002;
26-FEB-2002;
26-FEB-2002;
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15-MAR-2002; 2
17-APR-2002; 2
                                                                                                                                                                        26-FEB-2002;
27-FEB-2002;
27-FEB-2002;
28-FEB-2002;
                                                                            14-DEC-2001;
14-DEC-2001;
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28-FEB-2002;
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(ALSO/)
(ANDE/)
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(BOLD/)
(BURG/)
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(GANG/)
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(GORM/)
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The invention relates to human NOVX polypeptides and the polynucleotides encoding them. The invention also relates to antibodies specific to the NOVX polypeptides. The polypeptides, polynucleotides and antibodies are useful for manufacturing a medicament for treating a syndrome associated with a human disease, such as pathology associated with the NOVX polypeptide. The sequences are useful for diagnosing, treating or preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host dispets. Alzheimer's disease, Parkinson's disease, graft-versus-host chrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia, obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated cachexia, multiple sclerosis or fertility. The nucleic acids may be used a hybridisation probes, in chromosome mapping, in tissue typing, in preventive medicine or in pharmacogenomics. This sequence represents a human NOVX polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1839 AAGCGGCCGCTCGAGTCTAGAGGCCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCT 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human NOVX polypeptides and nucleic acid molecules, useful for diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson DW, Berghs C, Boldog FL,
EA, Gerlach V, Gorman L, Rothberg BG, G,
DM, Li L, Macdougall JR, Miller CE, Or
N Pena CEA, Peyman JA, Rieger DK,
SG, Smithson G, Spaderna SK, Spytek KA,
Vernet CAM, Voss EZ, Zhong M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2017 BP; 345 A; 613 C; 617 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 349; 610pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vernet CAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Agee ML, Alsobrook Jr, Eurgess CE, Catterton E, Dip
Bllerman K, Gangolli EA, Ger
Herrmann JL, Halvorsen Y, Ji
Larochelle WJ, Lepley DW, Li
Padigaru M, Patturajan M, Pi
Rothenberg ME, Shenoy SG, Si
Stone DJ, Taupier RJ, Verne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 101; Conservative
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STONE D J.
TAUPIER R J.
VERNET C A M.
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                                                                                                                                                                                                                                                                                                                                                                                                                      ZHONG M.
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(VOSS/)
(ZHON/)
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TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC 101

61

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GUO X S. HERRMANN J L.

(ROTH/) (GUOX/) (HERR/)

ROTHBERG B G.

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New human NOVX polypeptides and nucleic acid molecules, useful for dagnosing, preventing or treating NOVX-associated disorder, e.g. cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or scleroderma.
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P-PSDB; ADO42507.
28-MAY-2002;
29-MAY-2002;
29-MAY-2002;
                                                                                                                                                                                                                                                                                                                            (PENA/)
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(STON/)
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(MACD/)
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Human; NOVX; gene; ss; cancer; atherosclerosis; diabetes; Alzheimer's disease; Parkinson's disease; graft-versus-host disease; scleroderma; hypertenation; haemophilia; idiopathic thrombocytopenic purpura; immunodeficiency; AIDS; dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia; cancer-associated cachexia; multiple sclerosis; fertility.
1899 TCTAGTTGCCAGCCATCTGTTTTGCCCCTCCCCCGTGCC 1939
                                                                                   Human NOVX polynucleotide #178.
                                                                                                                                                                                                                                                                                    2001US-0339611P.
2001US-0340981P.
2001US-0341346P.
2001US-0340390P.
2001US-0340440P.
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2001US-034164P.
2001US-0341477P.
2001US-0341477P.
2001US-0341540P.
2001US-034154P.
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2002US-0353286P.
2002US-0353288P.
2002US-0359599P.
2002US-0359626P.
                                     ADO42506 standard; cDNA; 2022
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2001US-0338989P.
2001US-0339022P.
2001US-0339314P.
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2002US-0360924P.
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2002US-0381495P
2002US-0383534P
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                                                                    15-JUL-2004 (first entry)
                                                                                                                                                                      US2004058338-A1.
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11-DEC-2001; 2
11-DEC-2001; 2
12-DEC-2001; 2
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20-DEC-2001; 2
31-DEC-2001; 2
01-FEB-2002; 2
01-FEB-2002; 2
26-FEB-2002; 2
26-FEB-2002; 2
27-FEB-2002; 2
27-FEB-2002; 2
27-FEB-2002; 2
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07-DEC-2001;
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2002;
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                                                    AD042506;
                              ADO42506
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Guo XS;
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29-MAY-2002; 2002US-0383829F.
29-MAY-2002; 2002US-0384024P.
29-MAY-2002; 2002US-0384024P.
06-AUG-2002; 2002US-040135P.
07-AUG-2002; 2002US-0401788P.
20-AUG-2002; 2002US-0404676P.
23-AUG-2002; 2002US-0405684P.
23-AUG-2002; 2002US-0405684P.
23-AUG-2002; 2002US-0405684P.
23-AUG-2002; 2002US-0405684P.
23-AUG-2002; 2002US-0405684P.
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PEYMAN J A.
RIEGER D K.
ROTHENBERG M E.
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MILLER C E.
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LAROCHELLE W J.
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HERRMANN J L.
HALVORSEN Y.
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ELLERMAN K.
GANGOLLI E A.
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SMITHSON G.
SPADERNA S K.
STONE D J.
TAUBLER R J.
VERNET C A M.
VOSS E Z.
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BOLDOG F L.
BURGESS C E.
CATTERTON E.
DIPIPPO V A.
EDINGER S R.
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ROTHBERG B G.
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PATTURAJAN M.
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19-JUL-2001.

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The invention relates to human NOVX polypeptides and the polymucleotides encoding them. The invention also relates to antibodies specific to the NOVX polypeptides. The polypeptides, polymucleotides and antibodies are useful for manufacturing a medicament for treating a syndrome associated with a human disease, such as a pathology associated with the NOVX polypeptide. The sequences are useful for disposable, treating or preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host disperse, such as the promotory purpura, immunodeficiencies, AIDS, dyslipidemia, obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated cachexia, multiple sclerosis or fertility. The nucleic acids may be used a shybridisation probes, in chromosome mapping, in tissue typing, in preventive medicine or in pharmacogenomics. This sequence represents a human NOVX polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1843 AAGCGGCCGCTCGAGTCTAGAGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCT 1902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/note= *Ampicillin promoter that corresponds to the non-essential mucleotide sequence that have been removed in the novel DNA plasmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription termination; immunostimulatory sequence; ISS; antiviral; non-essential nucleotide; molecular biology application; gene therapy; DNA vaccine; cloning; gene expression; in vitro protein production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCGGTGATCAGCCTCGACTGTGCCT
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/note= "3' non-coding region of lacZ gene from pUCl8
corresponds to the non-essential nuclectide sequence
have been removed in the novel DNA plasmid vector"
5144. .5258
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid; cyclic; circular; replicon; exogenous gene; marker gene;
                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 101; DB 12; Length 2022; 100.0%; Pred. No. 2.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; pVAX1/Lac2; cytomegalovirus promoter; lac2 gene;
                                                                                                                                                                                                                                                                                                                                           Sequence 2022 BP; 347 A; 614 C; 618 G; 443 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1903 TCTAGTTGCCAGCCATCTGTTTGCCCCTCCCCCGTGCC 1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCGTGCC 101
                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= a
note= "Corresponds to the
Claim 20; SEQ ID NO 355; 610pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Commercial plasmid vector pVAX1/LacZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD10237 standard; DNA; 6050 BP
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                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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The present invention relates to plasmid DNA vectors comprising essentially of a replicon and at least one other component selected from promoter. intron, exogenous gene, transcription termination sequence, selectable marker gene, detectable marker gene and an immunostimulatory sequence (ISS) where the non-essential nucleotide sequences have been substantially removed from these vectors. The plasmid DNA vectors are useful in most molecular biology applications, e.g. gene therapy, DNA vaccines, cloning and expression of genes, and in the in vitro production of polypeptides and/or proteins. The present sequence is a commercial plasmid DNA vector pVAXI/Lacz which comprises Cytomegalovirus promoter, the lacz gene, pUC origin of replication and the kanamycin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCGGCCGCTCGAGTCTAGAGGCCCCGTTTAAACCCGCTGATCAGCCCTCGACTGTGCCT 3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid E2CLBDAS; fusion protein; nucleotide-binding domain; NBD; ligand-binding domain; LBD; transcription regulating domain; TRD; zinc finger protein; ZFP; ligand-activated transcriptional regulator; gene regulation; gene therapy; cell proliferative disorder; cancer; psoriasis; pemphigus vulgaris; Behcet's syndrome; lipid histicoytosis; E2C_ZFP; human; oestrogen receptor; ER; VP16; TA; transactivation domain;
                                                                                                                                                                                                                applications,
genes, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCCGCTGATCAGCCTCGACTGTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid E2CLBDAS encoding fusion protein comprising E2C ZFP-ER LBD-TA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6050 BP; 1346 A; 1597 C; 1696 G; 1411 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101; DB 5; Length 6050; Pred. No. 3.2e-24;
                                                                                                                                                                                                              New plasmid DNA vectors, useful for most molecular biology e.g. gene therapy, DNA vaccines, cloning and expression of the in vitro production of polypeptides and/or proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                       Example 2; Page 39-41; 50pp; English
                                                                                                        (ELIM-) ELIM BIOPHARMACEUTICALS INC.
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Rhesus macaque polyoma virus.
                                  09-JAN-2001; 2001WO-US001255
                                                                     10-JAN-2000; 2000US-00480879
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Matches 101; Conservative
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                                                                                                                                           Sun I,
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to fusion protein comprising a nucleotide-binding domain (NBD). A ligand-binding domain (TBD) of an intracellular receptor (ICR) and a transcription regulating domain (TBD). NBD is a polydactyl zinc finger protein (ZPP), or a modular part of it, that interacts fusion protein functions as a ligand-activated transcriptional regulator. The fusion protein and the nucleic acid encoding it, are used to regulate gene expression, particularly in gene therapy for treating malignant cell carcinoma) and non-malignant cell proliferative diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The fusion protein and its DNA are also useful for treating diseases caused by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein and tes DNA are also useful for treating diseases. The fusion protein and can be made to have different selectivity or specificity exogenous or exogenous ligands. The present sequence is BZCLBDAS construct encoding fusion protein comprising SZC zinc finger protein received the sequence ezc, human osebratory is not a function of the sequence ezc, human osebratory is not a function of the sequence ezc, human osebratory is not a function of the sequence ezc, human osebratory is not an analydra and the sequence ezc, human osebratory is not an analydra and the sequence ezc, human osebratory is not an analydra and the sequence ezc, human osebratory is not an analydra and an analydra and an analydra and an analydra and an analydra and an analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra and analydra a
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                                                                                                                                                                                                                                                                                    New fusion protein containing nucleotide-binding and ligand-binding domains, useful e.g. in gene therapy of cancer, provides ligand-activated control of gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor LBD fragment and VP16 transactivation domain (TA) from Herpes simplex virus. The ZFP serves as NBD and VP16 TA domain functions as transcription activator. The EZCLEDAS construct is based on plasmid poDNA3.1 that comprises sequences from cytomegalovirus, bacteriophage T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAGCGGCCGCTCGAGTCTAGAGGGCCCGGTTTAAACCCGCTGATCAGCCTCGACTGTGCCT
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ligand-binding domain; LBD; transcription regulating domain; TRD;
zinc finger protein; ZFP; ligand-activated transcriptional regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                              Claim 25; Page 186-187; 218pp; English.
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                                                      23-OCT-2000; 2000WO-EP010430.
                                                                                            25-OCT-1999; 99US-00433042.
02-JUN-2000; 2000US-00586625.
                                                                                                                                                                                                              Beerli
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                                                                                                                                                (NOVS ) NOVARTIS AG. (SCRI ) SCRIPPS RES INST.
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Best Local Similarity
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                                                                                          25-OCT-1999;
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                03-MAY-2001.
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ID AADO
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The invention relates to fusion protein comprising a nucleotide-binding domain (NBD), a ligand-binding domain (LBD) of an intracellular receptor (ICR) and a transcription regulating domain (TRD). MBD is a polydactyl zinc finger protein (ZFP), or a modular part of it, that interacts cancer protein functions as a ligand-activated transcriptional regulator. The fusion protein functions as a ligand-activated transcriptional regulator. The fusion protein and the nucleic acid encoding it, are used to regulate gene expression, particularly in gene therapy for treating malignant cell carcinoma and non-malignant cell proliferative diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The carcinoma and its DNA are also useful for treating diseases caused by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein and its DNA are also useful for treating diseases. The fusion protein can be designed to target any selected gene (endogenous or exogenous ligands. The present sequence is CTLBDAS.

Corrector LBD fragment and vile transactivation domain (TA) from Herpes which is a variant of murine Cys2-His2 ZFP Zif268, human oestrogen creeptor in the ZFP serves as NBD and VP16 TA domain functions as transcription activator. The CTLBDAS construct is based on plasmid companies of the comprises sequences from cytomegalovirus, bacteriophage T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion protein containing nucleotide-binding and ligand-binding domains, useful e.g. in gene therapy of cancer, provides ligand-activated control of gene expression.
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gene regulation; gene therapy; cell proliferative disorder; cancer; psortasis; pemphigus vulgaris; behcet's syndrome; lipid histiocytosis; C7 ZFP; Zifz68; murine; human; oestrogen receptor; ER; VP16; TA; transactivation domain; cyclic; circular; ds.
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Pred. No. 3.2e-24;
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Enterobacteria phage T7.
Rhesus macaque polyoma virus.
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02-JUN-2000; 2000US-00586625.
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(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                    Herpes simplex virus.
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                                                                                                                                                                                                                             sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                identified
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The invention relates to fusion protein comprising a nucleotide-binding domain (NBD), a ligand-binding domain (LBD) of an intracellular receptor (ICR) and a transcription regulating domain (LBD) of an intracellular receptor zinc finger protein (ZFP), or a modular part of it, that interacts specifically with a contiguous sequence of at least 3 nucleotides. The cusion protein functions as a ligand-activated transcriptional regulator. The fusion protein and the nucleic acid encoding it, are used to regulate correct for a strength of the contiguant cell proliferative diseases (e.g. colon cancer, prostate cancer, renal-cell carcinamia) and non-malignant cell proliferative diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The carcinomal and non-malignant cell proliferative diseases caused by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein and its DNA are also useful for treating diseases caused by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein can be made to have different selectivity or specificity for endogenous or exogenous ligands. The present sequence is EZCLBDBS construct encoding fusion protein comprising EZC zinc finger protein construct encoding fusion protein comprising EZC zinc finger protein construct encoding fusion protein comprising EZC zinc finger protein construct encoding fusion protein comprising EZC zinc finger protein construct as simplex virus. The ZPP serves as NBD and VP16 TA domain functions as creeptor LBD fragment and VP16 transactivation domain functions as companies and simian virus 40 (SV40)
                                                                                                                                                                                                                                     ligand-binding domain; LBD; transcription regulating domain; TRD; zinc finger protein; ZFP; ligand-activated transcriptional regulator; gene regulation; gene therapy; cell proliferative disorder; cancer; psoriasis; pemphigus vulgaris; Behcet's syndrome; lipid histiocytosis; E2C ZFP; human; oestrogen receptor; BR; VPL6; TA; transactivation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion protein containing nucleotide-binding and ligand-binding domains, useful e.g. in gene therapy of cancer, provides ligand-activated control of gene expression.
                                                                                                                                                                      Plasmid E2CLBDBS encoding fusion protein comprising E2C ZFP-ER LBD-TA.
                                                                                                                                                                                                                 Plasmid E2CLBDBS; fusion protein; nucleotide-binding domain; NBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; Page 188-189; 218pp; English.
                                      AAD06055 standard; DNA; 6639 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barbas CF, Kadan M, Beerli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacteria phage T7.
Rhesus macaque polyoma virus.
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                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                            Unidentified.
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                                                                                                                             31-JUL-2001
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RESULT 9
                      AAD06055
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                                                                                                                                                         Gaps
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                           Sequence 6639 BP; 1546 A; 1749 C; 1718 G; 1626 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                    TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC
                                                                                        Score 101; DB 4;
Pred. No. 3.2e-24;
; Mismatches 0;
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                                                                100.0%; Sco
100.0%; Pre
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Rhesus macaque polyoma virus.
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02-JUN-2000; 2000US-00586625.
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                                                                                                                          Similarity
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                                                                                        Query Match
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WPI; 2001-308618/32

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proliferative diseases (e.g. colon cancer, prostate cancer, renal-cell carcinoma) and non-malignant cell proliferative diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The fusion protein and its DNA are also useful for treating diseases caused that its protein and its DNA are also useful for treating diseases caused by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein can be designed to target any selected gene (endogenous or exogenous), and can be made to have different selectivity or specificity construct encoding fusion protein comprising C7 zinc finger protein (ZPP) which is a variant of murine Cyp2-His2 ZFP Zif268, human ocestrogen receptor LBD fragment and VP16 transactivation domain (TA) from Herpes camplex virus. The ZFP serves as NBD and VP16 TA domain functions as transcription activator. The C7LBDBS construct is based on plasmid the comprises and expense of the comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprise and comprises and comprises and comprises and comprise and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprises and comprise and comprises and comprises and comprises and comprises and comprises and comprise and comprises and comprises and comprise and comprises and comprise and comprises and comprise and comprises and comprise and comprises and comprise and comprise and comprises and comprise and comprise and comprise and comprise and comprise and comprise and comprise and comprise and comprise and comprise and comprise and comprise and compris
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Matches 101;
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Plasmid C7LBDBSG400V, fusion protein; nucleotide-binding domain; NBD; ligand-binding domain; LBD; transcription regulating domain; TRD; zinc finger protein; ZFP, ilgand-activated transcriptional regulator; gene regulation; gene therapy; cell proliferative disorder; cancer; psoriasis; pemphisgus vulgaris; Behcet's syndrome; lipid histiocytosis; C7 ZFP; Zifz68; murine; human; oestrogen receptor; ER; mutant; mutein; VP16; TA; transactivation domain; cyclic; circular; ds.
                                                                                                                                                                                                                                                                                                                                      Plasmid C7LBDBSG400V encoding fusion protein.
                                                                                 AAD06057 standard; DNA; 6695 BP.
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RESULT 11
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Barbas CF, Kadan M, Beerli R;
                                                                                                                Enterobacteria phage T7.
Rhesus macaque polyoma virus.
                                                                                                                                                                  23-OCT-2000; 2000WO-EP010430,
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                                                                                                                                                                                                  SCRIPPS RES INST.
                                                                                                      Herpes simplex virus.
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                                                                                                            Cytomegalovirus.
                                                                                                                                            WO200130843-A1
                                                                                           Homo sapiens.
Synthetic.
                                                                                                                            Unidentified
                                                                                                                                                       03-MAY-2001.
                                                                                      Mus sp.
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ligand-binding domain; LBD; transcription regulating domain; TRD; zinc finger protein; ZFP; ligand-activated transcriptional regulator; gene regulation; gene therapy; cell proliferative disorder; cancer; psoriasis; pemphigus vulgaris; Behcet's syndrome; lipid histiocytosis; C7 ZFP; ZiE288; murine; human; oestrogen receptor; ER; mutant; mutein; VP16; TA; transactivation domain; cyclic; circular; ds.

Enterobacteria phage T7. Rhesus macaque polyoma virus. Unidentified.

Herpes simplex virus.

Homo sapiens. Synthetic.

gb. Mus Cytomegalovirus.

Plasmid C7LBDBSG521R; fusion protein; nucleotide-binding domain; NBD;

Plasmid C7LBDBSG521R encoding fusion protein.

31-JUL-2001 (first entry)

AAD06058;

AAD06058 standard; DNA; 6695 BP

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The invention relates to fusion protein comprising a nucleotide-binding domain (NBD), a ligand-binding domain (LBD) of an intracellular receptor (ICR) and a transcription regulating domain (TRD). NBD is a polydactyl zinc finger protein (ZPP), or a modular part of it, that interacts specifically with a contiguous sequence of at least 3 nucleotides. The fusion protein functions as a ligand-activated transcriptional regulator. The fusion protein and the nucleic acid encoding it, are used to regulate gene expression, particularly in gene therapy for treating malignant cell carcinoma) and non-malignant cell proliferative diseases (e.g. colon cancer, prostate cancer, renal-cell carcinoma) and non-malignant cell proliferative diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The tusion protein and its DNA are also useful for treating diseases caused by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein can be designed to target any selected gene (endogenous or exogenous ligands. The present sequence is C7LBDBSG400V construct encoding fusion protein comprising C7 zinc finger protein (ZFP) which is a variant of murine Cyg2-His2 ZFP Zif268, human oestrogen receptor LBD fragment containing G400V mutation and Herpes simplex virus can plannid and plants of the containing G400V mutation and Herpes simplex virus or mularmid and plants. The C7LBDBSG400V construct is based can plannid and plants.
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                                                 New fusion protein containing nucleotide-binding and ligand-binding domains, useful e.g. in gene therapy of cancer, provides ligand-activated control of gene expression.
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                                                                                                                                                                 Claim 25; Page 191-193; 218pp; English.
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Plasmid C7LBDAL; fusion protein; nucleotide-binding domain; NBD;

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The invention relates to fusion protein comprising a nucleotide-binding domain (NBD), a ligand-binding domain (LBD) of an intracellular receptor (CTCR) and a transcription regulating domain (TRD). NBD is a polydactyl zinc finger protein (ZFP), or a modular part of it, that interacts seed the contiguous sequence of at least 3 nucleotides. The responsive protein and the nucleic acid encoding it, are used to regulate the fusion protein and the nucleic acid encoding it, are used to regulate gene expression, particularly in gene therapy for treating malignant cell proliferative diseases (e.g. colon cancer, prostate cancer, renal-cell carcinoma) and non-malignant cell proliferative diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The fusion protein and its DNA are also useful for treating diseases caused by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein can be designed to target any selected gene (endogenous or exogenous ligands. The present sequence is C7LBDBSG521R construct encoding fusion protein comprising C7 zinc finger protein (ZFP) which is a variant of murine Cys2-His2 ZFP Zif268, human osetrogen receptor LBD fragment contenting G221R mutation and Herpes simplex virus contentivation domain (TAM) The ZFP serves as NBD and VPDE TA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                domains, useful e.g. in gene therapy of cancer, provides ligand-activated control of gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             functions as transcription activator. The C7LBDBSG521R construct is based on plasmid pCDNA3.1 that comprises sequences from cytomegalovirus,
                                                                                                                                                                                                                                                                                                                                                                                                           fusion protein containing nucleotide-binding and ligand-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacteriophage T7 and simian virus 40 (SV40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Page 193-195; 218pp; English.
                                                                                                                                                                                                                                                                                                                   Barbas CF, Kadan M, Beerli R;
                                                                                                                               23-OCT-2000; 2000WO-EP010430.
                                                                                                                                                                               25-OCT-1999; 99US-00433042.
02-JUN-2000; 2000US-00586625.
                                                                                                                                                                                                                                               (NOVS ) NOVARTIS AG. (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-308618/32
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  Chimeric.
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                                                                       1 AAGCGGCCGCTCGAGTCTAGAGGCCCCGTTAAACCCCGCTGATCAGCCTCGACTGTGCCT
                                      Gaps
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100.0%; Score 101; DB 4; Length 6695; 100.0%; Pred. No. 3.2e-24;
                                  0; Indels
                                                                                                                                                              2359 TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCGGGCC 2399
                                                                                                                                            61 TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC 101
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Plasmid C7LBDAL encoding fusion protein comprising C7 ZFP-ER LBD-TA.
        AAD06048 standard; DNA; 6746 BP
                                                  (first entry)
                                                  31-JUL-2001
                            AAD06048;
AAD06048
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2350 AAGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCT 2409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New fusion protein containing nucleotide-binding and ligand-binding domains, useful e.g. in gene therapy of cancer, provides ligand-activated control of gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to fusion protein comprising a nucleotide-binding domain (NBD), a ligand-binding domain (LBD) of an intracellular receptor (ICR) and a transcription regulating domain (TBD). NBD is a polydactyl zinc finger protein (ZFP), or a modular part of it, that interacts specifically with a contiguous sequence of at least 3 nucleotides. The fusion protein functions as a ligand-activated transcriptional regulator. The fusion protein and the nucleic acid encoding it, are used to regulate gene expression, particularly in gene therapy for treating malignant cell proliferative diseases (e.g. colon cancer, prostate cancer, renal-cell carcinoma and non-malignant cell proliferative diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and lipid histicoycosis). The fusion protein and its DNA are also useful for treating diseases caused
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein can be designed to target any selected gene (endogenous or exogenous), and can be made to have different selectivity or specificity for endogenous or stope is c7LBDAL
                  ligand-binding domain; LBD; transcription regulating domain; TRD; zinc finger protein; ZFP; ligand-activated transcriptional regulator; gene regulation; gene therapy; cell proliferative disorder; cancer; psoriasis; pemphigus vulgaris; behcet's syndrome; lipid histiocytosis; C7 ZFP; Zif268; murine; human; oestrogen receptor; ER; VPI6; TA; transactivation domain; cyclic; circular; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; Page 174-176; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beerli R;
                                                                                                                                                                                                                                                        Enterobacteria phage T7.
Rhesus macaque polyoma virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and simian virus 40 (SV40)
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                                                                                                                                                                                                               Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kadan M,
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                                                                                                                                                                                                                                        Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                     WO200130843-A1.
                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                03-MAY-2001
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The invention relates to fusion protein comprising a nucleotide-binding domain (NBD), a ligand-binding domain (LBD) of an intracellular receptor (TCR) and a transcription regulating domain (TRD). MBD is a polydactyl zinc finger protein (ZFP), or a modular part of it, that interacts specifically with a contiguous sequence of at least 3 nucleotides. The fusion protein functions as a ligand-activated transcriptional regulator. The fusion protein and the nucleic acid encoding it, are used to regulate gene expression, particularly in gene therapy for treating malignant cell proliferative diseases (e.g. colon cancer, prostate cancer, renal-cell proliferative diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The fusion protein and its DNA are also useful for treating diseases caused by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein can be designed to target any selected gene (endogenous or exogenous) and can be made to have different selectivity or specificity construct encoding fusion protein comprising C7 zinc finger protein (ZFP) which is a variant of murine Cys2-His2 ZFP Zif268, human osetrogen receptor LBD fragment and VP16 transactivation domain (TA) from Herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion protein containing nucleotide-binding and ligand-binding domains, useful e.g. in gene therapy of cancer, provides ligand-activated control of gene expression.
                                                                                                                                                                                                                                                                                   Plasmid C7LBDBL; fusion protein; nucleotide-binding domain; NBD; ligand-binding domain; LBD; transcription regulating domain; TRD; zinc finger protein; ZFP; ligand-activated transcriptional regulator; gene regulation; gene therapy; cell proliferative disorder; cancer; psoriasis; pemphigus vulgaris; Behcet's syndrome; lipid histiocytosis; C7 ZFP; Zif268; murine; human; oestrogen receptor; ER; VPI6; TA; transactivation domain; cyclic; circular; ds.
                                                                                                                                                                                                                                                   Plasmid C7LBDBL encoding fusion protein comprising C7 ZFP-ER LBD-TA.
                    2410 TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC 2450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Page 178-180; 218pp; English.
                                                                                                                                   AAD06050 standard; DNA; 6818 BP
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Rhesus macaque polyoma virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Herpes simplex virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytomegalovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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simplex virus. The ZFP serves as NBD and VP16 TA domain functions as transcription activator. The C7LBDBL construct is based on plasmid pCDNA3.1 that comprises sequences from cytomegalovirus, bacteriophage T7 and simian virus 40 (5040)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligand-binding domain; LBD; transcription regulating domain; TRD; zinc finger protein; ZFP; ligand-activated transcriptional regulator; gene regulation; gene therapy; cell proliferative disorder; cancer; psoriasis; pemphigus vulgaris; behcet's syndrome; lipid histiocytosis; 2C7 ZFP; Zif268; murine; human; oestrogen receptor; ER; VPL6; TA; transactivation domain; cyclic; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid 2C7LBDAS encoding fusion protein comprising 2C7 ZFP-ER LBD-TA.
                                                                                                                                                                                        1 AAGCGGCCGCTCGAGTCTAGAGGCCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCT
                                                                                                                                                         Gaps
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0
                                                                                    Sequence 6818 BP; 1580 A; 1796 C; 1775 G; 1667 T; 0 U; 0 Other;
                                                                                                                     ; Score 101; DB 4; Length 6818; Pred. No. 3.3e-24; 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                            2482 TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC 2522
                                                                                                                                                                                                                                                              TCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCC 101
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Rhesus macaque polyoma virus.
Unidentified.
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02-JUN-2000; 2000US-00586625.
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Matches 101, Conservative
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(SCRI ) SCRIPPS RES INST.
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fusion protein functions as a ligarda-activated transcriptional regulator. The fusion protein and the nucleic acid encoding it, are used to regulate gene expression, particularly in gene therapy for treating malignant cell proliferative diseases (e.g. psoriasis, proliferative diseases (e.g. psoriasis, pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The tusion protein and its DNA are also useful for treating diseases caused by viruses in humans/plants, genetic and/or acquired diseases. The fusion protein can be designed to target any selected gene (endogenous or exogenous), and can be made to have different selectivity or specificity for endogenous or exogenous ligands. The present sequence is 2C7LBDAS construct encoding fusion protein comprising 2C7 zinc finger protein construct encoding fusion protein comprising 2C7 zinc finger protein receptor LBD fragment and VP16 transactivation domain (TA) from Herpes implex virus. The ZFP serves as NBD and VP16 TA domain functions as transcription activator. The 2C7LBDAS construct is based on plasmid polyna; and simian virus 40 (SV40) specifically with a contiguous sequence of at least 3 nucleotides. The 

Sequence 6828 BP; 1585 A; 1816 C; 1746 G; 1681 T; 0 U; 0 Other;

Gaps ö 0; Indels 100.0%; Score 101; DB 4; 100.0%; Pred. No. 3.3e-24; trive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 101; Conservative

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Search completed: July 14, 2005, 07:01:43 Job time : 143.448 secs

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CK0778129 pgn2c.pk0
BM887817 TM53 Hum
CK192687 Forward 8
CK092687 Forward 8
CK032687 Forward 8
BM887768 TM397 Hum
CK673248 Forward 8
CK070494 Forward 8
EX898352 Forward 8
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                                                                                                                                                        1 aagoggcogctcgagtctag......gtttgcccctcccccgtgcc 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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CR014355 Forward 8 CR014355 Forward 8 ER819796 K-EST0087 CR160587 Forward 8 EX084480 Forward 8 CR117924 Forward 8 CR13954 Forward 8 CR13954 Forward 8 CR13954 Forward 8 CR13954 Forward 8 CR012517 Forward 8 CR012517 Forward 8 CR014919 Forward 8 CR01749 Forward 8 CR081749 Forward 8 CR1609197 Forward 8 CR1609197 Forward 8 CR180417 Forward 8 CR160012 Forward 8 CR160012 Forward 8 CR160012 Forward 8	TS	CF315931  HD-05-A13.bl OsHDAC1-overexpressing transgenic rice plasmid cDNA Library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD-05-A13. mRNA sequence.  CF315931.1 G1:33687692  EST:  ENARTORIA (japonica cultivar-group) Oryza sativa (japonica cultivar-group) ENGADIA (Japonica cultivar-group)  Kim, J.S., Jun, K.M. Cheong.p. J. Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequenting Analysis of Rice ESTS  Unpublished (2003) COOntact: Nahm B.H.  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division Orngin, Kyeonggi, Korea Tel: 82 31 320 6139  Fax: 82 31 321 6355  EMA: Sin 6159  EMA: Sin 6159  EMA: Sin 6159  EMA: Sin 6159  Location/Qualifiers  1. 378  // Contact: Nahm B.H.  // Contact: Nakm B.H.  // Contact: Namm B.H.	DB 7; Length 378;
158 9 CR018574 197 4 BM819796 664 9 CR014355 284 9 CR0160587 284 9 CR117924 1199 9 CR017320 141 9 CR012517 160 9 CR012517 100 9 CR011087 89 9 CR180417 113 9 CR180417 113 9 CR180417 113 9 CR180417 113 9 CR180417 114 9 CR180417 115 9 CR180417 117 9 CR180417 118 9 CR180417 118 9 CR180417 119 9 CR180417 119 9 CR180417 110 9 CR180362 110 9 CR180362 110 9 CR180362 110 9 CR180362	ALIGNMENTS	CF315931  HD05-A13. DI OSHDACI-overexpressing transge library (HD) Oryza sativa (japonica cultivar-grass)  CF315931  GF315931. GI:33687692  EST.  Oryza sativa (japonica cultivar-group)  Bukaryota; Viridiplantae; Streptophyta; Embi Spermatophyta; Magnoliophyta; Liliopsida; Pintarge-scal (japonica cultivar-group)  ENT.  Oryza sativa (japonica cultivar-group)  Bukaryota; Viridiplantae; Streptophyta; Embi Spermatophyta; Magnoliophyta; Liliopsida; Pintarge-scal (japonica cultivar-group)  Kim,J.S., Jun,K.M., K.M., Kim,YK. and Nahm,B.H.  Large-scale Sequencing Analysis of Rice ESTFUNDUBLISHED (2003)  Contact: Nahm B.H.  Genomics and Genetics Institute, GreenGene For Bioscience and Bioinformatics, Myongji Uryongji, Kyenagi, Korea  Tel: 82 31 330 6133  Fax: 82 31 330 6133  Fax: 82 31 321 6355  Email: bhnahm@ggblo.com, bhnahm@bio.myongji, Location/Qualifiers    Analyong Analyon Companies of Colone HDACI-overexpressing Cultivar="Nackedong"   Analyong Haxef="Haxon: 39947"   Alab-host="E.coli DH108"	98.0%; Score 99;
5.88 5.72 5.73 5.74			tch
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De Regan, S.

RESULT 2 CK719567

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VERSION

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CR074510.1 GT:49808100
S GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
ISM Mus musculus (house mouse)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CE 1 (bases 1 to 132)
Onkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CE10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Solanum tuberosum"
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/mol_type="mRNA"
/ullivar="Blaepody"
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/note="vector: pBluescript II SK(+) XR; Site 2: Xho1; supplier: Developmental series: Plants from pathogen-free Solanum tuberosum var. Shepody, clone 1756, nuclear stock were grown in a screenhouse under natural conditions. RNA was isolated from stolon tissue."
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                                                                         Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; afteride; lamiids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 400)
Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De Koeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S. Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                     Contact: Barry Flinn
The Canadian Pocato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 629, CANADA
Email: bflinn@bioatlantech.nb.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 400;
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/organism="Mus musculus"
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/clone_lib="MHPP"
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Location/Qualifiers
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(Dases 1 to 605)
Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., Dekoeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and
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Gaps
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19817 Swollen Stolon Solanum tuberosum cDNA, mRNA sequence.
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The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Predericton, ON, E3B 629, CANADA
Email: bilinmobloatlantech.nb.ca
Clones can be requested from BioAtlantech via
bflinmobloatlantech.nb.ca
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/cultivar="Shepody"
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Unpublished (2002)
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BM888450
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Brogers, J. and Bradley, A.
Direct Submission
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Porward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP263n05, genomic survey sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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Warayotas, Metazozas, Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                93 ACGACCCCATGCATCGCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCCAGCCATCTGT
                                                                              Gaps
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                  Length 132;
                                                8; Indels
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Morgan, R.W. and Burnside, J.
Chicken ESTs from lymphoid tissue- 3' sequence Unpublished (2004)
               67.5%; Score 68.2; DB 9;
90.1%; Pred. No. 1.9e-11;
ive 0; Mismatches 8;
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Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
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/clone_lib="MHPP"
                                                                                                                                            81 TGTTTGCCCCTCCCCGTGCC 101
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CN778129
CN778129.1 GI:47548763
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73; Conservative
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Best Local Similarity
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/clone lib="Muman Trabecular Meshwork cDNA library"
/clone lib="Westor: pcDNA3; Site_1: EcoRI; Site_2: EcoRI; Human
cdNA library made from mRNA isolated from trabecular
meshwork cells established fom eyes from 6 individuals,
ages 2 weeks to 2 years. Cells were harvested at passages
3 through 6. Invitrogen made a unidirectional cDNA library
from the mRNA from the frozen cells using a pcDNA3 vector
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I (bases I to 519)
Wirtz,M.K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.
Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library
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/lab.host="R.coli EMDH108"
/clone lib="chicken Lymphoid cDNA library (pgn2c)"
/note="Vector: pCMVSPORT 6"
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TM108 Human Trabecular Meshwork cDNA library Homo sapiens cDNA
clone 104447 5', mRNA sequence.
BM888450
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/sex="Male and Female"
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Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-6818
Fax: 503-494-6875
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/dev stage="2 week to 2 year old infants"
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Best Local Similarity 93.2%; Pred. No. 1.1e-10;
Matches 69; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           organism="Gallus gallus"
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/organism="Homo sapiens"
University of Delaware
Townsend Hall, Newark, DE 19717,
Tel: 302-831-1341
Fax: 302-831-2822
Email: morgan@udel.edu, www.chick
Location/Qualifiers
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Query Match
Best Local Similarity
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/note="Vector: pcDNA3; Site 1: BcoRI; Site 2: BcoRI; Human
cdNA library made from mRNA isolated from frabecular
meshwork cells established fom eyes from 6 individuals,
ages 2 weeks to 2 years. Cells were harvested at passages
3 through 6. Invitrogen made a unidirectional cDNA library
from the mRNA from the frozen cells using a pcDNA3 vector
and TPO10F'' host cells."
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TMS53 Human Trabecular Meshwork cDNA library Homo sapiens cDNA
clone 122060 5', mRNA sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Wirtz, M.K., Samples, J.R., Xu, H., Severson, T. and Acott, T.S.
Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library
Unpublished (2002)
Contact: Wirtz MK
Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Tervilliger Blvd., Portland, OR 97201-4197, USA
Pax: 503-494-6875
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                                                 Length 519;
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Ceal type="trabecular meshwork"
/dev_stage="2 week to 2 year old infants"
/lab_host="TOP10F;"
                               Score 66; DB 5; Lengtu err,
Pred. No. 1.38-10;
Transches 5; Indels
                                                                               0; Mismatches
and TPO10F'' host cells."
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/mol_type="mRNA"
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Seg primer: T7 Reverse
High quality sequence stop: 350.
Location/Qualifiers
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                                               65.3%;
93.2%;
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Matches 69; Conserva
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                                                              Similarity
                                                                               69;
                                                 Query Match
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CR154962 233 bp DNA linear GSS 06-JUL-2004 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP182j09, genomic survey sequence.
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 05-JUL-2004
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Pred. No. 1.5e-10;
0; Mismatches 9; Indels (
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87.7%; Pred. No. 2.2e-10;
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                                                                                                                                                                                                                                                   GSS; genome survey sequence; MICER. Mus musculus (house mouse)

    .233
    /organism="Mus musculus"

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/db_xref="taxon:10090"
/clone="MHPP182j09"
/clone_lib="MHPP"
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/db_xref="taxon:10090"
/clone="MHPP224h16"
/clone_lib="MHPP"
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Mus musculus
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Best Local Similarity 88.8%;
Matches 71; Conservative 0
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mRNA sequence.
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Best Local Similarity
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BM887768
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/note="Vector: pcDNN3; Site 1: EcoRI; Site 2: EcoRI; Human
cdNA library made from mRNN-isolated from trabecular
meshwork cells established fom eyes from 6 individuals,
ages 2 weeks to 2 years. Cells were harvested at passages
3 through 6. Invitrogen made a unidirectional cDNA library
from the mRNA from the frozen cells using a pcDNA3 vector
and TPO10F'' host cells."
                                                                                                                                                                                                  BM887701 534 bp mRNA linear EST 08-MAR-2002
TM304 Human Trabecular Meshwork cDNA library Homo sapiens cDNA
clone 107917 5', mRNA sequence.
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1 (bases 1 to 534)
Witz,M.K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.
Witz,M. Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabcular Meshwork Library
Unpublished (2002)
                                                           97
                                              0; Gaps
 Gaps
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Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
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| Ceall type="trabecular meshwork"
| dev stage="2 week to 2 year old infants"
| lab_host="TOP10F'"
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 10; Indels
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Pred. No. 4.2e-10;
0; Mismatches 6;
 0; Mismatches
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/db_xref="taxon:9606"
/clone="107917"
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                                                                                                                       96 retrirecccirccccciacic 76
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Email: wirtzm@ohgu.edu
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l Similarity 91.9%;
68; Conservative
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71; Conservative
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Best Local Similarity
Matches 68; Conserv
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KEYWORDS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Bar (bases 1 to 329)

E Jambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Pigott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
Whil kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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Location/Qualifiers
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1 (Dases 1 to 600)

Wirtz,M.K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.

Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library
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TM397 Human Trabecular Meshwork CDNA library Homo sapiens CDNA
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Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-4698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com
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/clone_lib="Mus musculus 129Sv/Ev"
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Pred. No. 4.5e-10;
0; Mismatches 3;
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/organism="Mus musculus"
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/strain="129Sv/Ev"
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                                                       Mus musculus (house mouse)
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BM887768.1 GI:19271512
CG632479.1 GI:37456328
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95.7%;
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GTGCC 101
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Direct, Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516 GCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTNTAGTTGCCAGCCATCTGTTGGTTGC 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR037248 linear GSS 05-JUL-200 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP31109, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 CGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTTGCCCCCTCCCCC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 CGCTGATCAGCCTCGACTGTGCCTTATAGTTGCCAGCCATTTGTTGTTTGCCCCCCC 15
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Pred. No. 2.1e-09;
0; Mismatches 2; Indels
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                                                                                                                                                                                          /organism="Homo sapiens"
Fax: 503-494-6875
Email: wirtzm@ohsu.edu
Seq primer: T' Reverse
High quality sequence stop: 400.
                                                                                                                                                                                                                 /mol_type="mRNA"
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/clone="119752"
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CR037248.1 GI:49770303
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l Similarity 96.9%;
63; Conservative (
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CR106833 87 bp DNA linear GSS 05-JUL-2004 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP37h18, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 87)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
                                                                                                                                                                                                                                                                    CRIO6833.1 GI:49854244
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus (house course)
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
Musculus metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 ACGACCCCATGCATCGCGATGATCAGCCTCAGCTCTGCCTTCTAGTTGCCAACCATCTGT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
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Pred. No. 2.1e-09;
0; Mismatches 12;

    .87
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Job time : 961.667 secs
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Best Local Similarity 85.2%;
Matches 69; Conservative
14 GTGCC 10
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Unclassified.
1 (bases 1 to 142)
Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
Rosen, C.A.
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                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus polynucleotides and sequences Patent: US 6593114-A 2608 15-JUL-2003; Location/Qualifiers
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100.0%; Pred. No. 8.7e-20;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                               AR356490 142 bp DNA
Sequence 2608 from patent US 6593114.
AR356490
                                                                                                                                                                                                                                                     ALIGNMENTS

    142
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PATN2PN1B
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       AY589493
AY538698
AY538700
AY538701
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AF535127
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AR371489
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AF104441
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                                           AY538702
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AX260150 Sequence
A43386 Sequence 11
AX11675 Sequence
AX559717 Fseudomon
X97254 S.marcescen
Z92776 Caenorhabdi
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AR538046 Sequence
E00019 DNA coding
M10199 Plasmid pMM
E00018 DNA coding
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E00892 Synthetic D
                                                           July 14, 2005, 04:39:07; Search time 756.618 Seconds (without alignments) 6468.225 Million cell updates/sec
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                                                                                                                 1 agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                             4708233 segs, 24227607955 residues
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                            US-09-482-682-47_COPY_7889_7989
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BD195256
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Maximum Match 100%
Listing first 45 summaries
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AR116755
AY559171
SMTEMAQGE
CEC11F10
                                           nucleic search, using sw model
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E00019
PMM0ENDO
E00018
I01644
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AX260150
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E01156
E01274
E01302
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Maximum DB :
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PAT 17-AUG-2003

linear

AY628199 Escherich AF628199 Escherich AY235127 Klebsiell AY243512 Klebsiell AY628175 Escherich AY101764 Klebsiell AR371489 Sequence AX729027 Proteus m X54606 Pseudomonas X54604 Pseudomonas X54604 Pseudomonas

AF027199 Klebsiell

AY536698 Serratia AY538700 Serratia AY538701 Serratia AY538702 Serratia AY538699 Serratia AY34610 Klebsiell AJ30858 Becherich AY32531 Streptoco AY452662 Streptoco AY45265 Streptoco AY45265 Streptoco

PAT 08-OCT-2004

linear

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9 48

Gaps

; 0

0; Indels

Length 142;

BCT 26-APR-1993

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other sequences; plasmids.

1 (bases 1 to 240)

Kemper, b., Jensch, F., von Depka-Prondzynski, M., Fritz, H.J.,

Borgmeyer, U. and Mizuuchi, K.

Resolution of Holliday structures by endonuclease VII as observed
in interactions with cruciform DNA.

Cold Spring Harb. Symp. Quant. Biol. 49, 815-825 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAAATAG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                    PMMOENDO 240 bp DNA linear BCT 26-APR-:
Plasmid pMM110 region of endo VII cleavage sites near cruciform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 251)
Uorutaa, G. and Karen, T.
SYNTHESIS OF SELECTIVE AGED PROTEIN OR POLYPEPTIDE IN BACTERIA
Patent: JP 1981154999-A 1 30-NOV-1981;
UNIV HARVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-1980 US 80 139225
UORUTAA GIRUBAATO, KAREN TARUMATSUJI
C12P21/00,C07H21/00,C12N1/00,C12N15/00//C12R1/19; CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 101; DB 1; Length 240; 100.0%; Pred. No. 8.7e-20; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E00018 251 bp DNA linear DNA coding for Escherichia coli penicillinase.
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                                                                                                                                                                                                                                                                                                                                                                                                   source text: Plasmid pMM110 DNA. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment_type: N-Terminal Fragment;
*source: clone=pKT241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Plasmid pMM110"
/mol_type="genomic DNA"
/db_xref="taxon:2599"
/plasmid="Plasmid pMM110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
JP 1981154999-A/1
30-NOY-1981
09-APR-1981 JP 1981052488
11-APR-1980 US 80 139225
UORUTAA GIRUBAATO, KAREN TAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR 11-ARR-1980 US 80
PI UORUTAA GIRUBAATO,
PC C12P21/00_C07H21/0
strandedness: Double;
CC topology: Linear;
CC anti-sense: No;
CC fragment_type: N-TCC
*source: Clone=pXT
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anti-sense: No;
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E00018.1 GI:2168326
JP 1981154999-A/1.
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hes 101; Conservative
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Escherichia coli
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Plasmid pMM110
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E00018/c
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DEFINITION
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KEYWORDS
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PMMOENDO/c
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Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                    107 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

I (basea 1 to 228)
Uorutaa, G. and Karen, T.
SYNTHESIS OF SELECTIVE AGED PROTEIN OR POLYPEPTIDE IN BACTERIA
                                                                                                                                                                                                                                                                                              Gaps
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30-NOV-1981
09-APR-1981 JP 1981052488
11-APR-1980 US 80 139225
UORUTAA GIRUBAATO, KAREN TARUMATSUJI
CI2P21/00,CO7H21/00,CI2N1/00,CI2N15/00//CI2R1/19; CC
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/product='E.coli penicilinase'.
Location/Qualifiers
                                                                  Rosen, C.A.
Staphylococcus aureus polynucleotides and sequences
Patent: US 6737248-A 2608 18-MAY-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                   61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 bp DNA line
DNA coding for Escherichia coli penicillinase.
E00019
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UNIV HARVARD
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/organism="Escherichia coli"

    142
    /organism="unknown"
    /mol_type="genomic DNA"

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/db_xref="taxon:562"
                                                                                                                      Location/Qualifiers
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anti-sense: No;
*source: clone=pKT218;
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JP 1981154999-A/2.
Escherichia coli
Escherichia coli
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Matches 101; Conservative
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AUTHORS
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E00019/c
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PAT 29-SEP-1997

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Matches 101; Conservative
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BD195256/c
LOCUS
DEFINITION
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                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 344)
Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L18624.1 GI:308338
STS; PCR primer; STS sequence; microsatellite marker;
microsatellite repeat; repeat polymorphism; sequence tagged site.
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Gilbert, W. and Talmadge, K.
Mature protein synthesis.
Patent: US 4338397-A 1 06-UUL-1982;
President and Fellows of Harvard College; Cambridge, MA
                                            /product='E.coli penicilinase' FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 101; DB 6; Length 251; 100.0%; Pred. No. 8.7e-20; ive 0; Mismatches 0; Indels C
                                                                                                                                                                            100.0%; Score 101; DB 6; Length 251; 100.0%; Pred. No. 8.7e-20; ive 0; Mismatches 0; Indels
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Human chromosome 8 STS UT5345, sequence tagged site.
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 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            101644 251 bp ss-DNA Sequence 1 from Patent US 4338397.
                                                                                                   /organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
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                                                           al 190. .196.
Location/Qualifiers
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Homo sapiens
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                                                                                                                                                                                           Best Local Similarity 100. Matches 101; Conservative
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Ballard, L., Melis, R., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Rodriguez, P., Albertsen, H., Lalouel, J.-M. and White, R. Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome crepeat containing sequence tagged sites from the human genome crepeat containing unpublished (1993)

L. Original source text: Homo sapiens DNA.
Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
3160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: GAGCARARACAGGAAAATGC
Primer B: TTGGGGAAATGCGGAACC
32P-label: B Primer
PCR PFILES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OS Unidentified
PN JP 2002513277-A/43
PD 08-MAY-2002
PP 08-MAY-2003
PP 21-NOV-1996 US 60/031626,14-OCT-1997 US 60/061953 PI
PR 22-NOV-1996 US 60/031626,14-OCT-1997 US 60/061953 PI
PATRICK J DILLOM,GIL H CHOI,RODNEY A WELCH
PC CI2N15/11,C121N15/63,C07K16/12,G01N33/569,G06F17/30,G11B7/00 CC
Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
CC Nucleotide sequence of Escherichia coli pathogenicity islands
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1 (bases 1 to 400)

1 (bases 1 to Choi, G.H. and Welch, R.A.

1 billon, p.J., Choi, G.H. and Welch, R.A.

1 Nucleotide sequence of Escherichia coli pathogenicity islands

Patent: JP 2002513277-A 43 08-MAY-2002;

HUMAN GENOWE SCIENCES INC, WISCONSIN ALUMNI RESEARCH FOUNDATION
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Nucleotide sequence of Escherichia coli pathogenicity islands.
BD195256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mg++: 2mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36. .224
/standard_name="STS UT5345"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial Denaturation: 94C 300sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36. .60
complement(202. .224)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR Cycles: 30
Denaturation: 94C 10sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BD195256.1 GI:33005021
JP 2002513277-A/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Annealing: 60C 10sec
Extension: 72C 20sec
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61 GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 101
  /db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
mat_peptide
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KEYWORDS
SOURCE
ORGANISM
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ACCESSION
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E01156/c
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State of Season 1 to 456)

Nath State of Season 1 to 456)

MITH SAME, AND PRODUCTION OF POLYPEPTIDE WITH MICROORGANISM PATHSEL AND PRODUCTION OF POLYPEPTIDE WITH MICROORGANISM PATHSEL, AND PRODUCTION OF POLYPEPTIDE WITH MICROORGANISM PATHSEL 1 JP 1986149089-A1 1 07-JUL-1986;

EARTH CHEM CORP LTD

OS Artificial Sequence; Genes.

No 1986149089-A1

D 07-JUL-1986

PT 07AL HIDEO, MOMOTA YUTAKA, KUMAKURA TAKESHI,

PI TOCHIFUSA NORIYUKI,

PI TOCHIFUSA NORIYUKI,

PI TOCHIFUSA NORIYUKI,

PI TOCHIFUSA NORIYUKI,

PI KITAZAWA TOSHIKI, OJIDA KAZUHIDE, MATSUSHIRO AIZO PC

C12N15/00, C12N1/20, C12P21/00, (C12N1/20, C12R1:19), (C12P21/00, PC

C12N15/00, C12N1/20, C12P21/00, (C12N1/20, C12R1:19), (C12P21/00, PC

C12N15/00, C12N1/20, C12P21/00, (C12N1/20, C12R1:19), (C12P21/00, PC

C *Source: Strain-HH10;

CC *Source: Strain-HH10;

CF *Source: Strain-HH10;

CF *Source: Strain-HH10;

CF *Source: Strain-HH10;

CF *Source: Strain-HH10;

CF *Source: Strain-HH10;

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CF *Source: Strain-HH10;

CF *Source: Strain-HH10;

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                                                                                                                                                                                                                                                                                                                                         165 AGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 106
                                                                                                                                                                                                                                                                                                             1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product='signal peptide of beta-lactonase'
278. .435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product='beta-urogastrone mature peptide'.
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                                                                                                                                                                                                                    100.0%; Score 101; DB 6; Length 400; 100.0%; Pred. No. 8.7e-20; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                              /organism='Unidentified'
Location/Qualifiers
Location/Qualifiers
1. .400
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/mol_type="genomic DNA"
                                                                                                      /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 1986149089-A/1.
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synthetic construct
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Matches 101; Conserv
  Key
source
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  표단단
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ORGANISM
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VERSION
KEYWORDS
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E00892/c
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                                                                FEATURES
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OKAI HIDEO C12N1/20,C12P21/00,(C12N1/20,C12R1:19),(C12N1/20, PC
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JP 1987083890-A/1.
synthetic construct
synthetic construct
other sequences, artificial sequences.

(bases 1 to 456)
Yoshikawa, K., Momota, Y., Kajifusa, N., Koide, T. and Okai, H.
POLYPEPTIDE SECRETION EXPRESSION VECTOR, MICROORGANISM TRANSFORMED
BY SAID VECTOR AND PRODUCTION OF POLYPEPTIDE USING SAID
PATENT. JP 1987083890-A 1 17-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 114
                                                                                                                                        173 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 114
                                                                                               9
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                                                                                               1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTTTTAGAAAATAAACAAATAG
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09-OCT-1985 JP 1985225393
YOSHIKAWA KAZUTOSHI, MOMOTA YUTAKA, KAJIFUSA NORIYUKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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    Length 456;
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/note='beta lactamase promoter'
                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product='beta urogastrone'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209. .439
/product='beta urogastrone'
209. .277
278. .436
                                                                                                                                                                                      61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                              113 GGGTTCCGCGCACATTCCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                        456 bp DNA DNA fragment which secrets beta urogastrone.
Query Match 100.0%; Score 101; DB 6; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 101; DB 6;
Best Local Similarity 100.0%; Pred. No. 8.7e-20;
Matches 101; Conservative 0; Mismatches 0;
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    .456
    /organism="synthetic construct"

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/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Artificial gene
Artificial sequence, Genes.
JP 1987083890-A/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          topology: Linear;
hypothetical: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-sense: No;
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 11 E01274/c

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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OKAI HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, KOIDE TAKAO,
MOMOTA YUTAKA
CIZNI5/00,C07H21/04,CIZNI/00,CIZP21/02,(CIZNI/00,CIZRI:19), PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 114
                                                    Okai, H., Kumakura, T., Kawamoto, S., Koide, T. and Momota, Y.

QUYPEPTIDE.EXPRESSION VECTOR, HOST TRANSFORMED WITH SAID VECTOR
AND PRODUCTION OF POLYPEPTIDE USING SAID HOST
PALENT: JF 1987190083-A 1 20-AUG-1987;
EARTH CHEM CORP ITD
OS Artificial gene
OC Artificial sequence; Genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product='human beta-urogastrone'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product='human beta-urogastrone'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 101; DB 6; Length 456; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 101; Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
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/organism="synthetic construct"
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                  other sequences; artificial sequences.
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Patent: WO 0172774-A 60 04-OCT-2001,
Cyclacel Limited (GB)
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Sequence 60 from Patent WO0172774.
AX260098
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/db_xref="taxon:32630"
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200. .203
209. .277
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hypothetical: No;
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       synthetic construct
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                                                                                                   E01274 1997 29-SEP-1997 DNA linear PAT 29-SEP-1997 DNA encoding beta-urogastron fused with DNA encoding a promoter and signal peptide of beta-lactamase.
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31-JAN-1986 JP 1986021032
OKAI HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, ADACHI SHOJI, MATSUBARA AKIMASA, OJIDA KAZUHIDB, YANO MAKI, MIHARA SHIGERU, MATSUBHRO AIZO, YANAHHARA NOBORU
C12P21/00,C12N15/00,(C12P21/00,C12R1:91);
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                                                                                                                                                                                                                                             other sequences; artificial sequences.

1 (Dases 1 to 456)

Okai, H., Kumakurar, Kawamoto, S., Adachi, S., Matsubara, A., Ojida, K., Yano, M., Mihara, S., Matsushiro, A. and Yanaihara, N. PRODUCTION OF BETA-URCGASTRONE

Patent: JP 1987/179398-A 1 06-AUG-1987;

BARTH CHEM CORP LTD
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/product='beta-urogastron'
209. 439
/product='beta-urogastron'
Location/Qualifiers
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113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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Artificial sequence; Genes.
Homo sapiens
JP 1987179398-A/1
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200. .203
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hypothetical: No;
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JP 1987179398-A/1.
synthetic construct
synthetic construct
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PAT 26-OCT-2001

DEFINITION

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Search completed: July 14, 2005, 14:03:32
Job time : 756.618 secs
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Wagnoliophyta, eudicotyledons, core eudicots,
rosids, Myrtales, Lythraceae, Cuphea.
1 (bases I to 693)
Toepfer,R., Bautor,J., Bothmann,H., Filsak,E.,
Hoericke-Grandpierre,C., Klein,B., Martini,N., Mueller,A.,
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                                                                                                              1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                            100.0%; Score 101; DB 6;
100.0%; Pred. No. 8.7e-20;
iive 0; Mismatches 0;
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Cell cycle progression proteins
Parent: WO 0172774-A 112 04-OCT-2001;
Cyclacel Limited (GB)
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MAX PLANCK GESELLSCHAFT (DE)
Other publication CA 2169093 950316
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Sequence 112 from Patent WO0172774.
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Sequence 11 from Patent W09507357.
A43586.
A43586.1 GI:2298779
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1. .573
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                                                             Best Local Similarity 100.
Matches 101; Conservative
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AX260150/c
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A43586
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                                              l. .693
/organism="Cuphea lanceolata"
Other publication AU 7615494 950327.
Location/Qualifiers
1. .693
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Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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nucleic search, using sw model • nucleic ĕ

July 14, 2005, 04:35:42; Search time 142.398 Seconds (without alignments) 4198.742 Million cell updates/sec Run on:

US-09-482-682-47\_COPY\_7889\_7989

1 agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101 Perfect score: Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

4390206 segs, 2959870667 residues

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 88 08 08 Minimum Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* N Geneseq 16Dec04: geneseqn1990s:\* geneseqn1980s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:\* geneseqn2003cs:\*

geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2004as:

geneseqn2004bs:

SUMMARIES

## Aan60624 Plasmid p Aan71080 Sequence Aan70833 Beta-urog Aan81765 Sequence Aba90413 Drosophil Aax21173 Polymucle Aba90456 Drosophil Aav76919 Staphyloc Aan10032 Sequence Aan10031 Sequence Aav31229 E. coli J Aan60624 Plasmid p Description AAN71080 AAN70833 AAN81765 ABA90413 AAX21173 AAX21149 ABA90456 AAN10031 AAV31229 AAV76919 AAN60624 В Query Match Length Score õ

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Aba14573 Human ner Aa834681 Human DNA Ada41574 Human sec Acc50905 Human sec Adc50905 Human sec Adb61140 Connectiv Adb94622 Novel hum Adc74663 Human sec Ada57709 BAC fragm Adm41551 Novel hum Aa8277818 DNA encod Aa8277818 DNA encod Aa827818 DNA encod Aa827818 DNA encod Aa827818 DNA encod Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Genomic s Aa841857 Human imm Aa8843434 Human imm Aa8843434 Human rep Aa107329 Human rep Aa107329 Human ner Aa834680 Human DNA Adb61139 Connectiv	. STI			.08.	ne; S.aureus infection; immunodetection; cod poisoning; osteomyelitis; therapy; infection; scalded skin syndrome;					n D.T. Fannon MP. Rosen Ch.		from Staphylococcus aureus - used in the production of anti-		ne of 5191 Staphylococcus aureus DNA sequences sequences are recorded on a computer readable d from a floppy or hard disk, random access mory (ROM) or CD-ROM. Homology searches using allows putative functions to be assigned so egulatory regions of commercial, therapeutic or
ABA14573 AAC34681 ACC50905 AAC50905 AB271508 AB271508 AB91869 AD891869 AD891869 AD891869 AD87709 AD830559 AD830559 AD830559 AD830559 AD830559 AD830559 AD830559 AD830539 AD830539 AAC36485 AAC36485 AAC36485 AAC66343 AAC66343 AAC66343 AAC66343 AAC6634 AAC66	ALIGNMENTS			SEQ ID #2608						SC. Dillon		derived ium and	English.	one of 5191 Staph sequences are rest from a floppy emory (ROM) or CI allows putative regulatory region
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			AAV76919; 16-MAR-199	Staphylococcus	Computer readable mcellulitis; eyelid skin infection; sur toxic shock syndrom	Staphylococcus EP786519-A2.	-JUL-199	7AN-199	7AN-199	מיי ל-מי	7		IM 1, P	sequence represents and invention. The DNA cum, preferably selectory (RAM), read-only many S.aureus DNA sequence. Protein-encoding or
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industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulities, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, acalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                         107 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The closest identifiable promoter for the penicilinase gene in pKT241 (AAN10031) is located in the region 14 to 20 nucleotides before its
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthesis of mature protein or polypeptide - by using bacterial host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning vehicle; bacterial vector; transformed host; penicillinase;
                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of the pKT218 EcoRI-PstI penicillinase gene fragment.
                                                                                                                                                                                                                       Length 142;
                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                          Sequence 142 BP; 45 A; 25 C; 26 G; 45 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                      61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transformed by cloned vehicle contg. DNA fragment etc
                                                                                                                                                                                                                                                                                                                                                      GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 7
                                                                                                                                                                                                                     Score 101, DB 2;
Pred. No. 2.1e-21;
0; Mismatches 0;
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/*tag= a
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225. .228
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                                                                                                                                                                                                                     100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAN10032/c
ID AAN10032 standard; DNA; 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                  Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilbert W, Talmadge K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1981-80125D/44.
                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAP10039
                                                                                                                                                              readable medium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-OCT-1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin; ds
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                                                                                                                                                                                                                                                                                                                                                                  47
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     8888888888888888888
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translational start signal. In the examples, the 3' end of pKT241 was attached to the signal DNA sequence of the DNA fragment (19) for rat preproinsulin (see AAN10033). The closest identifiable promoter for the penicillinase gene in pKT218 (AAN10032) is located in the region 14 to 2 nucleocides before its translational start signal. In the examples, the fragment (CB6) for rat preproinsulin (see AAN10034)
                                                                                                                                                                                                                                                      1 AGGGTTATTGTCTCATGAGCGGATACATATTTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthesis of mature protein or polypeptide - by using bacterial host transformed by cloned vehicle contg. DNA fragment etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning vehicle; bacterial vector; transformed host; penicillinase;
                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of the pKT241 EcoRI-PstI penicillinase gene fragment.
                                                                                                                                                                            Query Match 100.0%; Score 101; DB 1; Length 228; Best Local Similarity 100.0%; Pred. No. 2.3e-21; Matches 101; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                             GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                             Sequence 228 BP; 72 A; 37 C; 46 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                               GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN10031 standard; DNA; 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248. .251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HARD ) HARVARD COLLEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1981-80125D/44.
P-PSDB; AAP10038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP38182-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAN10031;
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                                                                                                                                                                                                                                                                                                                                                                115
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1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                     61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                       105 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACTGACGTC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= d
/label= Beta-lactamase signal peptide
278. .436
                                                                                                                                                                                                                                                                                                                                     Plasmid pUG201 sequence encoding beta-urogastrone.
                                                                                                                                                                                                                                                                                                                                                                      Beta-lactamase signal peptide; pGH54; pGH55; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohgai H, Momota H, Kuwakura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85WO-JP000696
                                                                                                                                                                                       AAN60624/c
ID AAN60624 standard; DNA; 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
209. .439
/*tag= c
209. .277
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1984;
                                                                                                                                                                                                                                                                               25-MAR-2003
29-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                              AAN60624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RBS
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                                                                                                                                                                           PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; vaccine; protective immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to elicit an immune
                                                                                                                                                        9
                                                                                                                                                       1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                        Gaps

    end of pKT218 was attached to the signal DNA sequence of the DNA
fragment (CB6) for rat preproinsulin (see AAN10034)

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0
                                                                                   Score 101; DB 1; Length 251;
Pred. No. 2.3e-21;
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                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 400 BP; 106 A; 77 C; 91 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                          61 GGGTTCCGCGCACATTTCCCCGGAAAGTGCCACCTGACGTC 101
                                                    Sequence 251 BP; 74 A; 45 C; 50 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                115 GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 75
                                                                                                                         ö
                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 101; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          E. coli J96 pathogenicity island contig #43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Page 140-141; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon PJ, Choi GH, Welch RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       response to pathogenic E. coli.
                                                                                                                                                                                                                                                                                                                                                    AAV31229 standard; DNA; 400 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US021347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9822575-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-1998.
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                                                                                                                                                                                                             The plasmid produces secreted beta-urogastrone in a transformed expression system. Similar plasmids may be constructed where the secertion signal may be coupled with eg. somatostatin, insulin, growth hormone, interferon, IL-2, gastric inhibitory peptide, influenza B SA, epidermal growth factor and thymosine-beta4. (Updated on 25-MAR-2003 to correct PA field.)
Recombinant vector for polypeptide secretion - contains signal peptide sequence directly bonded to peptide-coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                    Disclosure; Table 4; 79pp; Japanese
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Gaps

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Oshiden K;

Kitazawa T,

Kajifusa N,

BP.

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AAN70833/c
ID AAN70833 standard; DNA; 456
                            AAN70833;
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                                                                                                                                                           promoter
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           173 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 AGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence encodes beta-urogastrone under the control of a tac promoter. The peptide may be expressed from plasmid pUGT 150s in a transformed accoli host. The plasmid may carry several separately expressing sequences comprising a tac promoter, SD site, signal peptide, and coding sequence, to produce beta-UG in high yield. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression vector contg. multiple information units is used to transform host all for increased prodn. of polypeptides.
AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                       GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                 /*tag= b
/transl_except= (pos:434. .436,aa:Arg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTTCCGCGCACATTCCCCCGAAAGTGCCACCTGACGTC 101
                                                         GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 553; 34pp; Japanese.
                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                      Sequence encoding beta-urogastrone.
                                                                                                                                                                                                                                                                                                                                                                                         86JP-00031415.
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                                                                                                          AAN71080 standard; DNA; 456
                                                                                                                                                                   (first entry)
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Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (EART ) EARTH SEIYAKU KK.
                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                (revised)
                                                                                                                                                                                                          pUGT 150s; beta-UG; ds
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1987-273761/39.
                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                               JP62190083-A
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                                                                                                                                                          10-MAR-2003
13-MAY-1991
                                                                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                  20-AUG-1987.
                                                                                                                                                                                                                                        Synthetic
                                                                                                                             AAN71080;
 Н
                                       61
                                                         113
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                                                                                                                                                                                                                                                                     promoter
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                                                                                                 AAN71080/c
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An example of a sequence detected by a probe consisting of polyinosine, polydeoxyinosine, oligoinosine and/or oligodeoxyinosine is labeled. The sens and probe are hybridized and the existence of DNA in the product is detected. It can be used to detect the presence of malignant tumour. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGGTTATTGTCTCATGAGGGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of DNA and/or RNA - by converting to single strand form and using probe contg. labelled inosine deriv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 11; 11pp; Japanese.
                                                                                                                                                                                                           Location/Qualifiers
125. .170
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                                                                                                                           ds.
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ID AAN81765 standard; DNA; 456 BP.
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                                                                                                                           Tumour; inosine; DNA probe;
(revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                              /*tag= c
209. .439
/*tag= a
209. .277
/*tag= d
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(first entry)
                                                                                    3eta-urogastrone sequence
                                                                                                                                                                                                                                                                        .204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to correct PA field.)
                                                                                                                                                                                                                                                                        200.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1986;
                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                       JP62244398-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1986;
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13-DEC-1990
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  25-MAR-2003
                                         18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                        sig_peptide
                     10-MAR-2003
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280 AGGGTTATTGTCTCATGAGCGGATACATATTGAATGTATTTAGAAAAATAAACAAATAG 221
                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90366-ABA90260). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting the cell division cycle, or capable of inhibiting the cell division cycle, or capable of inhibiting mitosis and/or meiosis. They can also be used in a method for treating a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as (glomerulonephritis and rheumatoid arthritis), dermatological disorders disorders (such as psoriasis), antiinflammatory, antifungal and antiparasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                  Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ema pallidum infection; syphilis; Borrelia infection; animal; production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide sequence from the genome of Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 101; DB 6; Length 466;
Pred. No. 2.6e-21;
0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 466 BP; 135 A; 87 C; 93 G; 150 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 180
                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 99; 213pp; English.
                                                                                                                                                                                                      Midgley C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0050667P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                              23-MAR-2001; 2001WO-GB001297
                                                                                                                       24-MAR-2000; 2000GB-00007268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX21173 standard; DNA; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
nes 101; Conservative
                                                                                                                                                                                                    Glover DM,
                                                                                                                                                                                                                                          WPI; 2002-055132/07
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                                                                                                                                                               CYCLACEL
WO200172774-A2
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                                        04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX21173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                      Deak P,
                                                                                                                                                             (CXCI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser
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  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiînflammatory; antipsoriatic; dermatological; antifungal; mitosis; antiparastic; antimalarial; antirheumatic; antiarthitic; cell division; cell cycle progression protein; tumour; proliferative disorder; cardiovascular; autoimmune; dermatological disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 AGGGTTAFTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secretion inhibiting action, or cell proliferation promoting action. The deriv. has the same biological or pharmacological activities as betaurogastrone. It is not susceptible to denaturation by oxidn. and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
                     Sequence of HB101 (pGH201) encoding new beta-urogastrone deriv. Met(21),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New beta-urogastrone deriv. - has gastric acid secretion inhibition and proliferation promotion activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemically stable. Deriv. has resistance to proteolytic enzymes such as protease. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antiproliferative; cytostatic; cardiant; immunosuppressive; meiosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The deriv, has various biological activities such as gastric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 100.0%; Score 101; DB 1; Length 4 al Similarity 100.0%; Pred. No. 2.6e-21; 101; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                              Gastric acid secretion; cell proliferation; hormone; ds
                                                                                                                                                                                                                                                                   "New beta-urogastrone deriv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 685; 76pp; Japanese.
                                                                                                                                                             Location/Qualifiers
209. .277
                                                                                                                                                                                                                                                                                                                                                                                           86JP-00153783
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ID ABA90413 standard; DNA; 466
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                                                                                                                                                                                                                                                                 /product=
                                                                                                                                                                                                                         .439
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                                                                                                                       Synthetic
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Best Local S:
Matches 101
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antiinflammatory; antipsoriatic; dermatological; antifungal; mitosis; antiparasitic; antimalarial; antirheumatic; antiarthritic; cell division; cell cycle progression protein; tumour; proliferative disorder; cardiovascular; autoimmune; dermatological disorder; ds.
                                                                                                                                  Antiproliferative; cytostatic; cardiant; immunosuppressive; meiosis;
                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila cell cycle progression protein coding sequence #91
                                                                                                                                                                       61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                           ; Score 101; DB 2;
; Pred. No. 2.7e-21;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rolynucleotides encoding cell cycle treating a tumor or a proliferative
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                   100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                       ABA90456 standard; DNA; 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders (such as malaria)
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                 Query Match 100.
Best Local Similarity 100.
Matches 101; Conservative
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Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glover DM,
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                                                                                                                                                                                                                                                                                    ABA90456/
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                                   New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          33 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis,
                                                                                                                                                                       diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                  1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosi characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pallidum infection; syphilis; Borrelia infection; animal;
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                         Length 487;
                                                                                                                                                                                                                                                                                    Sequence 487 BP; 125 A; 127 C; 113 G; 121 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 223
                                                                                                                                                                                                                                                                                                                         100.0%; Score 101; DB 2; 100.0%; Pred. No. 2.6e-21;
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                  biosynthetic products such as enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1093; 1150pp; English.
                                                                                                              Claim 1; Page 1106; 1150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US013041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0050667P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX21149 standard; DNA; 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                               Conservative
WPI; 1999-081273/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-081273/07
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9859034-A2
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                                                                                                                                                                                                                                                                                                                                                           101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263
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                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                               Local
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RESULT 11 AAX21149/

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                                                              The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90366-ABA90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting the cell division cycle, or capable of their inhibiting a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as (glomerulonephritis and rheumatorid arthritis), dermatological disorders (such as psoriasis), antiinflammatory, antifungal and antiparasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
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2.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 573 BP; 154 A; 118 C; 116 G; 184 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 101; 100.0%; Pred. No. 2
Claim 1; Page 144; 213pp; English.
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Sequence 535 BP; 145 A; 108 C; 122 G; 155 T; 0 U; 5 Other;

biosynthetic products such as enzymes

progression proteins, useful for disorder.

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RESULT 14
                    AAS30560/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel method for the optimisation of primer libraries. Specifically, it refers to increasing the affinity of short oligonucleotide primers, also known as extendable oligos (Bos), for their template sequences. The present invention describes improved methods for sequencing and the linear and exponential amplification of DNA that can amplification for RT-PCR, ligation chain reaction (LCR), rolling circle amplification, strand displacement amplification and isothermal DNA amplification. Accordingly, these extendable oligos with improved specificity and affinity are particularly important in fields ranging from biotechnology and agriculture to medical research. This polynucleotide sequence is the electropherogram of a DNA sequencing reaction that used the pUCI9 plasmid and B154/T422 oligos, used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing the affinity of an extendable oligonucleotide (EO) for a target nucleic acid, for providing primers having improved specificity, comprises hybridization of the EO to a template oligonucleotide (TO) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                   ds; primer library; extendable oligos; EO; ligation chain reaction; LCR; rolling circle amplification; strand displacement amplification; sothermal DNA amplification; biotechnology; agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                   Electropherogram of a DNA sequencing reaction using E154 & T422.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                    295 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTTCCGCGCACATTCCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 359
GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 101; DB 12;
100.0%; Pred. No. 2.8e-21;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                            medical research; pUC19 plasmid
                                                                                                                         ADH58311 standard; DNA; 605 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2002; 2002AU-00002045.
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                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NUCL-) NUCLEICS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D, Thomas T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       extension of the EO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003093500-A1.
                                                                                                                                                                                                 25-MAR-2004
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61
                                                                                                                                                             ADH58311;
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                                                                                       RESULT 13
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antianaemic; dermatological; immunosuppressive; antiniflammatory; antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic; osteopathic; prostate gland; prostatitis, adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperpoliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative; ds.
                                                                                           Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
                                                                   DNA encoding novel prostate gland antigen, Seq ID No 418.
AAS30560 standard; DNA; 776 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US - 0217487P.
2000US - 0217496P.
2000US - 0218290P.
2000US - 0220964P.
2000US - 0220964P.
2000US - 02254518P.
2000US - 0225213P.
2000US - 0225214P.
2000US - 0225266P.
2000US - 022526P.
2000US - 022526P.
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2000US-0225758P.
2000US-0225759P.
2000US-0226279P.
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2000US-0227182P.
2000US-0227009P.
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2000US-0186350P.
2000US-0189874P.
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                                           21-NOV-2001 (first entry)
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                      Homo sapiens.
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18-APR-2000;
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06-SEP-2000;
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                       AAS30560;
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2000US-0230438P.
2000US-0231243P.
2000US-0231243P.
2000US-0231413P.
2000US-0231413P.
2000US-0231414P.
2000US-0232080P.
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2000US-0246526P.
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2000US-0246613P.
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                                                      2000US-0232397P
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                                                                                                                        2000US-0234998P
                                                                                                                                          2000US-0235836P
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06-SEP-2000; 208-SEP-2000; 208-SEP-2000; 208-SEP-2000; 208-SEP-2000; 208-SEP-2000; 208-SEP-2000; 214-SEP-2000; 214-SEP-2000; 2
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
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The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, chronic non-bacterial prostatitis, prostatodystonia, prostatosis, granulomatuus prostatitis, malacoplakia, benign prostatic chronic non-bacterial prostatitis, prostatodystonia, prostatophy or hyperprolasia, and prostatitis, malacoplakia, benign prostatic hypertrophy or hyperprolasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. (I), (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Ragease), authritis), blood-related disorders (sickle cell anaemia), archinitis), blood-related disorders (sickle cell anaemia), respiratory disorders (musculomephritis), cardiovascular disorders (arrhythmias), respiratory disorders, musculoskeletal system disorders (arrhythmias), respiratory disorders (Alzheimer's disease and Parkinson's disease), endocrine disorders (Addison's disease and Parkinson's disease), condocrine disorders (Addison's disease and Parkinson's disease), condocrine disorders (Addison's disease and Parkinson's disease), condocrine disorders (Alzheimer's diseases at the callular level, and wound healing and epithelial cell proliferation. (I) or (II) is cuseful to prevent skin aging, for preventing hair loss, to maintain organs before transplantation, and as food additive or preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 418; 512pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM
                                    2000US-0249264P.
2000US-0249265P.
2000US-0249297P.
2000US-0249299P.
                                                                                                                     2000US-0249300P.
2000US-0250160P.
2000US-0250391P.
2000US-0251030P.
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2000US-0256719P.
2000US-0251479P.
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2000US-0251868P.
2000US-0251869P.
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Best Local Similarity 100.0
Matches 101; Conservative
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                                                                                                                     17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
                                                                             17-NOV-2000;
17-NOV-2000;
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546 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 487

486

7819/c AAS27819 standard; DNA; 776 BP.

RESULT 15 AAS27819/C ID AAS27

1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG

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2000US-02320B1P. 2000US-023196BP. 2000US-0232397P. 2000US-0232398P. 2000US-0232400P. 2000US-0232400P.

2000US-0233063P. 2000US-0233064P. 2000US-0233065P.

2000US-0234223P. 2000US-0234274P. 2000US-0234997P.

2000US-0234998P

2000US-0235484P. 2000US-0235834P. 2000US-0235836P.

2000US-0236327P. 2000US-0236367P. 2000US-0236368P. 2000US-0236369P.

2000US-0236370P. 2000US-0236802P. 2000US-0237037P.

2000US-0237038P. 2000US-0237039P. 2000US-0237040P. 2000US-0239935P.

2000US-0241785P

2000US-0241826P. 2000US-0244617P. 2000US-0246474P.

2000US-0241809P

2000US-0246475P. 2000US-0246476P. 2000US-0246477P. 2000US-0246478P.

2000US-0246523P. 2000US-0246524P. 2000US-0246525P.

16526P.

2000US-024

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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis c; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; chromosomal abnormality, bown syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; Albs; ds; acquired immune deficiency syndrome.
                                                 DNA encoding novel signal transduction pathway protein, Seg ID 1479.
                                                                                                                                                                                                                                                                                                  2000US-0186350P.
2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
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2000US-0220964P.
2000US-0224518P.
2000US-0224519P.
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2000US-0225270P.
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2000US-0215135P.
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2000US-0218290P
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2000US-0225214P
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2000US-0225267P
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2000US-0226279P
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                             (first entry)
                                                                                                                                                                                                        WO200154733-A1
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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08-SEP-2000;
08-SEP-2000;
                                                                                                                                                                                      Homo sapiens.
                             07-NOV-2001
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         AAS27819;
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2000US-0246527P. 2000US-0246528P. 2000US-0246532P. 2000US-0246609P.

2000US-0246610P. 2000US-0246611P. 2000US-0246613P.

2000US-0249207P. 2000US-0249208P. 2000US-0249209P. 2000US-0249210P.

2000US-0249211P. 2000US-0249212P. 2000US-0249213P.

2000US-0249215P 2000US-0249216P 2000US-0249265P

2000US-0249214P

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The invention relates to novel isolated polypeptides (I), and diagnostic polynucleotides (II). (I) and the antibody to (I) are useful for diagnosting, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital and acquired immunodeficiencies, autoimmune contransplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host diseases, infectious diseases (e.g. chear blood-related disorders (e.g. disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Alzheimer's disease, Parkinson's disease), reproductive graft of an endormalities (e.g. Alzheimer's disease, Parkinson's disease), reproductive system disorders (e.g. Addison's epithelial cell proliferation, endocrine disorders (e.g. Addison's epithelial cell proliferation, endocrine disorders (cirrhosis), as stimulators of disease), reproductive system disorders (cirrhosis), as stimulators of mighter affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction pathway protein coding sequences and PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 101; DB 4; Length 776; 100.0%; Pred. No. 2.9e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1479; 880pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM;
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249300P.
11-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-025130P.
05-DEC-2000; 2000US-025130P.
05-DEC-2000; 2000US-025149P.
06-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
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Best Local Similarity 100.
Matches 101; Conservative
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486 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 446 61 GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC 101 ð

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Search completed: July 14, 2005, 07:01:43 Job time : 142.448 secs

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0; Gaps

0; Indels

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1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60

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100002303 100004K04 100003G03

CC810024 CC8116954 CC8116954 CC8116959 AL694813 AL694813 CC811633 CC811643 CC811778 CC811778 CC8117595 CC8117595 CC8117595 CC8117595 CC8117595 CC8117595 CC8117595 CC8117595 CC8117595 CC8117679 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508 CC8118508

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BM078095 30-NOV-2001
83374 Hebeloma cylindrosporum functional cDNA library Hebeloma
cylindrosporum cDNA 5', mRNA sequence.
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Agaricales; Cortinariaceae; Hebeloma.
1 (bases 1 to 300)
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Construction of a functional cDNA library from the ectomycorrhizal
fungus Hebeloma cylindrosporum
Unpublished (2001)
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Site_2: XhoI"
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| Lissue_type="Mycalia"
| Liab_host="B. contains"
| Clone_lib="Hebeloma cylindrosporum functional cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wipf D.
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
Fax: 49 7071 293287
Email: daniel.wipf@zmbp.uni-tuebingen.de
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/mol_type="mRNA"
/strain="H1"
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High quality sequence stop: 300
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CC817788
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                                                                                       July 14, 2005, 05:15:57; Search time 961.667 Seconds (without alignments) 3997.736 Million cell updates/sec
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                                                                                                                                                                       1 agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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BU964094
FR0009140
                                                                nucleic search, using sw model
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length: 2000000000
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Scoring table:

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CC819058 CC819270 CC816848

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Query Match 100.0%; Score 101; DB 4; Length 300; Best Local Similarity 100.0%; Pred. No. 8.1e-19; Matches 101; Conservative 0; Mismatches 0; Indels

ORIGIN

100002L01 DKFZp469H

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL COMMENT

FEATURES

ORIGIN

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RESULT 2 BU963956/c

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DEFINITION

ACCESSION

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Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning Genome Res. 9 (10), 960-971 (1999) 99455097
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Direct Submission
Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource Centre Hintston, Cambridge, CBIO 1SB. Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 AGGGTTATTGICTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 111
                                                                                    A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis
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Bouchireb, N., Cottage, A., Yeo, G.S., Umrania, Y., Williams, G. and
Agaricales; Cortinariaceae; Hebeloma.
1 (bases 1 to 300)
Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and
Frommier, W.B.
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library"
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                                                                                                                                                                                                                                                                               Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
Fax: 49 7071 293287
Email: daniel.wipf@zmbp.uni-tuebingen.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC, 101
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                                                                                                                                                                           Unpublished (2002)
Contact: Wipf D
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Hebeloma cylindrosporum"
/mol type="mRNA"
/strain="H1"
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GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:76867"
                                                                                                                                                                                                                                                                                                                                                                                      no homology below 1e-10.
Location/Qualifiers
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AUTHORS
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Hebeloma cylindrosporum
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
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Agaricales, Cortinariaceae, Hebeloma.
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     A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis
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homolog to Enterobacteria phage f1 ; ampicillinase (1e-10)
Location/Qualifiers
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ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
Fax: 49 7071 293287
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                                                                                 61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                              114 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Hebeloma cylindrosporum"
|mol_type="mRNA"
|strain="H1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Mycelia"
/lab_host="E. coli XL1-Blue"
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                                                                                                                                                                                                                                                                                                                                                                                                                Hebeloma cylindrosporum
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BU964094.1 GI:24204891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                         BU963956
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

BU964094/c DEFINITION

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Gaps

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GSS 25-FEB-2004

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Query Match
Best Local Similarity
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84112, USA
                                                                                                                                                                                                                                               sequence.
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                                                                                                                                                RESULT 6
CC819240/c
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email S. Wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 bp mRNA linear EST 04-SEP-2003 nonym: hlcc2) Homo sapiens cDNA clone
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1 (bases 1 to 391)
Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH10B"
/clone_lib="313 (synonym: hlcc2)"
/note="vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No si sequence available.

This clone (DKFZp31371611) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                    1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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                                                                                                                                                                                                                                           Length 309;
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                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   99 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 139
                                                                                                                                                                                                                                                                                                                                                                                               61 GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                           100.0%; Score 101; DB 9;
100.0%; Pred. No. 8.2e-19;
ive 0; Mismatches 0;
                                                                                      1. .309
/organism="Takifugu rubripes"
                                                                                                                        /mol_type="genomic_DNA"
/db_xref="taxon:31033"
/clone="010H20aC4"
/clone_lib="cosmid_010H20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .391
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:966"
/clone="DKFZp313J1611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKFZp313J1611_rl 313 (synonym: hl
DKFZp313J1611_5', mRNA sequence.
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA-collection"
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Homo sapiens
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101; Conserv
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                                                                                          source
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AUTHORS
TITLE
JOURNAL
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AL597149
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1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 60

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Oxytricha plasmid UUGC10 library."
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|473114|qb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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9
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Contact: Robert B. Weiss
Contversity of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Sterkiella histriomuscorum
Bukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichiad; Oxytrichidae; Sterkiella.

1 (bases 1 to 414)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes
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                                                                                                                                 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sterkiella histriomuscorum"
/mol type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Plate: 0005 row: D column: 19
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quulity sequence stop: 414.
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CC819240.1 GI:32899308
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Fax: 801 585 7177
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                                                                                                                                                                               Eukaryota; Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi, Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Perciformes; Labroidei; Cichlidee; Haplochromis.

E 1 (bases 1 to 417)

S Watanabe,M., Kobayashi,N., Shin-i,T., Kohara,Y. and Okada,N. Orf sequences of cichlid in Lake Victoria are essentially same Contact: Tadasu Shin-i

Contact: Tadasu Shin-i

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
                  BJ684174 BJ684174 HCEST library Haplochromis chilotes cDNA clone no90c12,
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella.
1 (bases 1 to 491)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Haplochromis chilotes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone lib="HCEST library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:257977"
/clone="no90c12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="jaw"
                                                                                                   BJ684174.1 GI:46527295
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Matches 101; Conservative
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Tel: 801 585 5606
                                                             mRNA sequence.
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/organism="Sterkiella histriomuscorum"
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Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
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Email: webmaster@estarray.org, URL: http://www.estarray.org
Seg primer: M13 forward primer.
Location/Qualifiers
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Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
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Contact: Haitao Dong, Debao Li
Bioinfomatics and Gene Network Research Group
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Plate: 0006 row: J column: 13
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 491.
Location/Qualifiers
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Pred. No. 8.4e-19;

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Best Local Similarity 100.
Matches 101; Conservative
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/clone="UUGCXCONITYALDS"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone="Uuce-XoyTricha plasmid UUGCIO library."
/clone="Ubector: PWDAJANY, Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymuclecide kinase. Adaptor
oligonuclectides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (qi|4732114|qb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli Xil0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Sterkiella histriomuscorum
Bukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida, Oxytrichidae; Sterkiella.
1 (bases 1 to 495)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
                                                                                                                                                                                               Gaps
/tissue_type="Stem"
/dev_stage="3-5 leaf stage"
/clone_lib="Stem library from Oryza sativa (3-5 leaf
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University of Utah Genome Center
University of Utah
University of Utah
Rm. 304 biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                     61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                 Score 101; DB 4;
Pred. No. 8.4e-19;
Mismatches 0;
                                                                                                                              100.0%; Sco...
100.0%; Pred. No. c.
0; Mismatches
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Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 495.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Unpublished (2003)
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                                                                                                                                    Query Match
Best Local Similarity 100.
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100.0%; Score 101; DB 9; Length 495;

Query Match

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DNA from Oxytricha trifallax was blunt end-repaired with
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oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                     392 AGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 333
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Stichotrichida, Oxytrichidae, Sterkiella.
                                                    Gaps
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100004L13R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC10004L13 R, genomic survey
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Paired end reads from plasmid inserts of Oxytricha trifallax
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100.0%; Pred. No. 8.4e-19;
iive 0; Mismatches 0;
                                                  Mismatches
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Plate: 0004 row: L column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
100.08;
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Unpublished (2003)
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Matches 101; Conservative
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Fax: 801 585 7177
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Bukaryota, Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 515)
    histriomuscorum genomic clone UUGC100003C16 R, genomic survey
                                                                                                                                                                                                                   Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes
Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                               Sterkiella histriomuscorum (Oxytricha trifallax) Sterkiella histriomuscorum
                                                                       CC817752.1 GI:32897039
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Fax: 801 585 7177
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84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               macronuclear chromosomes
Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                  Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Eukaryota; Alvoclata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 503)
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Paired end reads from plasmid inserts of Oxytricha trifallax
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100.0%; Score 101; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 8.4e-19;
Matches 101; Conservative 0; Mismatches 0; Indels C
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Tel: 801 585 5606
Fax: 801 585 7177
Faxil ddunn@genetics.utah.edu
Flate: 0006 row: N column: 08
Seg primer: CACACAGGAAACAGCTATGACC
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High quality sequence stop: 503.
Location/Qualifiers
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CC817752/c
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/mol_type="genomic DNA"
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DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWM42 (gil4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Sterkiella histriomuscorum
Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
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100002D21R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100002D21 R, genomic survey
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Plate: 0003 row: C column: 16
Seq primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
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completed: July 14, 2005, 23:23:06
ne : 962.667 secs
          University of Utah
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DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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84112, USA
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Sterkiella histriomuscorum
Eukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella.
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Stichotrichida, Oxytrichidae, Sterkiella.
1 (bases 1 to 518)
Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
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Paired end reads from plasmid inserts of Oxytricha trifallax
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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University of Utah Genome Center
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Location/Qualifiers
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                                                                                                        macronuclear chromosomes
Unpublished (2003)
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Fax: 801 585 7177
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Best Local Similarity
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/Lab host="E. Col; strain XL10-Gold, T1-resistant, F-"
/Llone lib="Wortricha plasmid UUGCIO library"
/note="Vector: PWD42ny: Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligomucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Biomedical Polymers Research Bldg., 20
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                                                                                                                                                                                                                                                                                                                                        organism="Sterkiella histriomuscorum"
                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@generics.utah.edu
Plate: 0002 row: J column: 19
Seq priner: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 519.
                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:94289"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="UUGC100002J19"
                                                                                                                                                                                                                                                                             Location/Qualifiers
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Best Local Similarity 100.0
Matches 101; Conservative
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Tissue sp

Sequence

OM nucleic

Run on:

Sequence:

Title:

Searched:

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AX060344 Sequence
M33236 Cloning vec
AX133940 Sequence
AR071323 Sequence
BD238492 Expressio
AX24391 Sequence
A31754 Sequence
BD085110 Vertebrat
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                              AR207834 Sequence
BD009731 Tissue sp
A38214 Sequence 58
AX286570 Sequence
AX743954 Sequence
AR062871 Sequence
                                                                                                                                                                                                                                                AX319694 Sequence
L36555 Cloning vec
A44171 Sequence 1
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Method of production of a protein in cells which inducibly express the cell cycle inhibitor protein, p21
Patent: WO 02099100-A 2 12-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 105
                                                                                                                                                                                          AX951626 Sequence
U89673 Cloning vec
BD234590 Screening
                                                                                                                                                                                M83237 cDNA expres
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                           AX026821 Sequence
BD195386 Composit
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                     AR098192
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                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol type="unassigned DNA"
/db xref="taxon:10095"
/note="Rous Sarcoma Virus LTR promoter"
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Sequence 2 from Patent WO02099100.
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A91754
BD085110
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BD195386
AX319694
SYNTCRC
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BD238492
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Location/Qualifiers
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ALRPROLTB
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BD107647 FIV vacci
AX643582 Sequence
AX044426 Sequence
AX044425 Sequence
A83240 Cloning vec
AJ32038 Expressio
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AR207832 Sequence
BD009729 Tissue sp
A60213 Sequence 9
AR122289 Sequence
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AR098191 Sequence
AR207833 Sequence
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AX175190 Sequence
AX175195 Sequence
A85308 Sequence 6
                                                                     July 14, 2005, 04:39:07; Search time 749.127 Seconds (without alignments) 6468.225 Million cell updates/sec
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                                                                                                                                        1 ctgctccctgcttgtgtgtt......caattgcatgaagaatctgc 100
                                                                                                                                                                                                                  9416466
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                             4708233 segs, 24227607955 residues
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AX044425
SYNRSV3MV
EVE132038
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Maximum Match 100%
Listing first 45 summaries
                                                   - nucleic search, using sw model
                                                                                                                 US-09-482-682-64_COPY_1_100
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seq length: 200000000
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9b_ph; *

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9b_sk; *

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PAT 24-FEB-2003

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Minimum Maximum

Database

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9

Result

2

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE

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AUTHORS TITLE

JOURNAL MEDLINE

PUBMED REFERENCE MEDLINE PUBMED

JOURNAL

mRNA

ORIGIN

LTR

FEATURES

ACCESSION VERSION

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Rivera,V., Zoltick,P. and Wilson,J.M.
Methods for expression of genes in primates
Patent: WO 0142444-A 6 14-UDN-2001;
ARIAD GENE THERAPEUTICS, INC. (US); THE UNIVERSITY OF PENNSYLVANIA
                                                                                                                                                                  Rivera, V., Zoltick, P. and Wilson, J.M.
Methods for expression of genes in primates
Patent: WO 0142444-A 1 14-JUN-2001;
ARIAD GENE THERAPEUTICS, INC. (US) ; THE UNIVERSITY OF PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 CIGCICCCTGCTIGTGTGTGTGGGCGCGCTGAGTGCGCGGGCGAAATTTAAGCTACA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 100; DB 6; Length 648; Best Local Similarity 100.0%; Pred. No. 2.6e-25; Matches 100; Conservative 0; Mismatches 0; Indels
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"Organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="vector/RSV promoter/vector"

    .648
    /organism="synthetic construct"

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/db_xref="taxon:32630"
/note="MluI/RSV promoter/Bgll"
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synthetic construct
other sequences, artificial sequences.
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Sequence 6 from Patent WO0142444.
AX175195
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                         AX175190.1 GI:14598581
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A85308
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AX175195
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                                                                                                                                                 Yamamoto,T., de Crombrugghe,B. and Pastan,I.
Identification of a functional promoter in the long terminal repeat
of Rous sarcoma virus
(21 22 (3), 787-797 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobases 319 to 633)
Yamamoto,T., Jay,G. and Pastan,I.
Unusual features in the nucleotide sequence of a CDNA clone derived
from the common region of avian sarcoma virus messenger RNA
Proc. Natl. Acad. Sci. U.S.A. 77 (1), 176-180 (1980)
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[1] demonstrated the mRNA transcription initiation site shown in the Sites table using pSRI as a template. However, this is the 3' LITR, and the functional mRNA start site would be assumed to be on the 5' LIR at the homologous site.
                                                                                                                                                                                                                                                                                                                                     amamoto, T., Tyagi, J.S., Fagan, J.B., Jay, G., deCrombrugghe, B. and
                                                                                                                                                                                                                                                                                                                                                                                                              transforming gene of avian sarcoma virus as suggested by analysis of recombinant clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60
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J02025 J02022
J02025.1 GI:210255
C-myc proto-oncogene; long terminal repeat (LTR); src oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original source text: Rous sarcoma virus (Schmidt-Ruppin strai subgroup D) provirus, cDNA to 21S mRNA from infected chicken embryonic fibroblasts, clone pSR1.

[11] sites; mRNA start.

[12] istes; mRNA start.

[13] included 24 'g's on 5' end and 16 'c's end that were cDNA synthesis artifacts.

[2] also, sequenced a defective clone, pSR2, with the src gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                            Rous sarcoma virus
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
                                                                                                                                                                                                                                                                                                                                                                                        Molecular mechanism for the capture and excision of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 100; DB 14; Length 633; 100.0%; Pred. No. 2.6e-25; ive 0; Mismatches 0; Indels 0;
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'note="in vitro mRNA [1]; see comment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="terminally redundant repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rous sarcoma virus"
/mol_type="genomic RNA"
/db_xref="taxon:11886"
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Location/Qualifiers
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Sequence 1 from Patent WO0142444.
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'note="3' LTR"
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                                                                           Rous sarcoma virus
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Best Local Similarity 100.
Matches 100; Conservative
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PAT 03-JUL-2001

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PAT 24-NOV-2000
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Method of production of a protein in cells which inducibly express
the cell cycle inhibitor protein, p21
the cell cycle inhibitor protein, p21
Patent: WO 0210910-Al 12-DEC-2002;
Lonza Biologics plc (GB)
Location/Qualifiers
                                                                      77 CTGCTCCCTGCTTGTGTGTGTTGGAGGTCGCTGAGTAGTGCGGAGCGAAATTTAAGCTACA 136
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Patent: WO 0065752-A 18 09-NOV-2000;
AstraZeneca AB (SE) ; THE VICTORIA UNIVERSITY OF MANCHESTER (GB)
Location/Qualifiers
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/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
/noTe==R87-LTR promotor + intron + p21 cds + TKpoly(A)
LacSwitch II expression construct"
                                               1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
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//organism="synthetic construct"
/mol.type="unassigned DNA"
/db xref="taxon.35630"
/noTe="CPG2 with last exon of Thy-1 fused at 3' end"
            Gaps
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        0; Indels
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Sequence 18 from Patent WO0066752.
AX044426
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AX643582
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CC SST I - SST I FRAGMENT IN PLASMID CMV DEL. RT
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synthetic construct
other sequences, artificial sequences.
(bases 1 to 1070)
Neil,J.C., Rigby,M.A. and Jarrett,J.O.
FIV vaccine
PATENTY VOUSTONTY COURT OF THE UNIVERSITY OF GLASGOW
OS Artificial Sequence
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Rigby,M.A. and Jarrett,J.O.
FIV VACCINE
Patent: WO 940493-A 6 17-SEP-1998;
RIGBY MARK ALAN (GB); JARRETT JAMES OSWALD (GB)
Location/Qualifiers
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100.0%; Score 100; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.8e-25;
Matches 100; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db.xref="t-axon:32630"
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                                                                                                                                                                                                                                                                                    organism="unidentified"
|mol_type="unassigned DNA"
|db_xref="taxon:32644"
Sequence 6 from Patent WO9840493.
A85308
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15-JAN-2002
10-MAR-1998 JP 1998539351
11-MAR-1997 GB 9704977
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JP 2002501369-A/6.
                                               A85308.1 GI:6733916
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BD107647
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VERSION
KEYWORDS
SOURCE
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ORGANISM

RESULT 6 BD107647 LOCUS

TITLE JOURNAL

COMMENT

FEATURES

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AUTHORS REFERENCE

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Jacobson, S., Sekaly, R.P., Jacobson, C.L., McFarland, H.F. and
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864. .882
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/note="T7"
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EVE132038
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TITLE
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                                                           JOURNAL
MEDLINE
   AUTHORS
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Chemical compounds
Patent: WO 0066752-A 17 09-NOV-2000;
AstraZeneca AB (SB); THE VICTORIA UNIVERSITY OF MANCHESTER (GB)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="CPG2 mutant with last exon of Thy-1 fused at end"
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High efficiency DNA-mediated transformation of primate cells
Science 221 (4610), 551-553 (1983)
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   Length 2426;
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100.0%; Pred. No. 3.1e-25;
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other sequences; artificial sequences; vectors.
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                                                                                                                                         129 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 168
 100.0%; Score 100; DB 6; 1
100.0%; Pred. No. 3.1e-25;
ive 0; Mismatches 0;
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Sequence 17 from Patent WO0066752.
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New M13 vectors for cloning
Meth. Enzymol. 101, 20-78 (1983)
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Best Local Similarity 100.
Matches 100; Conservative
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               Similarity
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SYNRSV3MV
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Long, E.O.
HLA class II-restricted presentation of cytoplasmic measles virus antigens to cytotoxic T cells
J. Virol. 63 (4), 1756-1762 (1989)
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Submitted (27-FEB-1999) Zeng B.J., Gene Engineering Center,
Institute of Microbiology, Zhongguancun, Beijing, Beijing 100080,
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AMP gene; beta lactamase; ColEl origin of replication; multiple cloning site; SP6 promoter; SV40 origin of replication; T7 promoter; xanthine-guanine phosphoribosyl transferase; Xanthine-quanine phosphoribosyl transferase gene. Expression vector pCDPT

Expression vector pCDPT
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/function="ampicillin-resistance, replication origin"
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1. .3840
/organism="Expression vector pCDPT"
/mol_type="other RNA"
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Local Similarity 100.0%; Pred. No. 3.2e-25;
les 100; Conservative 0; Mismatches 0;
                                                                                                                                                  source text: Cloning vector DNA.
Location/Qualifiers
1. .3557
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/note="Multiple cloning site
                                                                                                                                                                                                                                     /organism="unidentified c
/mol_type="genomic DNA"
/mb_xref="taxon:45196"
1. 29
/function="polylinker"
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/evidence=experimental
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PAT 20-JUN-2002

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PD 21-MAR-2001
PP 13-MOV-1997 01
PP 13-MOV-1996 US 08/751517,14-FEB-1997 US 08/1
PR 15-NOV-1996 US 08/751517,14-FEB-1997 US 08/1
DOUGLAS ANTELMAN, RICHARD J GREGORY, KENNETH N WILLS PC CO7H21/04,C07K5/00,A61K38/00,A61K35/12
CC Strandedness: Single;
CC Topology: Linear;
FH Key CDS 209. 862.
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Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 3 21-MAR-2001;
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             61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                          141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
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; Pred. No. 3.3e-25;
0; Mismatches 0;
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Antelman, D., Gregory, R. J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 5 30-APR-2002;
Location/Qualifiers
                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                         /organism="unknown"
/mol_type="unassigned DNA"
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                                                                                                                    Sequence 5 from patent US 6379927.

    .3853
    /organism="unidentified"
/mol_type="genomic DNA"
/db xref="taxon:32644"

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Location/Qualifiers
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JP 2001503638-A/3.
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100.0%;
Best Local Similarity 100.0%;
Matches 100; Conservative 0
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                            product="beta-lactamase"
product="lacta-lactamase"
protein id="CAB51568.1"
db_xref="G1:5640090"
franslation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDABDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                      IELDLINSGKILESFRPEERFPWWSTFKVLLCGAVLSRIDAGGEGLGRRIHTSGNDLVE
SYPUTEKHITDGWIYRELCSAAITWSDNTAANLLTTIGGREELTAFLINMGDHYTRL
DRWEPELNEAI PINDEDTTWPVAAMTTLRKLITGELLTLASROGLIDWMEADKYAGPL
IRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATWDERNRQIA
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; Pred. No. 3.3e-25;
0; Mismatches 0;
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100.0%; Pred. No. 3.3e-25;
iive 0; Mismatches 0;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 5 13-JUN-2000;
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Sequence 5 from patent US 6074850.
AR098190
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/gene="amp"
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/note="ColE1"
                                                                                                                                                                                                         .644. .2729
note="SV40"
                                                                                                                                                                          450. .2775
note="SP6"
                                                                                                                                                                                                                                                                                              gene="amp"
                                                                                                                                          649. .1863
                                                                                                                                                           note="BGH"
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PAT 31-JAN-2002

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Best Local Similarity 100.0%; Pred. No. 3.3e-25;
Matches 100; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                    Collins, M.K., Weiss, R.A., Takeuchi, Y. and Cosset, F. EXPRESSION SYSTEMS
Patent: WO 97083304 06-MAR-1997;
CANCER RES CAMPALGN TECH (GB)
Location/Qualifiers
                                                                                                                                                                            linear
               Indels
                                                                                     61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 169
Best Local Similarity 100.0%; Pred. No. 3.3e-25; Matches 100; Conservative 0; Mismatches 0;
                                                                                                                                                                             DNA

    .3925
    /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

                                                                                                                                                                           A60213 3925 bp
Sequence 9 from Patent W09708330.
A60213.1 GI:3715221
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Job time : 751.127 secs
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A60213
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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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nucleic search, using sw model OM nucleic

Run on:

July 14, 2005, 04:35:42; Search time 140.988 Seconds (without alignments) 4198.742 Million cell updates/sec

1 ctgctccctgcttgtgtgtt......caattgcatgaagaatctgc 100 score: Sequence: Title: Perfect

US-09-482-682-64\_COPY\_1\_100

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 8 8 8 Minimum | Maximum |

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

geneseqn2003ds: geneseqn2003cs: geneseqn2004as: N\_Geneseq\_16Dec04:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2003as:\* geneseqn1980s:\* geneseqn1990s:\* geneseqn2002as: geneseqn2002bs: geneseqn2003bs: geneseqn2000s: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs

	Description	Abz23250 Nucleotid	Aah43951 Rous sarc	Aav58058 Plasmid C	Adm41035 Fungus nu	Adh11349 Vertebrat	Adm41037 Cytomegal	Adm41034 Human nuc	Abz23249 Lac repre	Adm41036 Cytomegal	Aad02037 Plasmid p	Aad02036 Plasmid p	Aat62937 3F4 human	Aat62932 2A2 human	Aav40006 Plasmid p	Aat90695 Plasmid C	Aav40007 Plasmid p	Aaq75974 pHLA-B7 e	Aav63466 Plasmid p	Aag62391 Vector pv	Aas17704 Vector pV
SUMMARIES	QI	ABZ23250	AAH43951	· AAV58058	ADM41035	ADH11349	ADM41037	ADM41034	ABZ23249	ADM41036	AAD02037	AAD02036	AAT62937	AAT62932	AAV40006	AAT90695	AAV40007	AAQ75974	AAV63466	AAQ62391	AAS17704
	DB	80	4	~	12	7	12	12	œ	12	4	4	N	~	~	7	7	~	7	N	9
	% Query Match Length DB	562	648	1070	1506	1600	1782	2241	2245	2294	2426	2427	3400	3400	3853	3925	4026	4059	4249	4341	4341
	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
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Abn83143 Plasmid p Add35599 Bicistron	Aaves/46 Nucleotid	Adr12380 Vector pM Aaf83146 Complete	Aaq75973 pHLA-B7/b	Adb33528 Expressio	Aazsebss perz expr Aas12839 DNA seque	Adh11417 Plasmid p	Adf10526 Plasmid p	Acc44637 Murine rD	Ads75099 Plasmid p	Abk88869 Topoisome	Ade83792 Plasmid p	Ado06721 Recombina	Acc44692 Plasmid p	Aat62933 2A2 human	Abv77540 Plasmid p	Abv77538 Plasmid p	Abv77547 Plasmid p	Abv77548 Plasmid p	Abv77549 Plasmid p	Aat62938 3F4 human
6 ABN83143 10 ADD35599	2 AAV69/46 4 AAF24901	13 ADR12380 4 AAF83146	2 AAQ75973	10 ADB33528	4 AAS12839	2 ADH11417	10 ADF10526	10 ACC44637	13 ADS75099	6 ABK88869	12 ADE83792	12 ADO06721	10 ACC44692	2 AAT62933	10 ABV77540	10 ABV77538	10 ABV77547	10 ABV77548	10 ABV77549	2 AAT62938
4341	4597	4825 4840	4965	5015	5070	5082	5162	5162	5172	5173	5173	5173	5192	5250	5271	5283	5292	5293	5293	5300
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
22 22 23	22.2	25 26	27	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

p21; RSV; LTR promoter; cell cycle inhibitor protein; protein production; anchorage-independent producer cell line; ss. Nucleotide sequence of the Rous sarcoma virus (RSV)-LTR promoter. ABZ23250 standard; DNA; 562 BP. 03-JUN-2002; 2002WO-EP006054. 01-JUN-2001; 2001GB-00013318. (first entry) Rous sarcoma virus. WO200299100-A2. 12-DEC-2002. 24-MAR-2003 ABZ23250; ABZ23250 

Al-Rubeai M, Shuttleworth J; WPI; 2003-148669/14.

(LONZ ) LONZA BIOLOGICS PLC.

Producing recombinant protein, particularly for maximizing or enhancing e.g. therapeutic protein production, by co-expressing protein with recombinant cell cycle inhibitor protein (p21) in producer cell line.

Disclosure; Page 32-33; 33pp; English.

promoter. The present sequence is used to produce vectors for use in the method of the invention. The specification describes a method for producing a protein, preferably a recombinant protein, in a mammalian anchorage-independent producer cell line. The method comprises coexpressing with the producer the producer cell line a recombinant cell cycle inhibitor protein (preferably p21). The method is useful for producing a recombinant protein in a producer cell line. This is The present sequence represents the Rous sarcoma virus (RSV)-LTR

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present invention
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11-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                            AAV58058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neil JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                provirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                       AAV5805E
     SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for genetically engineering a primate for expression of a desired gene comprising introducing into the primate a transgene comprising an Rous Sarcoma Virus (RSV) promoter and a nucleic acid sequence heterologous to RSV promoter. Also described is a primate cell (I) containing and capable of expressing a transgene comprising an RSV promoter operably linked to a recombinant nucleic acid encoding one or more fusion proteins, where the fusion proteins bind to a ligand and in the presence of the ligand modulate(s) the expression of a target gene. The method can be used for high level expression of genes in primates or for engineering primate cells. It is useful for increasing the efficacy of many gene therapy strategies, and for increasing the efficacy of intracellular immunisation agents, molecules
                                                                                                                                                                                                 1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetically engineering a primate for expression of a desired gene, comprises introducing into the primate a transgene comprising Rous Sarcoma Virus (RSV) promoter and a nucleic acid sequence heterologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  like ribozymes, antisense RNA, and dominant negative proteins, that act either stoichiometrically, or by competition. The method increases the efficacy of many gene therapy strategies by substantially elevating the expression of an expression therapeutic gene, and allowing expression to reach therapeutically effective levels. The present sequence represents specifically claimed RSV enhancer/promoter nucleotide sequence from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rous sarcoma virus; promoter; enhancer; RSV; primate; gene expression; transgene; genetic engineering; gene therapy; immunisation; ds.
particularly useful for maximizing or enhancing the production of e.g. therapeutic proteins at an industrial scale
                                                                                                                                  Gaps
                                                                                                                                  ö
                                                                                           Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rous sarcoma virus promoter nucleotide sequence SEQ ID NO:1.
                                                         Sequence 562 BP; 143 A; 109 C; 163 G; 147 T; 0 U; 0 Other;
                                                                                                                                0; Indels
                                                                                                                                                                                                                                             61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                  106 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 145
                                                                                                               Pred. No. 8.2e-28;
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                                                                                             В
                                                                                                                                0; Mismatches
                                                                                               Score 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ARIA-) ARIAD GENE THERAPEUTICS INC. (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0170019P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC-2000; 2000WO-US033256
                                                                                                                                                                                                                                                                                                                                                                           AAH43951 standard; DNA; 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zoltick P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-381673/40.
                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rous sarcoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200142444-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                              AAH43951;
                                                                                           Query Match
                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                       RESULT 2
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                                                                                                                                                                                             This is the nucleotide sequence of a SatI fragment of plasmid CMV-delRT, in which the immediate-early promoter of human cytomegalovirus replaces the 5' long termal repeat region of feline immunodeficiency virus (FIV) close F14-delRT (see AAVS805). FIV sequences downstream of the SatI site are identical to those in F14-delRT. Use of the CMV promoter was designed to enhance expression of FIV antigens, and to reduce the risk of reversion to a replicating provirus, in tissues after inoculation of DNA. Vaccine formulations for FIV-calated diseases include a defective feline immunodeficiency proviral (FIPV) polynucleotide comprising an in-frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIV; FIPV; vaccine; reverse transcriptase; diagnosis; therapy; CMV-delRT;
                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "CMV promoter fragment from pcDNA3 (BglII-KpnII)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protecting, e.g. cats, against feline immunodeficiency virus - by using vaccine comprising FIV pol gene containing deletion and/or insertion in reverse transcriptase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/note= "FIV sequences from primer binding site to SstI
                                                                                                                                                                1 CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                                                                                           Gaps
                                                                                                         .;
0
                                                    Length 648;
Sequence 648 BP; 163 A; 135 C; 179 G; 171 T; 0 U; 0 Other;
                                                                                                         Indels
                                                                                                                                                                                                                                                                               61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                         ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 189
                                              ; Score 100; DB 4;
; Pred. No. 8.6e-28;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
8. .896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid CMV-delRT SstI fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 4; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cytomegalovirus.
feline immunodeficiency virus.
                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV58058 standard; DNA; 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-GB000715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    918.
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                                                 Query Match
Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter; cat; ss.
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   the
                                                                                                                                                                                                                            CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 136
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deletion and/or insertion in the reverse transcriptase (RT) region of pol gene. Host cells comprising the FIPV are capable of producing FIV proteins, except for functionally competent RT, and thus release non-infectious FIV viral particles. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                             CTGCTCCCTGCTTGTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA
                                                                                                                                                               Gaps
                                                                                                                                                               ö
                                                                                                                               2; Length 1070;
                                                                                              Sequence 1070 BP; 275 A; 254 C; 268 G; 273 T; 0 U; 0 Other;
                                                                                                                                         le-27;
                                                                                                                               8
                                                                                                                                                             Mismatches .
                                                                                                                               Score 100;
Pred. No. 1
                                                                                                                                                               ö
                                                                                                                               100.0%;
100.0%;
                                                                                                                                                           Matches 100; Conservative
                                                                                                                                            Similarity
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                                                                                                                           Query Match
Best Local (
                                                                  field.)
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Fungus nucleotide sequence SEQ ID NO:3. ADM41035 standard; DNA; 1506 BP (first entry) 17-JUN-2004 ADM41035; RESULT 4 

engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; fungus; gene; ds.

Unidentified

WO2004027029-A2

01-APR-2004

19-SEP-2002; 2002US-0411790P

17-SEP-2003; 2003WO-US029251

(XIME-) XIMEREX INC.

Thompson SC; Ğ, Sosa Beschorner WE,

WPI; 2004-295402/27.

useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host. Engrafting foreign replacement cells within a fetal non-human

Disclosure; SEQ ID NO 3; 48pp; English

The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells in the cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present specification.

Sequence 1506 BP; 454 A; 277 C; 361 G; 414 T; 0 U; 0 Other;

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The present invention describes a vertebrate protein homologue of an UNC-53 protein of Caenorhabditis elegans or a functional equivalent, derivative or bioprecursor of UNC-53. Also described; (1) a CDNA sequence necoding a vertebrate homologue of the C. elegans UNC-53 protein; (2) a nucleic acid which hybridises to the CDNA of (1); (3) vector comprising the cDNA as in (1); (4) a host cell containing the vector as in (3); (5) a transgenic cell, tissue or animal comprising the vector as in (3); (6) a compound identified as an enhancer or inhibitor of the regulation of cell shape, motility or the direction of cell migration for use as a therbod for determination of whether a protein is an inhibitor or enhancer of regulation of cell behaviour, growth, shape or motility or the direction of migration by contacting a host cell expressing a homologue of UNC-53 and determining a change of phenotype; (8) a method for identification of a brotein which is
                                                              ö
                                                                                                                                                                                   81 crecrecerecergerereseses concercio de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de la crece de l
                                                                                                                            9
                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNC-53 vertebrate protein homologue; UNC-53; Caenorhabditis elegans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Verhasselt P;
Vandekerckhove JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell shape regulator; cell motility regulator; cell migration; cell behaviour regulator; phenotype; signal transduction pathway; signal transducing protein; signal integrator protein; neuronal regeneration; revascularisation; wound healing; chronic neurodegenerative disease; acute traumatic injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrate UNC-53 protein homologue related nucleotide sequence.
                                                              ;
0
Length 1506;
                                                              Indels
                                                                                                                                                                                                                                                    61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                               141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
Score 100; DB 12;
Pred. No. 1.2e-27;
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Luyten W, Geerts H,
                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buesa Arjol CM,
   100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH11349 standard; DNA; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibrotic disease; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maertens LJS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pujol NJR, Maercent
Tungen J, Bogaert TAOE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-362411/31.
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ADH11350.
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   Query Match
Best Local Simil
Matches 100; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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ID ADH1
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
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transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the

Sequence 1782 BP; 458 A; 399 C; 451 G; 474 T; 0 U; 0 Other;

specification.

8888888

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Gaps .. 0

Indels

; Score 100; DB 12; ; Pred. No. 1.2e-27; 0; Mismatches 0;

Query Match
Best Local Similarity 100.0%;
Matches 100; Conservative 0

Length 1782;

9

81 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 140

100

141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC

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1 CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGGAGCAAATTTAAGCTACA

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active in the signal transduction pathway of a cell of which a vertebrate homologue of UNC-53 is a component comprising: (i) contacting an extract of a cell with an antibody to the UNC-53 homologue; (ii) identifying an antibody/homologue complex, and (iii) analysing such a complex to identify any non-antibody protein bound to the complex. UNC-53 is a signal transducting or signal integrator protein involved in controlling directionality of cell migration and cell shape in C. elegans. Vertebrate homologues of UNC-53 can be used to promote neuronal regeneration, revascularisation or wound healing, to treat chronic neurodegenerative diseases or acute traumatic injuries or fibrotic diseases. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 CTGCTCCCTGCTTGTGTTGTGTGGCTCGCTGAGTGCGCGGAGGAAATTTAAGCTACA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 100; DB 2; Length 1600; 100.0%; Pred. No. 1.2e-27; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                      Sequence 1600 BP; 397 A; 409 C; 398 G; 396 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 100; Conservative
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engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
         141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
                                                                                                                                                                                                                                                                                                                                                              Cytomegalovirus nucleotide sequence SEQ ID NO:5.
                                                                                                                                                                      ADM41037 standard; DNA; 1782 BP
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                17-JUN-2004
                                                                                                                                                                                                                                 ADM41037;
                                                                                                     RESULT 6
                                                                                                                                         ADM41037
g
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engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; human; gene; ds.

Human nucleotide sequence SEQ ID NO:2.

(first entry)

17-JUN-2004

ADM41034;

ADM41034 standard; DNA; 2241

ADM41034 RESULT

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Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.
                                                                                                                                                                 Thompson SC;
                                                                                                                        17-SEP-2003; 2003WO-US029251.
                                                                                                                                      19-SEP-2002; 2002US-0411790P.
                                                                                                                                                                 Sosa CE,
                                                                                                                                                                              WPI; 2004-295402/27.
                                                                                                                                                    (XIME-) XIMEREX INC.
                                                                                              WO2004027029-A2.
                                                                                Cytomegalovirus
                                                                                                                                                                 Beschorner WE,
                                                                                                            01-APR-2004.
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The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2241 BP; 498 A; 630 C; 609 G; 504 T; 0 U; 0 Other;
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The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for

Disclosure; SEQ ID NO 5; 48pp; English.

Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.

Thompson SC;

Beschorner WE, Sosa CE, WPI; 2004-295402/27.

(XIME-) XIMEREX INC

17-SEP-2003; 2003WO-US029251.

WO2004027029-A2

01-APR-2004

Homo sapiens

19-SEP-2002; 2002US-0411790P.

Disclosure; SEQ ID NO 2; 48pp; English.

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ADM41036;
                                    Query Match
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                                                                                                                                                                                       RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a lac repressor operated p21-expression cassette comprising the Rous sarcoma virus (RsV)-LTR promoter. p21 is a cell cycle inhibitor protein. The present sequence is used to produce vectors for use in the method of the invention. The specification describes a method for producing a protein, preferably a recombinant protein, in a mammalian anchorage-independent producer cell line. The method comprises co-expressing with the protein in the producer cell line a recombinant cell cycle inhibitor protein (preferably p21). The method is useful for producing a recombinant protein in a producer cell line. This is useful for producing a recombinant protein in a producer cell line. This is particularly useful for maximizing or enhancing the production of e.g. therapeutic proteins at an industrial scale
                                                            81 CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 140
                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or enhancing
                                               GTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing recombinant protein, particularly for maximizing or enhanci: e.g. therapeutic protein production, by co-expressing protein with recombinant cell cycle inhibitor protein (p21) in producer cell line.
                          Gaps
                                                                                                                                                                                                                                                                     Lac repressor; p21; RSV; LTR promoter; cell cycle inhibitor protein; protein production; anchorage-independent producer cell line; ss.
                                                                                                                                                                                                                                               Lac repressor operated p21-expression cassette and RSV-LTR promoter.
                        ö
 Length 2241;
                        Indels
                                                                                           61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                       ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "thymidine kinase polyA site"
                                                                                                                                                                                                                                                                                                                                                                                                      t antigen intron"
Score 100; DB 12;
Pred. No. 1.3e-27;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              1052. .1907
/*tag= c
/note= "p21 coding sequence"
1908. .2245
                                                                                                                                                                                                                                                                                                                                                       *tag= a
note= "RSV-LTR promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 15-16; 33pp; English.
                                                                                                                                                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          '*tag= b
'note= "SV40 small
100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                           ABZ23249 standard; DNA; 2245 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shuttleworth J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001; 2001GB-00013318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2002; 2002WO-EP006054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LONZ ) LONZA BIOLOGICS PLC.
                                                                                                                                                                                                                                                                                                                                                                              64. .1051
                                                                                                                                                                                                                        (first entry)
                        100; Conservative
                                                                                                                                                                                                                                                                                                                                            . .563
                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-148669/14.
             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Al-Rubeai M,
                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyA_signal
                                                                                                                                                                                                                         24-MAR-2003
                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                  ABZ23249;
Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                             promoter
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                       Matches
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The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells in the cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                                                                                                                                                                                                                                                                                       46 CTGCTCCCTGCTTGTGTGTGTAGAGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
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                                                                                                                                                                                                                1 CIGCICCCIGCTIGIGIGITGGAGGICGCTGAGIAGIGCGCGAGCAAAATTTAAGCTACA
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                       Length 2245;
C; 625 G; 533 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2294 BP; 466 A; 680 C; 641 G; 507 T; 0 U; 0 Other;
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                               61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                   106 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 145
                                                                                                                                               ö
                                                                    Score 100; DB 8;
Pred. No. 1.3e-27;
; Mismatches 0;
                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytomegalovirus nucleotide sequence SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thompson SC;
                                                                                                  Best Local Similarity 100.0%; Pr
Matches 100; Conservative 0;
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   Sequence 2245 BP; 532 A; 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM41036 standard; DNA; 2294
                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-295402/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (XIME-) XIMEREX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004027029-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-2004
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61
                                                                                                        RESULT 11
                                                                                                                               AAD02036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a gene directed enzyme prodrug therapy (GDEPT) using post translational glycosylphosphatidylinositol (GPI) addition to a prodrug activating enzyme which enables anchorage of the enzyme at the call surface. Carboxypeptidaes G2 (CPG3) is a preferred prodrug activating enzyme. The invention also relates to an expression vector for expression of a GPI enzyme hybrid capable of anchorage to the surface of a mammalian cell. The expression vector comprise polynucleotide sequences encoding a signal peptide, an enzyme capable of activating a prodrug, and a post-translational GPI addition motif. The expression vector is useful in the manufacture of a medicament for cancer therapy in a mammalian host. The present DNA sequence is a plasmid pug3/RC/CGO2-THY1 comprising CPG2 nucleic acid sequence with the last excon of rat Thy 1 gene at its 3' end. (Updated on 11-SEP-2003 to
                    CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 140
                                                                                                                                                                                                                                                                                                                                                               Carboxypeptidase G2; CPG2; gene directed enzyme prodrug therapy; GDEPT; glycosylphosphatidylinositol; GPI; cancer; therapy; rat; Thyl gene; plasmid; ds.
CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGGAGCAAAATTTAAGCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene directed enzyme prodrug therapy using post translational glycosylphosphatidylinositol addition to prodrug activating enzyme enable anchorage of enzyme at cell surface for cancer therapy.
                                                                                                                                                                                                                                                                                                                              Plasmid pNG3/RC/CPG2-Thyl comprising CPG2 DNA with rat thyl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 100; DB 4; Length 2426; 100.0%; Pred. No. 1.4e-27; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2426 BP; 557 A; 705 C; 668 G; 495 T; 0 U; 1 Other;
                                                                                               ACAAGGCAAGCTTGACCGACAATTGCATGAAGAATCTGC
                                                                      ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1e; Page 59-60; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lowenstein PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASTR ) ASTRAZENECA AB.
(UYMA-) UNIV VICTORIA MANCHESTER.
                                                                                                                                                                                                  AAD02037 standard; DNA; 2426 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-2000; 2000WO-GB001640.
                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Castro MG, Emery SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-015983/02.
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Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200066752-A2
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                                                                                                                                                                                                                                                                         11-SEP-2003
26-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria.
                                                                      61
                                                                                                        141
                                                                                                                                                                                                                                      AAD02037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric.
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                                                                                                                                                                RESULT 10
                                                                                                                                                                                 AAD02037
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The present invention relates to a gene directed enzyme prodrug therapy (GDEPT) using post translational glycosylphosphatidylinositol (GPI) addition to a prodrug activating enzyme which enables anchorage of the enzyme at the cell surface. Carboxypeptidase G2 (CPG2) is a preferred prodrug activating enzyme. The invention also relates to an expression vector for expression of a GPI enzyme hybrid capable of anchorage to the surface of a mammalian cell. The expression vector comprise polymucleotide sequences encoding a signal peptide, an enzyme capable of activating a prodrug, and a post-translational GPI addition motif. The expression vector is useful in the manufacture of a medicament for cancer therapy in a mammalian host. The present DNA sequence is a plasmid bNG3/RC/CPG2 (G3) comprising CPG2 variant CPG2 (G3) and the last exon of rat Thy-1 at the 3' end. (Updated on 11-5EP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCTCCCTGCTTGTGTTTGGAGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 129
                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pNG3/RC/CPG2(Q3)-Thyl comprising CPG2 variant with rat thyl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carboxypeptidase G2; CPG2; gene directed enzyme prodrug therapy; GDEPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosylphosphatidylinositol; GPI; cancer; therapy; rat; Thyl gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene directed enzyme prodrug therapy using post translational glycosylphosphatidylinositol addition to prodrug activating enzyme enable anchorage of enzyme at cell surface for cancer therapy.
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129 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lowenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASTR ) ASTRAZENECA AB. (UYMA-) UNIV VICTORIA MANCHESTER.
                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPG2 (Q3) variant; plasmid; ds.
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                                                                                                                                                                                          AAD02036 standard; DNA; 2427
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                                                                                                                                                                                                                                                                                                                            (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-015983/02
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les 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200066752-A2.
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                                                                                                                                                                                                                                                                                                                     11-SEP-2003
26-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                        AAD02036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric.
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CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGGAGCAAAATTTAAGCTACA 128

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1 CTGCTCCCTGCTTGTGTGTTTGGAGGTCGCTGAGTAGTGCCGCGAGCAAAATTTAAGCTACA

100; Conservative

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Gaps

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148 CTGCTCCTGCTTGTGTTGGAGGTCGCTCGGTAGTGCGCGCGAGAAATTTAAGCTACA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies binding to porcine but not human cell interaction proteins useful to treat and assay for rejection of xenografted porcine organs, tissues or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rother RP, Matis LA;
                                          1 CIGCICCCIGCTIGIGIGITIGGAGGICGCIGAGIAGIGCGCGAGCAAAATTTAAGCTACA
 Length 3400;
                                                                                                                                                                                                                                                      Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis; ss.
                                                                                                                                                                                                                                    2A2 human G2/G4 chimeric antibody expression plasmid insert.
                      Indels
                                                                                  61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                              ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 247
; Score 100; DB 2;
; Pred. No. 1.5e-27;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mueller JP, Evans MJ, Mueller EE, Rollins S,
                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         *tag= c
codon_start= 1318
                                                                                                                                                           AAT62932 standard; DNA; 3400 BP.
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 100; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US015575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0004489P
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                                                                                                                                                                                                               (first entry)
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2991. .3
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286.
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2984.
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                                                                                                                                                                                                       (revised)
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P-PSDB; AAW14934.
                                                                                                                                                                                                                                                                                                   Homo; sapiens
                                                                                                                                                                                                    17-OCT-2003
16-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9711971-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1996;
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                                                                                                                                                                                                                                                                                                             Mus sp.
Chimeric.
                                                                                                     208
                                                                                                                                                                                AAT62932;
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                                                                                                                                     RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A DNA sequence (AAT62937) comprises a 3F4 human G2/G4 (see also AAT62936) chimeric antibody expression plasmid insert sequence. The chimeric antibody (AAW14940) is specific for porcine vascular cell adhesion molecule (VCAM) and is useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplantation of porcine cilsusues and organs into human recipients. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matis LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies binding to porcine but not human cell interaction proteins useful to treat and assay for rejection of xenografted porcine organs,
                                                                                                                        Xenotransplantation, graft rejection, cell interaction, pig, vascular cell adhesion molecule, VCAM, monoclonal antibody; chimeric antibody; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3400 BP; 759 A; 1012 C; 909 G; 720 T; 0 U; 0 Other;
                                                                                                     3F4 human G2/G4 chimeric antibody expression plasmid insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rother RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mueller EE, Rollins S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 58-61; 105pp; English.
                                                                                                                                                                                                                                                        /*tag= b
1286. .2055
/*tag= c
/codon_start= 1350
2056. .2447
/*tag= 2448
                                                                                                                                                                                                               ocation/Qualifiers
                                AAT62937 standard; DNA; 3400 BP.
                                                                                                                                                                                                                                                                                                                                          2484. .2601
/*tag= f
2602. .2928
/*tag= g
2929. .3025
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2929. .3025
/*tag= h
3026. .3348
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                                                                       (revised)
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2484. ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-212855/19.
P-PSDB; AAW14940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissues or cells.
                                                                                                                                                                        Homo; sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1995;
26-SEP-1996;
                                                                      17-OCT-2003
16-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mueller JP,
                                                   AAT62937;
                                                                                                                                                                                          Chimeric.
                                                                                                                                                                                  gb.
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           RESULT 12
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This is the nucleotide sequence of pCTM, a plasmid which contains a CMV promoter, a tripartite adenovirus leader flanked by T7 and SP6 promoters, and a multiple cloning site with a bovine growth hormone polyA site and downstream SV40 polyA site. It has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastoma protein (BP, see AAW62465) and ESF transcription factor (see AAW62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, specifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the ESF promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGAAAATTTAAAGCTACA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Packaging-deficient construct; viral gag-pol gene; packaging cell line; moloney murine leukaemia virus; MoMLV; viral env gene; helper construct; gene therapy; humna cytomegalovirus; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                                                                                                                                                                                New fusion polypeptide of, e.g. transcription factor - used to treat, e.g. hyper-proliferative disease such as cancer and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 100; DB 2; Length 3853; 100.0%; Pred. No. 1.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3853 BP; 936 A; 986 C; 942 G; 989 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CANC-) CANCER RES CAMPAIGN TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeuchi Y,
                                                                                                                     Wills KN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid CMV10A1 coding sequence.
                                                                                                                                                                                                                                                            Example 1; Fig 4; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT90695 standard; DNA; 3925 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-GB002061
                  96US-00751517
97US-00801092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 100; Conservative
                                                                                                                     Gregory RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weiss RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-179287/16
                                                                                                                                                             WPI; 1998-297858/26
                                                                              (CANJ-) CANJI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collins MKL,
                  15-NOV-1996;
14-FEB-1997;
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                                                                                                                     Antelman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                   A DNA sequence (AAT62931) comprises a 2A2 human G2/G4 (see also AAT62931) chimeric antibody expression plasmid insert sequence. The chimeric antibody (AAM14934) is specific for porcine vascular cell adhesion molecule (VCAM) and is useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplants and for improving xenotransplantation of porcine tissues and organs into human recipients. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                             148 crecrecrecristraterresassics and respected cases and respectation 207
                                                                                                                                                                                                                                                                                                                                        1 CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 60
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                          100.0%; Score 100; DB 2; Length 3400; 100.0%; Pred. No. 1.5e-27;
                                                                                                                                                                                                                    Sequence 3400 BP; 776 A; 993 C; 899 G; 732 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function= "tripartite leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                       61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                             208 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= d
/note= "pUC19 backbone H3 to AatII"
complement(2857. .3717)
                                                                                                                                                                                                                                                                                                 0; Mismatches
                Disclosure; Page 44-47; 105pp; English
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*tag= c
note= "SP6 promoter"
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'note= "CMV promoter"
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unidentified bacteriophage; SP6.
Macaca mulatta; polyoma virus.
Bos taurus.
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/note= "AMP-ORF"
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15-FEB-1999
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                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                Local
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AAV40006

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9

0; Gaps

Indels

Selectable retroviral packaging cell lines and expression constructs - comprise selectable gene downstream of gene of interest, are selectable due to the in-efficiency associated with translation re-initiation.

Claim 23; Fig 13; 79pp; English

This sequence represents the recombinant expression plasmid CWV10A. This sequence is a packaging-deficient construct having a viral env gene (in this cases from moloney marine leukaemia virus under how promoter control) and a selectable marker (SM). It is an example of a recombinant expression vector (REV) of the invention, used to create a packaging cell line. The REVS of the invention comprise a gene of interest (GOI) and a SM gene. The SM gene is arranged downstream of the GOI and a GOI associated stop codon is spaced from a start codon of the SM gene to ensure that the SM protein is expressed as a result of translation. The cell lines are transformed with two REVS, both are replication deficient, one contains the viral gag-pol gene, the other the CM rial env gene. By using helper constructs, such as the REV's, which are directly selectable and which provide for high expression of the viral gene, high titre retroviral vectors may be obtained. The packaging cell lines are useful for gene therspy. Prior packaging cell inces are useful for gene therspy. Prior packaging cell lines are useful for gene therspy. Prior packaging cell lines are useful for gene therspy. Prior packaging cell lines are useful for high expression of the viral lines using full lines are useful for packaging cell lines are useful for high expression of the viral lines using full lines are useful lines using full length retroviral genomes as helper genomes were isolated by cotransfecting them with plasmids encoding selectable markers. However, the helper functions can be lost during the passages of the cells in culture and the current packaging systems provide limited titres of infectious retroviral vectors. Co-transfection with a plasmid encoding a SM does not directly select the best gag-pol-env-expressing cells. The new retroviral packaging cell lines overcome these problems 

Sequence 3925 BP; 963 A; 1001 C; 959 G; 998 T; 0 U; 4 Other;

Gaps 0; Length 3925; Indels Score 100; DB 2; Pred. No. 1.6e-27; 100.0%; Scur. 100.0%; Pred. No. 1. 0; Mismatches Best Local Similarity 100. Matches 100; Conservative Query Match

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Search completed: July 14, 2005, 07:01:45 Job time : 143.038 secs

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602412672 AGENCOURT AGENCOURT

BG387788 CD643822 BU170446

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CN386746 CN386717 BF309673 CN386780 CD654097 CN386742 CN3656906 BGB20298 CB996419

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CB993607

RSH15G08 RTCNT1 28 BY703355

BY703355

AGENCOURT

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BQ222104 CD656102 BU189860 BM477450 CB239722

Run on:

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/note="Vector: DR-Script Amp SK+; Site 1: SrfI; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center
                                                                                                                                                                                                                                                                                                                    B67169 12-MAY-2000
CpG0047A CpIOWAgDNA2 Cryptosporidium parvum genomic, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' the insert, to correct miscalled bases and assign uncalled (N)
bases throughout the sequence, and to terminate when base-calling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida, Cryptosporidiidae, Cryptosporidium.

1 (bases 1 to 602)

Strong, W.B. and Nelson, R.G.

Preliminary profile of the Cryptosporidium parvum genome expressed sequence tag and genome survey sequence analysmol. Biochem. Parasitol. 107 (1), 1-32 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Cryptosporidium parvum"
/mol_type="genomic DNA"
/strain="IOWA"
                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 602.
Location/Qualifiers
                                                     CD654097
CN386742
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BU170446
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CD656102
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Cryptosporidium parvum
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B67169.1 GI:2642750
                     became ambiguous.
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Class: shotgun
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                                                      sequence.
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VERSION
KEYWORDS
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TITLE
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PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                             RESULT
B67169
B67169 CpG0047A Cp
B1333630 G02997459
CD655614 ACBNCOURT
CC242469 CH261-11F
CB387202 OSTF076E6
BQ310441 MRO-BT450
AQ946479 Sheared D
CC888514 SALK 1519
CK086063 RG11_C07
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CK086063 RG11_C07
AL25351 TECTRAGOON
F32722 HSPD25699 H
AA962465 0091805.8
CN386744 328755673
CB1611201 K-EST0220
CB161182 K-EST0220
AW500392 UI-HF-EN0
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CRS37056 DKFZ9459D
CR386728 17005326
BG933413 MR3-HT099
BI113747 602860946
CN386724 170006000
AM955076 EST367146
CN386730 170005316
                                                                         July 14, 2005, 05:15:57; Search time 952.146 Seconds (without alignments) 3997.736 Million cell updates/sec
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                                                                                                                                             1 ctgctccctgcttgtgtgtt......caattgcatgaagaatctgc 100
                                                                                                                                                                                                                           68479088
         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                  34239544 segs, 19032134700 residues
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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                                                   nucleic search, using sw model
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AQ946479
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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seq length: 200000000
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gb_htc:
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Result Š.

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http://sequence-www.stanford.edu/group/techdev/shear.htm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 CTGCTCCCTGCTTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 100
                  The randomly sheared gDNA was chromatographed on Sephacryl S-400 to remove any small fragments and DNA eluting in the void volume was blunt-ended with T4 DNA Polymerase, treated with alkaline phosphatase to prevent the ligation of multiple fragments, ligated to Srf I-digested pCR-Script Amp (SK+) vector and transformed into E. coll strain XLIO Gold. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 primers."
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/lab_host="DH108"
/clone lib="NUH MGC 12"
/note="Grgan: cervix, Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 60
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1 (bases 1 to 829)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 TTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbe-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Flate: LiAM133 row: £ column: 15
High quality sequence stop: 788.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                             Score 100; DB 8; Length 602;
Pred. No. 8e-24;
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                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                   Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 100; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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BI333630
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TITLE
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/LOUGY
This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 11541991) from WAO1 cell line. Undifferentiated human ES cell line WAO1 cell line. Undifferentiated human ES cell line WAO1/H1 was obtained from WiCell Research Institute, Inc., Wadison, Wi. cultured according to their instructions, on MEF feeders. They formed acondines with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. FPF3, SSEA-1, TUBB3, MES, GRAPA, POXI, NCAM, MSX1, FF13, SSEA-1, TUBB3, MES, GRAPA, EDXI, NCAM, MSX1, FF13, SSEA-1, TUBB3, MES, GRAPA, ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIZO1 Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199]) Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 1.1.1573-158] (2001). [PMID:11544199]) primer [Invitrogen: 1.1.1573-158] (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Geneitute / NIH
National Cancer Institute / NIH
Bldg. 31 Rm.DA07 Betheeda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
CDNA Library Preparation: Yulan Piao and Minoru Ko
cDNA Library Preparation: Yulan Piao and Minoru Ko
cDNA Library Preparation: Yulan Piao and Minoru Ko
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC c
can be found through the I.M.A.G.E. Consortium/Linla at:
http://mage.llnl.gov
Plate: NDAMSO6 row: k column: 14
                                                                                                                                                                                                                                                                                       CD655614 823 bp mRNA linear EST 18-JUN-2003 AGENCOURT_14551032 NIA Human H1 Embryonic Stem Cell cDNA Library (Long) Homo saplens cDNA clone IMAGE:30424285 5', mRNA sequence. CD655614
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/cell line="WAO1"
/lab_fost="DH10B (T1 phage-resistant)"
/clone_lib="NIA Human H1 Embryonic Stem Cell cDNA Library
(Long)"
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217 TTGGGCGTCCCAGAATTGTTGGTGAGCAAACTTCAAGTTGCTGCCTGGGAAGTCCTGACT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 823)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
1. .823
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD655614.1 GI:31896113
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                                                                                                                                           157 GACA 154
                                                                     79 GACA 82
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616 AAACACTTAAACGCCAACTCCACAGAGAA 588
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Best Local
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BQ310441/c
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                                                         RESULT 5
CB387202
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(Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb.
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CH261-118 RM1.1 CH261 Gallus gallus genomic clone CH261-11F8,
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                                                                                                                                                                                                                                                             524 GAGCTAACTGAATTGTATGGGAGCAGCATTTAACATATTCCTAGTCAAGGACTGGATGGG 465
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1 (Dases 1 to 1165)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus, Gallus BAC End Reads
Unpublished (2003)

Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                          22 GAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGAC
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                                                                                                                                                                                        28; Indels
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Pred. No. 26;
                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Sequencing Center
Washington University School of Medicine
Bmail: submissions@watson.wustl.edu
Insert Lenghi: 182000 Std Brror: 0.00
Seq primer: RM1 TACGACTATAGGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db xref="taxon:901"
/clone="CH261-11F8"
                                                                                                                                                                                      0; Mismatches
                                                                                                                                                 Score 30.2; 1
Pred. No. 18;
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High quality sequence stop: 738.
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Gallus gallus
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                                                                                                                                                                                                                                                                                                 82 AATTGCATGAAGAAT 96
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Best Local Similarity 58.4
Matches 52; Conservative
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Best Local Similarity
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67 CAAGGCTTGACCGACAATTGCATGAAGAA 95

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Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Harley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Tolias, P. P., Chevet, E., Papasotiropoulos, V., Tolias, P. P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFecome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marc Vidal Laboratory
Dana Parber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Bmail: Marc-Vidaledfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
POLYĀ-NO.
CB387202 401 bp mRNA linear EST 15-MAY-2003
OSTF076E6_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/stssue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into pPC86"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ITGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGG
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0
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29.4; DB 6; Length 4
Pred. No. 30;
0; Mismatches 31; Indels

    .401
    /organism="Caenorhabditis elegans"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . (2003) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 ATTTCCTGACAATTTCATG 366
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BQ310441.1 GI:20853032
                                                                                        CB387202.1 GI:30728912
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/clone="Sheared DNA-906"
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/clone="Netared DNA-906"
/note="Vector: pUCIB: Site 1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma bruce: (TREU927/4 GUTat 10:1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
1 (bases 1 to 754)
El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gersayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gersaca,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
Donelson,J., Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
Unpublished (1999)
Other_GSSs: Sheared DNA-4906.TF
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Adorinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
ttp://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Reverse
Class: shotgun.
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                                                                                                                                                                                                                                                                                       Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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/mol_type="genomic DNA"
/strāin="TREU927/4 GUTat 10.1"
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Unpublished (2001)
Contact: Joseph R. Ecker
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                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MRO&t2=MRO-BT4502-220601-202-b02&t3=2001-06-22&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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High quality sequence start: 48
High quality sequence stop: 530.
Location/Qualifiers
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   KEYWORDS
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GSS 01-SEP-2000

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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
207F02 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                    267 dadgadriccaadaagcaaacrgaagccagaargaagagaggcrggacrrgcaaggccaaa 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, catinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontidae, Tetraodon.
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Submitted (12-ARP-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 ENRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 339-949 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                        31 GAGTAGTGCGCGAGCAAATTTAAGCTACAACAAGGCAAGGCTTGACCGACAATTGCATG
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="207F02"
/clone="1b="G"
/note="Genoscope sequence_ID : COAG207DC01SP1~end :
PUC-Ori"
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                                          Length 657;
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                                          DB 7;
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                                          Score 29; DB
Pred. No. 44;
0; Mismatches
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Pred. No. 47;
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Tetraodon nigroviridis
Tetraodon nigroviridis
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                                      29.0%;
ilarity 63.8%;
Conservative
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Best Local Similarity 63.8%;
Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              207 AAAAATTTG 199
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                            Query Match
Best Local Similarity
Matches 44; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Cucurbitales, Cucurbitaceae, Cucumis.
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Horticulture Department, Michigan State University, Bast Lansing,
MI 48824, US 8824, US 8824, US 8824, US 8827, 
                                                                                                                                                                                                     This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of Atlg03960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:3702"
/clone="SALK 151964.54.50.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="POR was performed on Arabidopsis thaliana lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 TGAGTAGTGCGCGAGCAAATTTAAGCTACAACAAGGCAAGGCTTGACCGACAATTGCAT
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/note="Vector: pAD-GAL4; Site_1: EcoRI; Site_2: XhoI"
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RG11 CO7 Cucumber leaf Cucumis sativus cDNA, mRNA sequence.
CK086063
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29.2%; Score 29.2; DB 9; Length 426;
Best Local Similarity 64.2%; Pred. No. 35;
Matches 43; Conservative 0; Mismatches 24; Indels
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
ecotype="Col-0"
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/strain="Straight 8"
/db_xref="taxon:3659"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Grumet, R. and McGrath, M.
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                                                                                                                                                                                                                                                                    Class: TDNA tagged
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AA962465.1 GI:3134629
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Homo sapiens
                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
        mRNA sequence.
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Matches 46; Conserv
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TITLE
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1 (Dases 1 to 340)
Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
1Gentification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=_vector: pcDNAII (Invitrogen); Site 1: BstXI;
Site 2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated
oligo-dT-NotI primer
(5' biotin-AACCCGGCTCGAGCGCCGCTTTTTTTTTTTTTTT-3'). The
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                                                                                                                                                                                                  F32722 340 bp mRNA linear EST 13-MAY-1999
HSPD25699 HM3 Homo sapiens CDNA clone 83000037G06, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector."
22 GAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGAC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at http://grup.bio.unipd.it.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttissue type="pectoral muscle (after mastectomy)"
clone Tib="HM3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .340
/organiam="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="83000037G06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
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                                                                                                                                                                                                                                                            F32722.1 GI:4818348
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                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                139 TGAAAGAGA 131
                                                           74 TGACCGACA 82
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F32722/c
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: No.-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llni.gov/bbrpy/mage/f/mage.html
Insert Length: 1045 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Patima Bonaldo. "
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1 (bases 1 to 436)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 408) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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328755673 GRN_EB Homo sapiens CDNA 5', mRNA sequence.
CN386744
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llarity 61.3%; Pred. No. 57;
Conservative 0; Mismatches
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/organism="Homo sapiens"
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clone lib="L18POOLIn1"
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illarity 61.3%;
Conservative 0
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                                                                                                                                                                                                                                                                                      82 AATTGCATGAAGAAT
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Best Local S
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CB161182
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                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1. H7 and H9 cells"
/clone_lib="GRN_EB"
/clone_lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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K-EST0221011 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-16-H03
Transcriptome characterization elucidates signaling networks that control human BS cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 GAGCTAACTGAATTGTATGGGAGCAGCATTTAACATATTCCTAGTCAAGGACAGGATGGG 74
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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/cell line="SNU-354+Cho-CK+Choi-CK+HLK-3"
/lab host="Top10F'"
                                           Query Match 28.6%; Score 28.6; DB 7; Length 4 Best Local Similarity 61.3%; Pred. No. 57; Matches 46; Conservative 0; Mismatches 29; Indels
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                                                                                                                                                                                                                  'organism="Homo sapiens"
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/organism="Homo sapiens"
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Plate: 16 row: H column: 03
High quality sequence stop: 514.
Location/Qualifiers
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Contact: Kim YS
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/note="Organ: Liver: vector: pT/T3-Pac; Site_1: EcoRI; Site_2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research collture."
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K-EST0220988 L18POOLIn1 Homo sapiens CDNA clone L18POOLIn1-16-F04
5', mRNA sequence.
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1 (bases 1 to 530)
1 (bases 1 to 530)
1 (bases 1 to 530)
1 (by W.Y., Chu,M.Y., Kim,M.Y., Kim,M.Y., Kim,M.Y., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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/clone_lib="LisPooLin!
/note="Organ: Liver; Vector: pT/T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
Aboratory and it was constructed as described by Bonaldo,
M.F. Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
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                                                                                                                                                                                                                                                                                                                                                                                                              261 GAGCTAACTGAATTGTATGGGAGCACCATTTAACATATTCCTAGTCAAGGACAGGATGGG 320
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                       Length 514;
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Pred. No. 59;
0; Mismatches
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/clone="L18POOL1n1-16-F04"
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/organism="Homo sapiens"
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Plate: 16 row: F column: 04
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Location/Qualifiers
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Search completed: July 14, 2005, 23:23:14 Job time: 960.146 secs

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Sequence Metastati

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Title:

Minimum DB Maximum DB

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AR240811 Sequence
BD221144 Human gen
AR370661 Sequence
AX784008 Sequence
AX752973 Sequence
AX74004 Lepilemur
AR036903 Sequence
AR141142 Sequence
AR11142 Sequence
AR111973 Sequence
AR19173 Sequence
AR19173 Sequence
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AR19187 Sequence
AR1978 Sequence
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AF143508 Cloning
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AR476645 Sequence
AR487271 Sequence
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Zygosaccharomyces bailii
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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    .299
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Sequence 1 from Patent BP 0356130.
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108488 Sequence 1
10880 Sequence 1
116794 Sequence 2
A60961 Sequence 27
A60977 Sequence 28
AR369178 Sequence
AR36918 Sequence
AR476628 Sequence
AR476638 Sequence
AR46038 Sequence
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AR154888 Sequence
E65413 Genome DNA
                                                                   July 14, 2005, 04:39:07; Search time 756.618 Seconds
(without alignments)
6468.225 Million cell updates/sec
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                                                                                                                                   gcgtgaccgctacacttgcc......ttccccgtcaagctctaaat 101
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        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                       4708233 segs, 24227607955 residues
                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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101
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Maximum Match 100%
Listing first 45 summaries
                                                 nucleic search, using sw model
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BD194797
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PAT 03-JUN-2004

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PAT 02-DEC-1994

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Gaps

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PAT 03-APR-1996

linear

ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

TITLE JOURNAL

FEATURES

ORIGIN

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54 GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTTCCT 113
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PROTEIN/(POLY) PRETIDE LIBRARIES
Patent: WO 9708320-A 270 06-MAR-1997;
MORPHOSYS PROTEINOPTHIRENUM (DE)
Location/Qualifiers
1. 470
| /organies="unidentified"
| mol_type="unidentified"
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100.0%; Score 101; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.2e-16;
Matches 101; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity 100.0%; Pred. No. 6.2e-16;
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Sequence 270 from Patent WO9708320,
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Patent: WO 8805085-A 1 14-JUL-1988;
Location/Qualifiers
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Patent: US 5478731-A 2 26-DEC-1995;
Location/Qualifiers
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                                                                  "ANO
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2 from patent US 5478731.
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Unclassified.
Unclassified.
I (bases 1 to 460)
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I mober, S.Cc., Holzschu, D.Lc. and Lalik, P.Hc.
A mobile fl phage single-strand DNA origin of replication
Patent: EP 0356130-A2 1 28-FEB-1990,
Location/Qualifiers
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1 (bases 1 to 461)

Sorge,J.A.M., Huse,W.M. and Short,J.M.

Sorge,J.A.M., Huse,W.M. 110 vivo excisable plasmids

Patent: EP 0286200-A2 1 12-OCT-1988;

Location/Qualifiers
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100.0%; Pred. No. 6.2e-16;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 1 from Patent WO 8805085.
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Sequence 1 from Patent BP 0286200.
105488
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Huse, W., Sorge, J.A. and Short, J.M.
 GI:589091
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DEFINITION

RESULT 3 IO5488

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PAT 06-MAR-1998

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ACCESSION VERSION KEYWORDS

RESULT 4 I08820

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58 GCGTGACCGCTACACTTGCCAGCGCCCTAGCCCCGCTCCTTTCGCTTTCTTCCCTTCCT 117
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Knappik,A., Pack,P., Ge,L., Moroney,S.
Protein/(poly)peptide libraries
Patent: US 6696248-A 270 24-FEB-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                  1 (bases 1 to 470)
Knappik,A., Pack,P., Ge,L., Moroney,S
Protein/(poly)peptide libraries
Patent: US 6300064-A 286 09-OCT-2001;
Location/Qualifiers
                                                                                                                                                        Sequence 286 from patent US 6300064.
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Sequence 270 from patent US 6696248.
AR476628
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Matches 101; Conservative
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ROTEIN/(FOLY) PREPTIDE LIBRARIES
Patent: WO 9708320-A 286 06-MAR-1997;
MORPHOSYS PROTEINOPTIMIERUNG (DE)
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Khappik,A., Pack,P., Ge,L., Moroney,S. and Pluckthun,A.
Protein/(poly)peptide libraries
Patent: US 6300064-A 270 09-OCT-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 101; DB 6; Length 470;
.larity 100.0%; Pred. No. 6.1e-16;
Conservative 0; Mismatches 0; Indels
           Length 470;
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100.0%; Pred. No. 6.1e-16;
tive 0; Mismatches 0;
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Sequence 270 from patent US 6300064.
AR369178.1 GI:34605134

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    /db_xref="taxon:32644"

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Sequence 286 from Patent WO9708320.
A60977.
A60977.1 GI:3715509
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AR369178
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Best Local Similarity 100.0%; Pred. No. 6.1e-16;
Matches 101; Conservative 0; Mismatches 0; Indels (
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Beach, P.H., Hannon, G.J., Conklin, D. and Mammalian viral vectors and their uses Patent: US 6255071-A 5 03-JUL-2001;
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Knappik,A., Pack,P., Ge,L., Moroney,S
Protein/(poly)peptide libraries
Patent: US 6706484-A 286 16-MAR-2004;
                                                                                                                                                                          1. .470
/organism="unknown"
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Sequence 5 from patent US 6255071.
AR160383
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BD194797
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                   GI:47252215
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1 (bases 1 to 472)
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Knappik,A., Pack,P., Ge,L., Moroney,S.
Protein/(polly)peptide libraries
Patent: US 6706484-A 270 16-MAR-2004;
                                                                                 DNA
                                                                                                                                                                                                       1 (bases 1 to 470)
Knappik,A., Pack,P., Ge,L., Moroney,S
Protein/(poly)peptide libraries
Patent: US 6696248-A 286 24 FEB-2004;
Location/Qualifiers
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AR476638
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Sequence 286 from patent US 6706484.
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AR487254
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REPERENCE

FEATURES TITLE

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KEYWORDS

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PAT 17-OCT-2001

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PAT 17-JUL-2003

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PN JP 2002514054-A/6
PP 14-MAY-2002
PP 22-SEP-1997 UP 1998515028
PR 20-SEP-1996 US 08/716926,19-MAR-1997 US 08/820931 PI
DAVID H BEACH, GRECORY J HANNON, DOUGLAS S CONKLIN, PEIQUING SUN PC
C12N15/86,C12N15/10,C07K14/025
CC Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
CC Viral vectors and their uses
FH Key Location/Qualifiers
FT Source 1. 472
FT Source 1. 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCCCTTTCGCTTTCTTCCCTTTCTT 122
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Beach, D.H., Hannon, G.J., Conklin, D.S. and Sun, P. Viral vectors and their uses Parent: JP 2002114054-A 6 14-MAY-2002; COLD SPRING HARBOR LABORATORY
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Bovine Bovine

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## RESULT 1 AAS3339

DNA encoding human secreted protein, Seq ID No 674. (first entry) 04-DEC-2001 AAS33391;

Homo sapiens.

02-AUG-2001

2000US-0209467P. 2000US-0214886P. 2000US-0215135P. 2000US-0216647P. 2000US-0180628P. 2000US-0184664P. 2000US-0186350P. 2000US-0189874P. 2000US-0190076P. 2000US-0198123P. 2000US-0205515P. 17-JAN-2001; 2001WO-US001347. 2000US-0216880P 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 9-MAY-2000; 07-JUN-2000; 28-JUN-2000; 0-JUN-2000; 04-FEB-2000; 

WO200155326-A2.

2000US-0217496P. 2000US-0218290P. 2000US-0220963P. 14-JUL-2000; 26-JUL-2000;

ALIGNMENTS

Bovine

Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina; rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmological; cytostatic; Alzheimer's disease; Parkhison's disease; human; cancer; multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; neurological disease; cerebrovascular disorder; thrombosis; wound healing; ds. BP. AAS33391 standard; DNA; 288

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Minimum Maximum

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SUMMARIES

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Rosen CA, Barash SC, Ruben SM

WPI; 2001-451931/48

New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions.

Disclosure; SEQ ID NO 674; 753pp; English

The invention relates to novel isolated nucleic acid molecules (I)

cncoding human secreted proteins (II). (I) and (II) are used to prevent,

treat or ameliorate a medical condition in e.g. humans, mice, rabbits,

goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in

the prevention, treatment and diagnosis of diseases associated with

inappropriate expression of secreted proteins. (I) and complementary

sequences may also be used as DNA probes in diagnostic assays (e.g.

polymerase chain reactions (PCR) to detect and quantitate the presence

of similar nucleic acid sequences in samples, and so which patients may

be production of antibodies and in assays to identify modulators

(agonists and antagonists) of the expression and activity of the secreted

can regulate expression and activity of (II) antibodies

may also be used as diagnostic agents for detecting the presence of (II)

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2000US-0241786P.
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in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The disorders include for example: immune/autoimmune diseases (e.g. HIV thuman immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, erginer's disease, thromosomial disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. cardiac arrest, tachycardia, angina and alsorders (e.g. cardiac arrest, viruses and fungi and ocular and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues.

AAS33043-AAS31486 represent human secreted protein coding sequences, PCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunomodulatory; human immunodeficiency virus; HIV; anaemia; angina;
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                      100.0%; Score 101; DB 4; Length 288; 100.0%; Pred. No. 4.4e-21; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                              TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAAT 133
                                                                                                                                                                                                                                                                                                                                                                         61 ITCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAAT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding human secreted protein, Seq ID No 675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS33392 standard; DNA; 288 BP.
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2000US-0189874P.
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2000US-0205515P.
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Best Local Similarity
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04-FEB-2000;
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The invention relates to novel isolated nucleic acid molecules (I)

cncoding human secreted proteins (II). (I) and (II) are used to prevent,

treat or ameliarate a medicial condition in e.g. humans, mice, rabbits,

gaats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in

the prevention, treatment and diagnosis of diseases associated with

the prevention, treatment and diagnosis of diseases associated with

the prevention, treatment and diagnosis of diseases associated with

the prevention, treatment and diagnosis of diseases associated with

sequences may also be used as DNA probes in diagnostic assays (e.g.

polymerase chain reactions (PCR)) to detect and quantitate the presence

of similar nucleic acid sequences in samples, and so which patients may

be in need of restorative therapy. (II) may also be used as antigens in

the production of antibodies and in assays to identify modulators

consists and antegonists of the expression and activity of the secreted

proteins. The anti-(II) antibodies and antagonists may also be used to

down regulate expression and activity of (II). The anti-(II) antibodies

consy also be used as diagnostic agents for detecting the presence of (II)

in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The

disorders include for example: Immune/autoimmune diseases (e.g. HIV

(human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions.
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                                          08-NOV-2000; 2000US-0246526P.

08-NOV-2000; 2000US-0246527P.

08-NOV-2000; 2000US-0246528P.

08-NOV-2000; 2000US-0246632P.

08-NOV-2000; 2000US-0246609P.

08-NOV-2000; 2000US-0246610P.
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06-DEC-2000;
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and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease, neurological diseases (e.g. Alzheimer's disease, Parkinson's disease and Charco-Marie-Tooth disease), cardio, cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). (I) and (II), agonists, antagonists and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues.

AAS33043-AAS33486 represent human secreted protein coding sequences, PCR
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                                                                                                                                                                                                                                                 GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCCCTTCCCT
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                                                                                                                                                      100.0%; Score 101; DB 4; Length 288; ilarity 100.0%; Pred. No. 4.4e-21; Conservative 0; Mismatches 0: Indels (
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2000US-0214886P.
2000US-0215135P.
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 101; Conserv
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17-MAR-2000;
18-APR-2000;
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28-JUN-2000;
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### 17-WOY-2009; 2000US-02423
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    Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42293
                            TICTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAAT 101
                                           TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAAT 133
                                                                                                                            AAK87481 standard; DNA; 288 BP
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                                                                                                                                                                                      (first entry)
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19-MAY-2000; 2
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28-UNN-2000; 3
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1-JUL-2000; 2
5-JUL-2000; 2
5-JUL-2000; 2
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4-AUG-2000; 2
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4-AUG-2000; 2
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17-MAR-2000;
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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Human; reproductive system related antigen; reproductive system disorder;
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                     cancer; gene therapy;
                                                                                             WO200155320-A2.
                                                           Homo sapiens.
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

activity, and can be used in gene therapy and vaccine production. (I)

proteins and polynucleotides may be used in the prevention, diagnosis and

treatment of diseases associated with inappropriate (I) expression. For

example, they may be used to treat disorders associated with decreased

expression by rectifying mutations or deletions in a patient's genome

that affect the activity of (I) by expressing inactive proteins or to

supplement the patients own production of (I). Additionally, (I)

cubylucleotides may be used to produce the secreted (I), by inserting the

nucleic acids into a host cell and culturing the cell to express the

protein. (I) proteins and polynucleotides may be used to prevent,

cancers and cancer metastases of haematopoietic-derived cells. AAK64703

cancers and cancer metastases of haematopoietic-derived cells. AAK64703

to AAK87694 represent human immune/haematopoietic antigen genomic

sequences from the present invention. AAK64942 to AAK64950 and AAM82169

represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM
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05-JAN-2001; 2001US-0259678P

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                                                                                          Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
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                                                                                                                                  Disclosure, SEQ ID NO 9716; 1297pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                       Query Match 100.0%; Score 101; DB 4; Length 288; Best Local Similarity 100.0%; Pred. No. 4.4e-21; Matches 101; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                         TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAAT 101
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                       (HUMA-) HUMAN GENOME SCI INC
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                                              Barash SC,
                                                                     WPI; 2001-465570/50
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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                                               Rosen CA,
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2000US-0235834P
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
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08-NOV-2000;
08-NOV-2000;
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molecule encoding a reproductive system antigen is reating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 9717; 1297pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 101; DB 4; Length 288; Best Local Similarity 100.0%; Pred. No. 4.4e-21; Matches 101; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 43 A; 87 C; 73 G; 85 T; 0 U; 0 Other;
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       2000US-0246478P.
2000US-0246523P.
2000US-0246524P.
2000US-024652F.
2000US-024652F.
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2000US-024652B.
2000US-024661P.
2000US-0246610P.
2000US-0246611P.
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2000US-0249211P.
2000US-0249212P.
2000US-0249213P.
2000US-0249214P.
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2000US - 0249216P.
2000US - 0249217P.
2000US - 0249218P.
2000US - 0249244P.
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2000US-0249297P
2000US-0249297P
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2000US-025060P
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in preventing, treating
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Gaps

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Indels

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Matches

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ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted protein genes, and ABP00947-ABP01363 represent the proteins they encode. ABZ73689-ABZ74687 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening and recombinant. The secreted proteins in drug screening and recombinant. The secreted proteins are thought to be involved in biological activities associated with cellular signalling, cellular differentiation, cell migration, prohormone activation and neurotransmitter activity. The secreted proteins, and modulators of protein fragments specific for the secreted proteins, and modulators of protein cargments specific for the secreted proteins, and modulators of protein fragments specific for the secreted proteins, and modulators of protein cations are useful for diagnosing or treating cancers or other heir nucleic acids may also be used in the treatment of autoimmune disorders, inflammatory disorders, diseases involving angiogenesis, ADDS (acquired immunodeficiency syndroms), hepatitis, anaemia, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying an molecular weight markers. The present sequence represents a human secreted protein genomic fragment referred to in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or
                                                                                                                                                                                                                                                                                                                          Human; secreted protein; cancer; tumour; hyperproliferative disorder; autoimmune disorder; inflammation; angiogenic diseases; AIDS; acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV; antianaemic; vulnerary; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human secreted proteins and nucleic acids, useful for detecting treating cancer or other hyperproliferative disorders, autoimmune disorders, inflammatory disorders, HIV disease, hepatitis or anemia.
                                                                                                                                                                                                                                                                                   Secreted protein gene 366 genomic fragment HUSGU40, SEQ ID NO:1750.
                      TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 288 BP; 43 A; 87 C; 73 G; 85 T; 0 U; 0 Other;
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                                                                                                                                                      ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2001; 2001US-0278650P
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12-SEP-2001; 2001US-00950083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                    ABZ74603 standard; DNA; 288
                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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61
                                                                                                                                                                                               ABZ74603;
                                                                                                        RESULT 7
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Score 101; DB 8; Length 288; Pred. No. 4.4e-21;

100.0%;

Query Match Best Local Similarity

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ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted protein genes, and ABP00947-ABP01363 represent the proteins they encode. ABZ73689-ABZ74687 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening and recombinant. The secreted proteins in drug screening and recombinant. The secreted proteins are thought to be involved in biological activities associated with cellular signalling, cellular differentiation, cell migration, prothormone activation and neurotransmitter activity. The escreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein crypty are useful for diagnosing or treating cancers or other hyperproliferative disorders. Additionally, the secreted proteins and their nucleic acids may also be used in the treatment of autoimmune disorders, inflammatory disorders, diseases involving angiogenesis, ADS (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological seamples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein genomic fragment referred to in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted proteins and nucleic acids, useful for detecting or treating cancer or other hyperproliferative disorders, autoimmune disorders, inflammatory disorders, HIV disease, hepatitis or anemia.
                                                                                                                                                                                                                                                                                                                                                             autoimmune disorder; inflammation; angiogenic diseases; AIDS; acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV;
                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; cancer; tumour; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                  Secreted protein gene 366 genomic fragment HUSGU40, SEQ ID NO:1749.
TICTCGCCACGTTCGCCGGCTTTCCCCGGTCAAGCTCTAAAT 101
                                          Trcrcgccacgrrcgccgcrrrccccgrcaagcrcraaar 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 2326; 2474pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                               antianaemic; vulnerary; gene; ds.
                                                                                                                                                             ВР
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12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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                                                                                                                                                          ABZ74602 standard; DNA; 288
                                                                                                                                                                                                                                                12-MAY-2003 (first entry)
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Indels

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Length 288;

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Matches

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RESULT 9 ADA98980

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muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; renal disorder; proliferative disorder; cancer; ds.
                                                                                                                 atherosclerosis, stroke, endocarditis, congestive heart failure, rheumatic heart disease, cardiomyopathy, hemorrhoids, varicose veins, migraine, thrombosis, neural disorder, immune system disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secreted polypeptide and nucleic acid molecules, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing, preventing, prognosticating or treating cardiovascular disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted protein; cardiovascular disorder; arrhythmia;
                                                                                               GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCCGCTCCTTTCGCTT
                                                                                                                                                                         TTCTCGCCACGTTCGCCGGCTTTCCCCCGTCAAGCTCTAAAT 101
                                                                                                                                                                                                  TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAAT 133
                Score 101; DB 8;
Pred. No. 4.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein-related DNA sequence #572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 1088; 1572pp; English
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                  BP.
                100.0%;
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12-SEP-2001; 2001US-00950083.
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                                                                                                                                                                                                                                                                                                                  ADA98979 standard; DNA; 288
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                     101, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-247946/24.
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003004623-A2
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                                                                                                                                    33
                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                         ADA98979;
                  Query Match
Best Local (
                                                       Matches
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                                                                                                                                                                                                                                                                                           ADA98979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises the amino acid and coding sequence of human secreted proteins. The DNA and protein sequences of the invention are useful in the treatment of cardiovascular disorders, such as: arrhythmia,
                                                                                                                                                         9
                                                                                                                                                                                            GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atherosclerosis, stroke, endocarditis, congestive heart failure, theumatic heart disease, cardiomyopathy, hemorrhoids, varicose veins, migraine, or thrombosis. The DNA and protein sequences may also be used for treating or preventing: neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, renal disorders, proliferative disorders and/or cancerous diseases. The present DNA sequence is used in the exemplification of the invention. NOTE: The present sequence is shown on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; secreted protein; cardiovascular disorder; arrhythmia; atherosclerosis; stroke; endocarditis; congestive heart failure; rheumatic heart disease; cardiomyopathy; hemorrhoids, varicose veins; migranie; thrombosis; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; renal disorder; proliferative disorder; ds
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human secreted polypeptide and nucleic acid molecules, useful f
diagnosing, preventing, prognosticating or treating cardiovascular
disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or
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0
                                                                          Length 288;
                                                                                                                                                         GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTT
                                                                                                                 Indels
                                                                                                                                                                                                                                                        TTCTCGCCACGTTCGCCGGCTTTCCCCCGTCAAGCTCTAAAT 133
                                   Sequence 288 BP; 43 A; 87 C; 73 G; 85 T; 0 U; 0 Other;
                                                                                                                                                                                                                                   TICTCGCCACGTTCGCCGGCTTTCCCCCGTCAAGCTCTAAAT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein-related DNA sequence #573.
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                                                                          , DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 1089; 1572pp; English
                                                                                             Pred. No. 4.4
Mismatches
                                                                            Score 101;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2001; 2001US-00950083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                 101; Conservative
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                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA,
invention
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                                                                          Query Match
Best Local S
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The invention comprises the amino acid and coding sequence of human secreted proteins. The DNA and protein sequences of the invention are useful in the treatment of cardiovascular disorders, such as: arrhythmia, atherosclerosis, stroke, endocarditis, congestive heart failure, rheumatic heart disease, cardiomyopathy, hemorrhoids, varicose veins, migraine, or thrombosis. The DNA and protein sequences may also be used for treating or preventing: neural disorders, immune system disorders, muscular disorders, reproductive disorders, jamune system disorders, pulmonary disorders, reproductive disorders, gastrointestinal disorders, cancercous diseases. The present DNA sequence is used in the exemplification of the invention. NOTE: The present sequence is shown on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 288 BP; 43 A; 87 C; 73 G; 85 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 101; DB 8;
Pred. No. 4.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
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Best Local Similarity
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NOTE: The present sequence is shown on

Sequence 288 BP; 43 A; 87 C; 73 G; 85 T; 0 U; 0 Other;

the WIPO website.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel genes and their fragments which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids and proteins are useful in the diagnosis, treatment and prevention of conditions are useful in the dispussibly treatment and prevention of conditions polymeuropathy, atherosclerosis, anamaia, stroke, gangrene, impotence, infection, cataract, renal disorders, or endocrine disorders. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A human secreted protein and nucleic acids useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating diabetes or conditions related to diabetes, e.g. hyperglycemia, obesity,
                             1 GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCT
                                                   GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCT
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 Gaps
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0; Indels
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                                                                                                        TTCTCGCCACGTTCGCCGGCTTTCCCCCGTCAAGCTCTAAAT 133
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                                                                                        TrcrccccacGrrccccGGCrrTccccGTCAAGCTCTAAAT 101
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                                                                                                                                                                                                                                                                                                                                  Neuroprotective; Cerebroprotective; Antianemic; ds.
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Mismatches
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                                                                                                                                                                                                                                                                                     Human secreted protein DNA SEQ ID 682.
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12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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                                                                                                                                                                                             ADA44489 standard; DNA; 288
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101; Conservative
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                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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The invention relates to novel genes and their fragments which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids and proteins are useful in the diagnosis, treatment and prevention of conditions related to diabetes, e.g. hyperglycaemia, obesity, retinopathy, polyneuropathy, atherosclerosis, anaemia, stroke, gangrene, impotence, infection, cataract, renal disorders, or endocrine disorders. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A human secreted protein and nucleic acids useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating diabetes or conditions related to diabetes, e.g. hyperglycemia, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGTGACCGCTACATTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCTTTCCT
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Neuroprotective; Cerebroprotective; Antianemic; ds.
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                                                                                                                               Human secreted protein DNA SEQ ID 681.
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Matches 101; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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                               ADA44488 standard; DNA; 288
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RESULT 12
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virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV; vulnerary; antibacterial; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; heparotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifumgal; antiparasitic; cardiant; immune disorder; infection; vaccine; cardiovascular disorder; neurological disease; nephrotropic;

gene therapy; gene; ds

WO200277186-A2

03-OCT-2002

Ното варіепв.

nootropic; neuroprotective; cytostatic;

secreted protein;

Human:

Human secreted protein encoding genomic DNA SEQ ID NO 1646.

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The invention relates to novel human genes (ABZ66891-ABZ68209) and the encoded secreted proteins (ABP99470-ABP99872) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and in the specification. The nucleic acids, proteins, antibodies and in the specification. The nucleic acids, proteins, antibodies and antibacists are useful in the disgnosis, treatment and prevention of:

(a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung or urogenital; (b) immune disorders e.g. Addison's disease,

(c) lung or urogenital; (b) immune disorders e.g. Addison's disease,

(c) alergies, autoimmune haemolytic ansemia, autoimmune thyroiditis,

diabetes mellitus, Crohn's disease, multiple sclerosis, rhemmatoid

arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial anoxia and epilepsy; and (f) infectious diseases such as viral,
                      Human; secreted protein; nootropic; neuroprotective; cytostatic; vurucide; dermatory; anti-HIV; vulnerary; antibacterial; antiparkinsonian; antisinflamatory; antibacterial; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflamatory; antiallergic; antidiabetic; antiuleer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; infection; vaccine; cardiovascular disorder; neurological disease; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g. AIDS, multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human secreted proteins encoded by genes contained in cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 288 BP; 43 A; 87 C; 73 G; 85 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterial, fungal and parasitic infections
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12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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                                                                                                                                                                                            gene therapy; gene; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        West Nile fever.
                                                                                                                                                                                                                                                                                      WO200277186-A2
                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                      03-OCT-2002,
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New human secreted proteins encoded by genes contained in cDNA clones (e.g. HGGAC19), useful for preventing, treating or diagnosing e.g. AIDS, multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or West Nile fever.

27-MAR-2001; 2001US-0278650P 12-SEP-2001; 2001US-00950082. 12-SEP-2001; 2001US-00950083. (HUMA-) HUMAN GENOME SCI INC

12-SEP-2001;

Rosen CA, Ruben SM; WPI; 2003-040583/03

26-MAR-2002; 2002WO-US009188

Disclosure; Page 2268; 2423pp; English

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The invention relates to novel human genes (ABZ66891-ABZ68209) and the encoded secreted proteins (ABP99470-ABP99872) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthur tris, and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
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Pred. No. 4.4e-21;
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Matches 101;
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100.0%; Score 101; DB 10; Length 288; 100.0%; Pred. No. 4.4e-21; cive 0; Mismatches 0; Indels 0;

Matches 101; Conservative

Query Match Best Local Similarity

9 92

33 GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCCCTTTTCGCTTTCTTCCCTTCCT 1 GCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCT

TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAAT 133 TTCTCGCCACGTTCGCCGGCTTTCCCCGGTCAAGCTCTAAAT 101

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g 8

ABZ68123 standard; DNA; 288

RESULT 14 ABZ68123

26-MAR-2003 (first entry)

ABZ68123;

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The invention relates to novel human genes (ABZ66891-ABZ68209) and the encoded secreted proteins (ABP99470-ABP99872) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the disapmosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung or urogenital; (b) immune disorders e.g. Addison's disease, altergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, carbritis and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anazia and epilepsy; and (f) infectious diseases such as viral,
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                                                                                                      Human; secreted protein; nootropic; neuroprotective; cytostatic; virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV; vulnerary; antibacterial; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antiheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antipparasitic; cardiant; immune disorder; infection; vaccine; cardiovascular disorder; neurological disease; nephrotropic; gene; ds.
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                                                                  Human secreted protein encoding genomic DNA SEQ ID NO 1533.
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12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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                      (first entry)
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Best Local Similarity 100.
Matches 101; Conservative
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                      26-MAR-2003
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Search completed: July 14, 2005, 07:01:48 Job time : 145.448 secs

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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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Best Local Similarity 100.0%; Pred. No. 9.1e-18;
Matches 101; Conservative 0; Mismatches 0; Indels (
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BI940501 daf71e02.
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B83638 RPCII1-16L2
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AQ279924 CITBI-E1-
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Copyright (c) 1993 - 2005
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Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 116)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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Seg primer: M13 Reverse
Class: BAC ends.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Other GSSs: CITBL-E1-2503C21.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200
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AQ265335 11-00T-1998 CITBL-E1-2508M1.TR CITBL-E1 Homo sapiens genomic clone 2508M1, genomic survey sequence.

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Homo sapiens (human)

1SM Homo sapiens

Bukaryota, Metzaca; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metzaca; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

2E 1 (bases 1 to 142)

3A Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,

Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and

Venter, J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready

Map Building

Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel. 301 838 0206

Eax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 150)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
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Contact: Mark Adams
Department of Eukaryotic Genomics
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Seg primer: MI3 Reverse
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
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/clone="2508M1"
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GI:3793535
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61 TTCTCGCCACGTTCGCCGGCTTTCCCCGGTCAAGCTCTAAAT 101
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/sex="Male"
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nes 101, Conserv
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
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Contract: Mark Adams
Contract: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 3101 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                              Email: mdadams@figr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                       http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: MI3 Reverse
Class: BAC ends.
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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CalTech Human BAC Library D"
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Use of a random BAC End Sequence Database for Sequence-Ready Map
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                9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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The Institute for Genomic Research
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/db xref="taxon:9606"
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1. .158
                                                                                                                                                                                                                                                                                  /sex="male"
/cell_type="sperm"
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AQ026683.1 GI:3266905
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Homo sapiens
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AQ061259 11-JUL-1998 CIT-HSP Homo sapiens genomic clone 2352N1, genomic survey sequence.
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K. Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
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/clone_lib="CIT-HSP"
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HindIII
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/clone_llb="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
Email: mdadams@tigr.org
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/db_xref="taxon:9606"
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DEFINITION

AQ196514

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

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Murphy Chiapelli MCCarter="
/note="vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI;
Site_2: EcoRI; The library was constructed by Claire
Murphy, Brandi Chiapelli, and Dr. James McCarter at
Washington University, St. Louis Oligo(dT)-SLI PCR based
library. Pristionchus pacificus mixed stage cDNA PCR
products of size >400 uncleotides containing SLI on the
s' end and oligo(dT) on the 3' end were non-directionally
cloned into pCRII-TOPO(Invitrogen) following the Topo TA
is McCarter, J., Cliffon, S., Chiapelli, B., Pape, D., Martin, J.,
Wyle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoo, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.,
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The library was constructed by Claire Murphy, Brandi Chiapelli, and Dr. James McCarter at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center Seq primer: -40RP from Gibco High quality sequence stop: 161.
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
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100.0%; Pred. No. 9.4e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (bas) 1 to 163) Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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                                                                                                                                              LETHEP-2385C23.TR CIT-HSP Homo sapiens genomic clone 2385C23, genomic survey sequence.
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/clone_lib="CIT-HSP"
hindte="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII
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Pristionchus pacificus
Eukaryota: Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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  112 TTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAAT 152
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100.0%; Pred. No. 9.4e-18;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BM812626.1 GI:19148640
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Best Local S:
Matches 101
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GSS 29-AUG-1998

VERSION KEYWORDS SOURCE ORGANISM

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Murphy Chiapelli McCarter"

Murphy Chiapelli McCarter"

Ante="Vector: pCRIT-TOPO (Invitrogen); Site 1: ECORI;

Site 2: ECORI; The library was constructed by Claire

Murphy, Brandi Chiapelli, and Dr. James McCarter at

Mashington University, St. Louis. Oligo(dT)-SLI PCR based

Dibrary. Pristionchus pacificus mixed stage cDNA PCR

products of size >400 nucleotides containing SLI on the
5' end and oligo(dT) on the 3' end were non-directionally

cloned into pCRII-TOPO(Invitrogen) following the TOPO TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ310689 173 bp DNA linear GSS 22-DEC-1998
CITBL-E1-2520L11.TR CITBL-E1 Homo sapiens genomic clone 2520L11,
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Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Mupublished (1998)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Eax: 301 838 0200
Email: hbe@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 173)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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Seg primer: M13 Reverse
Class: BAC ends.
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    168
    organism="Pristionchus pacificus"

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0
                                                                                                          /mol_type="mRNA"
/db_xref="taxon:54126"
/dev_stage="Mixed stage"
/lab_host="DH108"
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          High quality sequence stop: 167.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="2520L11"
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/cell_type="sperm"
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The library was constructed by Claire Murphy, Brandi Chiapelli, and
Dr. James McCarter at Washington University, St. Louis. DNA
Sequencing by: Washington University Genome Sequencing Center
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Unpublished (1998)
Other GSSs: CIT-HSP-2376E2.TF
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
17e1: 301 838 0200
Fax: 301 838 0208
Fax: 301 838 0208
Email: madams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
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Neodiplogasteridae; Pristionchus.
Neodiplogasteridae; Pristionchus.
Neodiplogasteridae; Pristionchus.
I (bases I to 188)
McCarter, J. (21ifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Mirter, E., Bennett, J., Franklin, C., Wylie, T., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., McCann, R., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13.Reverse
Class: BAC ends.
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/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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100.0%; Pred. No. 9.4e-18;
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AQ280347 linear GSS 22-NOV-1998
CITBI-E1-2518K3.TR CITBI-E1 Homo sapiens genomic clone 2518K3,
                                                                                                                                                                       AQ278442 200 bp DNA linear GSS 22-NOV-1998 CITBI-E1-2519N1.TR CITBI-E1 Homo sapiens genomic clone 2519N1,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butherlai, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 200)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry, K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 211)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Map Building
Unpublished (1998)
Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
      68 TTCTCGCCACGTTCGCCGGCTTTCCCCGGTCAAGCTCTAAAT 108
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/cell type="sperm"
/clone lib="CITB1-B1"
/note="Vector: pBeloBAC11; Si
CalTech Human BAC Library D"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2519N1"
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GSS.
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Homo sapiens
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Homo sapiens
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CITBI-E1-2518K13.TR CITBI-E1 Homo sapiens genomic clone 2518K13,
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Department of Eukaryotic Genomics
Search 301 838 0200
Examil: mdadams@tign.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
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Clones are available from Research Genetics (info@resgen.com). BAC end search are completed as a complete are completed as a complete are completed as a completed as a complete are completed as a complete are completed as a complete are completed as a complete are completed as a completed are completed as a completed as a completed are completed as a completed are completed as a completed as a completed are completed as a completed as a completed are completed as a completed as a completed are completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a completed as a compl
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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Map Building
/clone lib="CITBI-B1"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
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CalTech Human BAC Library D"
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                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 9.4e-18;
Matches 101; Conservative 0; Mismatches 0;
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Other GSSs: CITBI-E1-2518K13.TF
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Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Map Bullding
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                      http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
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/note="Vector: PBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
calTech Human BAC Library D"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Cilfton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
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Endocrine Pancreas Consortium
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db_xref="taxon:9606"
clone="2518K3"
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Note: Organ: pancreas; Vector: pSPORTI (GIBCO); Site_1:
Not I; Site_2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and SalI linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-SalI sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/-. The wt library is in
pSPORTI, T7 promoter is 5'."
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2000) Library was constructed by Catherine Lee DNA sequencing by: washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Scearce (mscearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 207.
Location/Qualifiers
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/clone_lib="Kaestner ngn3 wt"
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100.0%; Pred: No. 9.6e-18;
iive 0; Mismatches 0;
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/mol_type="mRNA"
/strain="129/Sv x CD1"
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1 (bases 1 to 142)
Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
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iive 0; Mismatches 0;
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Sequence 2608 from patent US 6593114.
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Sequence 2608 from patent US 6737248.
AR538046
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PATN2PN1B
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AF104442
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E00019 DNA coding
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AY559171 Pseudomon
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Z92776 Caenorhabdi
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                                                           July 14, 2005, 04:39:07; Search time 756.618 Seconds (without alignments) 6468.225 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                            4708233 seqs, 24227607955 residues
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X54604 Pseudomonas AF027199 Klebsiell

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                                                    1 (bases 1 to 142)
Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and Rosen,C.A.
Staphylococcus aureus polynucleotides and sequences
Patent: US 6737248-A 2608 18-MAY-2004;
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/product='E.coli penicilinase'.
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JP 1981154999-A/2.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Butteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Butteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Butteria; I (bases 1 to 251)

University of SELECTIVE AGED PROTEIN OR POLYPEPTIDE IN BACTERIA

Datem: JP 1981154999-A 1 30-NOV-1981;

UNIV HARVARD

OS Escherichia coli

PN JP 1981154999-A/1

PN JP 1981154999-A/1

PN JP 1981154999-A/1

PP 09-ARR-1980 US 80 139225

PI UNGVTAA GIRUBAATO, KAREN TARUMATSUJI

PC C12P21/00,C07H21/00,C12N1/00,C12N15/00//C12R1/19; CC

strandedness: Double;

CC tropology: Linear;

CC fragment type: N-Terminal Fragment;

CC **Source: clone=PKT241;
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                                                                                                                        BCT 26-APR-1993
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                                                                                                                                                                                                                                                                      other sequences; plasmids.

1 (bases 1 to 240)

Remper_B. Jensch,F., von Depka-Prondzynski,M., Fritz,H.J.,

Borgmeyer,U. and Mizunchi,K.

Resolution of Holliday structures by endonuclease VII as observed
in interactions with cruciform DNA

Cold Spring Harb. Symp. Quant. Biol. 49, 815-825 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rrmuknUO 240 bp DNA linear BCT 26-APR-1
Plasmid pMM110 region of endo VII cleavage sites near cruciform
structures.
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115 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E00018 251 bp DNA line
DNA coding for Escherichia coli penicillinase.
E00018 I GI:2168326
JP 1981154999-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
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Best Local Similarity 100.0%; Pred. No. 8.7e-20;
Matches 101; Conservative 0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               source text: Plasmid pMM110 DNA. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .240
/organism="Plasmid pMM110"
/mol_type="genomic DNA"
/db_xref="taxon:2599"
/plasmid="Plasmid pMM110"
                                                                                                                                                                                  M10199
M10199.1 GI:150826
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Escherichia coli
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Plasmid pMM110
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KEYWORDS
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/map="8"
                                                                                                                                                                                                                                     Initial Denaturation: 94C 300sec
PCR Cycles: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36. .60
complement (202. .224)
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BD195256.1 GI:33005021
JP 2002513277-A/43.
unidentified
                                                                                                                                                                                                                                                                                  Annealing: 60C 10sec
Extension: 72C 20sec
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Matches 101; Conservative
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primer_bind
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BD195256/c
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 344)
Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L18624.1 GI:308338
STS; PCR primer; STS sequence; microsatellite marker;
microsatellite repeat; repeat polymorphism; sequence tagged site.
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Gilbert, W. and Talmadge, K.
Mature protein synthesis
Patent: US 4338397-A 1 06-JUL-1982;
President and Fellows of Harvard College; Cambridge, MA
                             210. .>252
/product='E.coli penicilinase' FT
                                                                                                                                                                                     Query Match 100.0%; Score 101; DB 6; Length 251; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 101; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMUT5345 344 bp DNA linear ;
Human chromosome 8 STS UT5345, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                   61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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 Location/Qualifiers
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                                                                                                        /organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                              101644 251 bp sk
Sequence 1 from Patent US 4338397
101644
                                                             al 190. .196.
Location/Qualifiers
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/organism="unknown"
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Homo sapiens
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Matches 101; Conservative
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                                                             TATA_signal
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 Key
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HUMUTS345
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I01644/c
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Ballard, L., Melis, R., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Rodriguez, P., Albertsen, H., Lalouel, J.-M. and White, R. Genetic and physical mapping of simple sequence repeat containing sequence tagged site from the human genome cropeat containing sequence tagged site from the human genome containing upublished (1993)

L. Original source text: Homo sapiens DNA.
Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: GAGCARAAACAGGAACAGAAATGC
Primer B: TTGGGGAAATGTGCGGAACC
32P-label: B Primer
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PN JP 2002513277-A/43

PD 08-MAY-2002

PP 21-NOV-1996 US 60/031626,14-OCT-1997 US 60/061953 PI

PATRICK J DILLON,GIL H CHOI,RODNEY A WELCH

PC C12N15/11,C12N15/63,C07K16/12,G01N33/569,G06F17/30,G11B7/00 CC

CT Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

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CC Topology: Linear;
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Dillon, P.J., Choi, G.H. and Welch, R.A.
Nucleotide sequence of Escherichia coli pathogenicity islands
Patent: JP 2002513277-A 43 08-MAY-2002;
HUMAN GENOME SCIENCES INC, WISCONSIN ALUMNI RESEARCH FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Nucleotide sequence of Escherichia coli pathogenicity islands.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gel: Acrylamide 7%, Formamide 32%, Urea 34%
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/standard_name="STS UT5345"
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/db_xref="taxon:32630"
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mat_peptide
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Matches 101; Conserv
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                      ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other sequences.

other sequences.

other sequences.

I (bases 1 to 456)

Skai,H., MomcLay,Y., Kumakura,T., Tochifusa,N., Kitazawa,T.,
Ojida,K. and Matsushiro,A.

POLYPEPTIDE SECRETION DEVELOPMENT VECTOR, MICROORGANISM

POLYPEPTIDE SECRETION DEVELOPMENT VECTOR, MICROORGANISM

AL HOROCOGNANISM

EARTH CHEM CORP LTD

OS Artificial gene

OC Artificial gene

OC Artificial sequence; Genes.

PN JP 1986149089-A/1

PD 07-JUL-1986

PF 21-DEC-1984 JP 1984271206

PF 21-DEC-1984 JP 1984271206

PF 07-JUL-1986

PF 07-JUL-1986

PF 07-JUL-1986

CC Artificial sequence; Genes.

PN JP 1986149089-A/1

PN JP 198614908-A/1

PN JP 198614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E00892 Anthetic DNA encoding fused polypeptide between E coli beta-lactamase and human beta-urogastrone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product='beta-urogastrone mature peptide'.
                                                                                                                                                                                                                                                                                                      1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product='beta-urogastrone precursor' FT 209. .277
                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                 100.0%; Score 101; DB 6; Length 400; 100.0%; Pred. No. 8.7e-20; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         61 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 101
                                   /organism='Unidentified'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
/mol_type="genomic DNA"

    .400
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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JP 1986149089-A/1.
synthetic construct
synthetic construct
                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 101; Conservative
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  Key
source
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FT
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표보보
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                       Bource
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E00892/c
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                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                               PAT 29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other sequences; artificial sequences.

1 (bases 1 to 456)
Yoshikawa,K., Momota,Y., Kajifusa,N., Koide,T. and Okai,H.
POLYPEPTIDE SECRETION EXPRESSION VECTOR, MICROORGANISM TRANSFORMED
BY SAID VECTOR AND PRODUCTION OF POLYPEPTIDE USING SAID
PATENT: JP 1987083890-A 1 17-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                            1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OKAI HIDEO
C12N15/00, C12N1/20, C12P21/00, (C12N1/20, C12R1:19), (C12N1/20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-1987
09-OCT-1985 JP 1985225393
YOSHIKAWA KAZUTOSHI, MOMOTA YUTAKA, KAJIFUSA NORIYUKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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    Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125. .170
/note='beta lactamase promoter'
                                                                                                                                                                                                                                                                                                                                                 linear
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product='beta urogastrone'
209. 277
peptide 278. 436
7product='beta urogastrone'
Location/Qualifiers
                                                                                                                                                                                    61 GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                 113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                               801156 456 bp DNA li
DNA fragment which secrets beta urogastrone.
E01156
100.0%; Score 101; DB 6;
larity 100.0%; Pred. No. 8.7e-20;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .456
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Artificial Sequence; Genes. JP 1987083890-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209. .439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *source: clone=pUG201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                topology: Linear;
hypothetical: No;
                                                                                                                                                                                                                                                                                                                                                                                                               E01156.1 GI:2169415
JP 1987083890-A/1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct
synthetic construct
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AX260098.1 GI:16509129
                                                                                                                             Homo sapiens
JP 1987190083-A/1
                                                                                                                                                                                                                                                           topology: Linear;
hypothetical: No;
                                                                                                                                                                                                                                                                                    anti-sense: No;
     synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                        209. .439
                                                                                                                                                                                                                                                                                                                                                 sig_peptide
mat_peptide
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                                                                                                                                                                                                                                                                                                                           Promoter
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AX260098/c
LOCUS
DEFINITION
ACCESSION
VERSION
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ORGANISM
   ORGANISM
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AUTHORS
TITLE
                                       AUTHORS
TITLE
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                                                                       801274 1997 29-SEP-1997 DNA linear PAT 29-SEP-1997 DNA encoding beta-urogastron fused with DNA encoding a promoter and signal peptide of beta-lactamase.
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                                                                                                                                                                                                                                                                                                                     06-AUG-1987
31-JAN-1986 JP 1986021032
OKA1 HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, ADACHI SHOJI, MATSUBARA AKIMASA, OXIDA KAZUHIDE, YANO MAKI, MIHARA SHIGERU, MATSUSHIRO AIZO, YANAIHARA NOBORU
C12P21/00,C12N15/00,C12P21/00,C12R1:91);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                            other sequences; artificial sequences.

1 (Dases I to 456)

Okai, H., Kumakura, T., Kawamoto, S., Adachi, S., Matsubara, A., Ojida, K., Yano, M., Mihara, S., Matsushiro, A. and Yanaihara, N. PRODUCTION OF BETA-URCGASTRONE
Patent: JP 1987179398-A I 06-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E01302 456 bp DNA linear PAT 29-5 DNA encoding human beta-urogastrone fused with DNA encoding promoter and signal peptide of beta-lactamase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 101; DB 6; Length 456; 100.0%; Pred. No. 8.7e-20; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278. .436
/product='beta-urogastron'
209. .439
/product='beta-urogastron'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 GGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 456
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                       Artificial gene
Artificial sequence; Genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125. .170
200. .203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    strandedness: Double;
                                                                                                                                                                                                                                                                                                            JP 1987179398-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                topology: Linear;
hypothetical: No;
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JP 1987190083-A/1.
synthetic construct
                                                                                                                           E01274.1 GI:2169533 JP 1987179398-A/1.
                                                                                                                                                    synthetic construct
synthetic construct
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mat_peptide
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Best Local Similarity
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Matches
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VERSION
KEYWORDS
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VERSION
KEYWORDS
SOURCE
                                                   RESULT 11
E01274/c
                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                        AUTHORS
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20-AUG-1987
14-FEB-1986 JP 1986031415
OKAI HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, KOIDE TAKAO, MOMOTA YUTAKA
CI2NI5/00,C07H21/04,C12N1/00,C12P21/02,(C12N1/00,C12R1:19), PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 26-OCT-2001
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                                            Okai, H., Kumakura, T., Kawamoto, S., Koide, T. and Momota, Y. POLYPEPTIDE-EXPRESSION VECTOR, HOST TRANSFORMED WITH SAID VECTOR AND PRODUCTION OF POLYPEPTIDE USING SAID HOST PATENT: JP 1987190083-A 1 20-AUG-1987;

BARTH CHEM CORP LID
OS Artificial gene
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product='human beta-urogastrone'
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .456
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
other sequences; artificial sequences.
1 (bases 1 to 456)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX260098 466 bp
Sequence 60 from Patent WO0172774.
AX260098
                                                                                                                                                          Artificial gene
Artificial sequence; Genes.
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200. .203
209. .277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   C12R1:19);
strandedness: Double;
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Query Match
                 FEATURES
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                                                                                                                                                                                                                                                                                                              PAT 26-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cuphea lanceolata
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Myrtales; Lythraceae; Cuphea.
1 (bases 1 to 693)
Toepfer, R., Bautor, J., Bothmann, H., Filsak, E.,
Schulte, W., Voetz, M., Walek, J. and Schell, J.,
PROMOTERS
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                                                                                                                                                    280 AGGGTTATTGTCTCATGAGGGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 221
                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                   Length 466;
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/organism="Drosophila melanogaster"
/mol_type="unassigned DNA"
/db_xref="taxon:7227"
                                                100.0%; Score 101; DB 6;
100.0%; Pred. No. 8.7e-20;
tive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 8.8e-20;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deak, P., Glover, D.M. and Midgley, C.
Cell cycle progression proteins
Patent: WO 0172774-A 112 04-OCT-2001;
Cyclacel Limited (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: WO 9507357-A 11 16-MAR-1995;
MAX PLANCK GESELLSCHAFT (DE)
Other publication CA 2169093 950316
                                                                                                                                                                                                                                                                                                       Sequence 112 from Patent WO0172774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A43586 693 bp
Sequence 11 from Patent WO9507357.
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                              AX260150.1 GI:16509172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A43586.1 GI:2298779
                                                                Best Local Similarity 100.
Matches 101; Conservative
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Best Local Simil
Matches 101;
                                                  Query Match
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AX260150/c
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AUTHORS
TITLE
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A43586
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JOURNAL
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AUTHORS
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Run on:

July 14, 2005, 04:35:42; Search time 142.398 Seconds (without alignments) 4198.742 Million cell updates/sec

US-09-482-682-64\_COPY\_7131\_7231 101

score: Perfect

1 agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04:\* .: geneseqn1980s:\* : geneseqn1990s:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2000s:\* geneseqn2001as:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:\*

geneseqn2004bs:

geneseqn2003cs:\* geneseqn2004as:

geneseqn2003bs:\*

SUMMARIES

Aav76919 Staphyloc	Aan10032 Sequence	Aan10031 Sequence	Aav31229 E. coli J	Aan60624 Plasmid p	Aan71080 Sequence	Aan70833 Beta-urog	Aan81765 Sequence	Aba90413 Drosophil	Aax21173 Polynucle	Aax21149 Polynucle	Aba90456 Drosophil	Adh58311 Electroph	Aas30560 DNA encod	Aas27819 DNA encod	Abk42984 Genomic s	Aal07344 Human rep	Aal03229 Human rep	Aal06588 Human rep	Aal07340 Human rep
AAV76919	AAN10032	AAN10031	AAV31229	AAN60624	AAN71080	AAN70833	AAN81765	ABA90413	AAX21173	AAX21149	ABA90456	ADH58311	AAS30560	AAS27819 ·	ABK42984	AAL07344	AAL03229	AAL06588	AAL07340
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142	228	251	400	456	456	456	456	466	487	535	573	605	176	176	776	116	116	116	176
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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100.0         450         2         AAN31229         Aav31229           100.0         456         1         AAN60524         Aan60624           100.0         456         1         AAN71080         Aan71080           100.0         456         1         AAN71083         Aan71083           100.0         456         1         AAN81765         Aan81765           100.0         487         2         AAX21173         Aax51173           100.0         487         2         AAX21173         Aax51173	100.0         142         2         AAV76919         Aav76919           100.0         228         1         AAN10032         Aan10032           100.0         251         1         AAN10031         Aan10031           100.0         456         1         AAN31229         Aav31229           100.0         456         1         AAN71080         Aan66624           100.0         456         1         AAN71080         Aan7083           100.0         456         1         AAN70833         Aan70833           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100.0 228 1 AAN10032 A 100.0 251 1 AAN10031 A 100.0 456 1 AAN70633 A 100.0 456 1 AAN71080 A 100.0 456 1 AAN71080 A 100.0 456 6 ABA90413 A 100.0 456 6 ABA90413 A 100.0 573 6 ABA90456 A 100.0 573 6 ABA90456 A 100.0 776 4 AAS30560 A

Abal4573 Human ner	Aas34681 Human DNA	Ada41574 Human sec	Acc50905 Human sec	Abz71508 Secreted	Adb91869 Human sec	Adb61140 Connectiv	Adb94622 Novel hum	Adc74663 Human sec	Ada57709 BAC fragm	Adn41551 Novel hum	Aas30559 DNA encod	Aas27818 DNA encod	Abk42983 Genomic s	Aas41807 Genomic s	Aas41855 Genomic s	Aak85485 Human imm	Aak85434 Human imm	Aal07343 Human rep	Aal06587 Human rep	Aal07339 Human rep	Aal03228 Human rep	Abal4572 Human ner	Aas34680 Human DNA	Adb61139 Connectiv
ABA14573	AAS34681	ADA41574	ACC50905	ABZ71508	ADB91869	ADB61140	ADB94622	ADC74663	ADAS7709	ADN41551	AAS30559	AAS27818	ABK42983	AAS41807	AAS41855	AAK85485	AAK85434	AAL07343	AAL06587	AAL07339	AAL03228	ABA14572	AAS34680	ADB61139
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176	176	176	176	176	176	176	176	176	176	176	845	845	845	845	845	845	845	845	845	845	845	845	845	845
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101
c 21	c 22	c 23	c 24	c 25	c 26	c 27	c 28	c 53	c 30	c 31	c 32	c 33	c 34	c 35	c 36	c 37	c 38	c 39	c 40	c 41	c 42	c 43	C 44	c 45
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## ALIGNMENTS

AAV76919/c ID AAV76919 standard; DNA; 142 (first entry) 16-MAR-1999 AAV76919; 

BP.

Staphylococcus aureus contig SEQ ID #2608.

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

Staphylococcus aureus

EP786519-A2.

30-JUL-1997

97EP-00100117. 07-JAN-1997;

96US-0009861P. 05-JAN-1996; (HUMA-) HUMAN GENOME SCI INC.

Rosen CA; Fannon MR, Dillon PJ, Barash SC, Choi GH, WPI; 1997-374922/35. Kunsch CA,

Polynucleotide(s) and proteins derived from Staphylococcus aureus -stored on computer readable medium and used in the production of anti-S.aureus vaccines.

Claim 1; Page 2287; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable endedium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or

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industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against 8. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, acalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The closest identifiable promoter for the penicilinase gene in pKT241 (AAN10031) is located in the region 14 to 20 nucleotides before its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthesis of mature protein or polypeptide - by using bacterial host transformed by cloned vehicle contg. DNA fragment etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning vehicle; bacterial vector; transformed host; penicillinase; insulin; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of the pKT218 EcoRI-PstI penicillinase gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 142 BP; 45 A; 25 C; 26 G; 45 T; 0 U; 1 Other;
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Pred. No. 2.1e-21;
0; Mismatches 0;
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225. :228
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AAN10032 standard; DNA; 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1981-80125D/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAP10039.
                                                                                                                                                                                                                                                                                                                                       readable medium
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translational start signal. In the examples, the 3' end of pKT241 was attached to the signal DNA sequence of the DNA fragment (19) for rat preproinsulin (see AAN10013). The closest identifiable promoter for the penicillinase gene in pKT218 (AAN10032) is located in the region 14 to 20 mucleotides before its translational start signal. In the examples, the 3' end of pKT218 was attached to the signal DNA sequence of the DNA fragment (CB6) for rat preproinsulin (see AAN10034)
                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The closest identifiable promoter for the penicilinase gene in pKT241 (AAN10031) is located in the region 14 to 20 nucleotides before its translational start signal. In the examples, the 3' end of pKT241 was attached to the signal DNA sequence of the DNA fragment (19) for rat preproinsulin (see AAN10033). The closest identifiable promoter for the penicillinase gene in pKT218 (AAN10032) is located in the region 14 to 2 nucleotides before its translational start signal. In the examples, the
                                                                                                                                                                                                                            1 AGGGTTATTGTCTCATGAGCGGGATACATATTTGAATGTATTAGAAAATAAACAAATAG
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthesis of mature protein or polypeptide - by using bacterial host transformed by cloned vehicle contg. DNA fragment etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning vehicle; bacterial vector; transformed host; penicillinase;
                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of the pKT241 EcoRI-PstI penicillinase gene fragment.
                                                                                                                                                             100.0%; Score 101; DB 1; Length 228; 100.0%; Pred. No. 2.3e-21;
                                                                                                                                                                                            Indels
                                                                                                                               Sequence 228 BP; 72 A; 37 C; 46 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                         61 GGGTTCCGCGCACATTTCCCCGGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                           GGGTTCCGCGCAAAAGTGCCACCTGACGTC
                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/label= sticky end
248. .251
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/label= sticky end
                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81EP-00301561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80US-00139225
                                                                                                                                                                                                                                                                                                                                                                                                   AAN10031 standard; DNA; 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1992 (first entry)
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Talmadge K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1981-80125D/44.
                                                                                                                                                                            Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insulin; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gilbert W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP38182-A.
                                                                                                                                                                                                                                                                                                                       115
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                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by the PAI open reading frames of the invention can be used in kits to detect uropathogenic E. coli. The proteins are used in vaccines to elicit a protective immune response in an animal to the uropathogenic E. coli strain J96
                                                                                                                                                                 New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to elicit an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR;
PAI V; pheV; vaccine; protective immune response; ds.
                                                                                                                                             Gaps
end of pKT218 was attached to the signal DNA sequence of the DNA igment (CB6) for rat preproinsulin (see AAN10034)
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                                                                               Length 251;
                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 400 BP; 106 A; 77 C; 91 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                             61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                               Sequence 251 BP; 74 A; 45 C; 50 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 75
                                                                              100.0%; Score 101; DB 1; 100.0%; Pred. No. 2.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                coli J96 pathogenicity island contig #43.
                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Page 140-141; 250pp; English.
                                                                                                                                                                                                                                                                                                         Matches 101; Conservative
                                                                                             Similarity
                 fragment
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Length 400;

100.0%; Score 101; DB 2; 100.0%; Pred. No. 2.5e-21;

Query Match 100. Best Local Similarity 100. Matches 101; Conservative

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                    165 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The plasmid produces secreted beta-urogastrone in a transformed expression system. Similar plasmids may be constructed where the secertion signal may be coupled with eg. somatostatin, insulin, growth hormone, interferon, IL-2, gastric inhibitory peptide, influenza B SA, epidermal growth factor and thymosine-beta4. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant vector for polypeptide secretion - contains signal peptide sequence directly bonded to peptide-coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oshiden K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kitazawa
                                             GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 101
                                                          GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 65
                                                                                                                                                                                                                                                                                                                                                                                /*tag= d
/label= Beta-lactamase signal peptide
278, .436
                                                                                                                                                                                                              Plasmid pUG201 sequence encoding beta-urogastrone
                                                                                                                                                                                                                                    Beta-lactamase signal peptide; pGH54; pGH55; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kajifusa N,
                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Table 4; 79pp; Japanese
                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85WO-JP000696
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ID AAN60624 standard; DNA; 456
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Best Local Similarity
Matches 101; Conservat
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(OHGA/) OHGAI H.
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29-OCT-1991
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ID AAN70833 standard; DNA; 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encodes beta-urogastrone under the control of a tac promoter. The peptide may be expressed from plasmid pUGT 150s in a transformed E.coli host. The plasmid may carry several separately expressing sequences comprising a tac promoter, SD site, signal peptide, and coding sequence, to produce beta-UG in high yield. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
 9
                                                                                                                                                                                                                                                                                                                                                                                                         Expression vector contg. multiple information units is used to transform host all for increased prodn. of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 1; Length 456; 100.0%; Pred. No. 2.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                   GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                    /*tag= b
/transl_except= (pos:434. .436,aa:Arg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                           GGGTTCCGCCCACATTCCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 553; 34pp; Japanese.
                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                      Sequence encoding beta-urogastrone.
                                                                                                                                                                                                                                                                                                                                                     86JP-00031415
                                                                                                                                                                                                                                                                                                                                   86JP-00031415
                                                                                        AAN71080/c
ID AAN71080 standard; DNA; 456
                                                                                                                                  (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                              .439
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                                                                                                                                                                                       pUGT 150s; beta-UG; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                       Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                JP62190083-A.
                                                                                                                                                                                                                                                                                                                                    14-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                     14-FEB-1986;
                                                                                                                                           10-MAR-2003
13-MAY-1991
                                                                                                                                                                                                                                                                                                                  20-AUG-1987.
                                                                                                                                    25-MAR-2003
                                                                                                                  AAN71080;
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                                                                              RESULT 6
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An example of a sequence detected by a probe consisting of polyinosine, polydeoxyinosine, oligoinosine and/or oligodeoxyinosine is labeled. The sens and probe are hybridized and the existence of DNA in the product is detected. It can be used to detect the presence of malignant tumour. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detection of DNA and/or RNA - by converting to single strand form and using probe contg. labelled inosine deriv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 11, 11pp, Japanese.
                                                                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                             Tumour; inosine; DNA probe;
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(first entry)
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209. .277
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                                                                                                                        Beta-urogastrone sequence
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Matches 101; Conservative
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209. .4
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                                                         revised)
                                          (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1986;
                                                                                                                                                                                                  Unidentified
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13-DEC-1990
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                                        25-MAR-2003
                                                             10-MAR-2003
                                                                               18-JAN-1991
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AAN70833;
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                                                                                                                                                                                                                                                           promoter
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RESULT 7

JP63012298-A

Synthetic

Key

(23)

19-JAN-1988.

30-JUN-1986; 30-JUN-1986;

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The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90366-ABA90520). The coding sequences and proteins are useful for identifying substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting the cell division cycle, or capable of inhibiting a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as (glomerulonephritis and rheumatoid arthritis), dermatological disorders (such as psoriasis), antiinflammatory, antifungal and antiparasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                    Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 466 BP; 135 A; 87 C; 93 G; 150 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 6;
Pred. No. 2.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                               Claim 1; Page 99; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Sci
100.0%; Pri
tive 0;
                                                                                                                                                                                           Glover DM, Midgley C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX21173 standard; DNA; 487 BP
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                                                                            23-MAR-2001; 2001WO-GB001297
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                                                                                                               24-MAR-2000; 2000GB-00007268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders (such as malaria)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
Les 101; Conservative
                                                                                                                                                                                                                              WPI; 2002-055132/07
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WO200172774-A2.
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                                      04-OCT-2001
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                                                                                                                                                                                           Deak P,
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요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The deriv. has various biological activities such as gastric acid secretion inhibiting action, or cell proliferation promoting action. The deriv. has the same biological or pharmacological activities as betaurogastrone. It is not susceptible to denaturation by oxidn. and is chemically stable. Deriv. has resistance to proteolytic enzymes such as protease. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New beta-urogastrone deriv. - has gastric acid secretion inhibition and proliferation promotion activity.
                Sequence of HB101 (pGH201) encoding new beta-urogastrone deriv. Met(21)
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                                                                        secretion; cell proliferation; hormone; ds
                                                                                                                                                                                                                                                  "New beta-urogastrone deriv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                 ocation/Qualifiers
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                                                                        Gastric acid
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12-FEB-2002

ABA90413;

RESULT 9 ABA90413/

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Query Match

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Length 466; Indels 9

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RESULT 11 AAX21149,

Length 535;

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Antiproliferative, cytostatic; cardiant; immunosuppressive; meiosis; antiinflammatory; antipooriatic; dermatological; antifungal; mitosis; antiparasitic; antimalarial; antirhumatic; antiarthritic; cell division; cell cycle progression protein; tumour; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90366-ABA90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as ciglomerulonephritis and rheumatorid arthritis), dermatological disorders (such as psoriasis), antiinflammatory, antifungal and antiparasitic
                                                                                                                                                     158 AGGCTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila cell cycle progression protein coding sequence #91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular; autoimmune; dermatological disorder; ds
                                                                                                                                                                                                    61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                              GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
                     Score 101; DB 2;
Pred. No. 2.7e-21;
                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Midgley C;
                                                                                                                                                                                                                                                                                                                                                               BP
                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
         Query Match
Best Local Similarity 100.(
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Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-055132/07
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                                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                 for the detection, diagnosis, characterisation, prevention and therapy of
T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 AGGTTATTGTCTCATGAGGGGATACATATTGAATGTATTTAGAAAAAATAAACAAATAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                            products
                                                                                                                                                                        AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                            New isolated Treponema pallidum nucleic acids - used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide sequence from the genome of Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                    Length 487;
                                                                                                                                                                                                                                                                                                                                       Sequence 487 BP; 125 A; 127 C; 113 G; 121 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 223
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                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 2; 100.0%; Pred. No. 2.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                           biosynthetic products such as enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1093; 1150pp; English.
                                                                                                                                   Claim 1; Page 1106; 1150pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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WPI; 1999-081273/07
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Gaps ö 9

Sequence 535 BP; 145 A; 108 C; 122 G; 155 T; 0 U; 5 Other;

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This invention relates to a novel method for the optimisation of primer libraries. Specifically, it refers to increasing the affinity of short oligonucleocide primers, also known as extendable oligos (EOs), for their template sequences. The present invention describes improved methods for sequencing and the linear and exponential amplification of DNA that can amplification, strand displacement amplification of DNA that can amplification. Accordingly, these extendable oligos with improved specificity and affinity are particularly important in fields ranging from biotechnology and agriculture to medical research. This polynucleotide sequence is the electropherogram of a DNA sequencing reaction that used the pUCL9 plasmid and B154/T422 oligos, used in an exemplification of the invention.
                                                                                                                                                                                                                                                                            ds; primer library; extendable oligos; EO; ligation chain reaction; LCR; xolling circle amplification; strand displacement amplification; isothermal DNA amplification; biotechnology; agriculture; medical research; pUCI9 plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Increasing the affinity of an extendable oligonucleotide (EO) for a target nucleic acid, for providing primers having improved specificity, comprises hybridization of the EO to a template oligonucleotide (TO) and
                                                                                                                                                                                                                                           Electropherogram of a DNA sequencing reaction using E154 & T422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 605 BP; 159 A; 133 C; 147 G; 148 T; 0 U; 18 Other;
                     295 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC
 GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 101; DB 12;
100.0%; Pred. No. 2.8e-21;
ive 0; Mismatches 0;
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                                                                                                                             ADH58311 standard; DNA; 605 BP
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                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extension of the EO
                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Escherichia coli.
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                                                                                                                                                                                                       25-MAR-2004
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                                                                                                                                                                  ADH58311;
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                                                                                          RESULT 13
                                                                                                             ADH58311
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GGGTTCCGCGCACATTCCCCCGAAAAGTGCCACCTGACGTC 101

61 319

Gaps

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0; Indels

Matches 101; Conservative

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Local Similarity

Query Match

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antianaemic; dernatological; immunosupressive; antinflammatory; antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic; osteogathic; prostate gland; prostatitis, adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative; ds.
                                                                                                  Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
                                                                           DNA encoding novel prostate gland antigen, Seq ID No 418.
          AAS30560 standard; DNA; 776 BP.
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2000US-0186350P.
2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
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2000US-0224518P.
2000US-0224519P.
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2000US-0225266P.
2000US-0225267P.
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                                                    21-NOV-2001 (first entry)
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AAS30560/
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06-SEP-2000; 2000US-0231242P.
08-SEP-2000; 2000US-0231242P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0232391P.
14-SEP-2000; 2000US-0232391P.
14-SEP-2000; 2000US-0232391P.
14-SEP-2000; 2000US-0232391P.
14-SEP-2000; 2000US-0232391P.
14-SEP-2000; 2000US-0232391P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233065P.
14-SEP-2000; 2000US-0233065P.
14-SEP-2000; 2000US-0233065P.
14-SEP-2000; 2000US-0233065P.
14-SEP-2000; 2000US-0234937P.
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2000US-0246475P.
2000US-0246476P.
2000US-0246477P.
2000US-0246477P.
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29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
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2000US-0240960P.
2000US-0241221P.
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2000US-0241786P.
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2000US-0246524P.
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
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26-SEP-2000;
27-SEP-2000;
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29-SEP-2000;
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08-NOV-2000;
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The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prognosis, procedution, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, prostatodystonia, prostatous prostatuous prostatitis, malacoplakia, benign prostatic non-bacterial prostatitis, prostatodystonia, prostatous, granulomatuus prostatitis, malacoplakia, benign prostatic chromas, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. (I), (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget si disease), attritis), blood-related disorders (sickle cell anaemia), hyperproliferative disorders (sickle cell anaemia), hyperproliferative disorders (sickle cell anaemia), respiratory disorders (musculomephritis), cardiovascular disorders (arrhythmias), respiratory disorders musculoskeletal system disorders (arrhythmias), respiratory disorders (Addison's disease and Parkinson's disease), endocrine disorders (Addison's disease and Parkinson's disease), condocrine disorders (Addison's disease and Parkinson's disease), condocrine disorders, liver disorders (biliary liver cirrhosis), condomined and shorders (biliary liver cirrhosis), condomined and inherited disorders (diseases at the cellular level, and wound healing and epithelial cell proliferation. (I) or (II) and organs before transplantation, and as food additive or preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated prostate gland related polypeptide useful for diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM
                                2000US-0249264P.
2000US-0249265P.
2000US-0249297P.
2000US-0249299P.
2000US-0249300P.
2000US-0250160P.
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2000US-0251988P.
2000US-0256719P.
2000US-0251479P.
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2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
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2000US-0254097P
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01-DEC-2000;
01-DEC-2000;
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05-DEC-2000;
06-DEC-2000;
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AAS27819 standard; DNA; 776 BP

AAS27819/ ID AAS27 RESULT 15

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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; ds; acquired immune deficiency syndrome.
                                                 DNA encoding novel signal transduction pathway protein, Seg ID 1479
                                                                                                                                                                                                                                                                       2000US-0179065P.
2000US-0180628P.
2000US-0184664P.
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2000US-0231244P
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                              07-NOV-2001 (first entry)
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08-SEP-2000;
08-SEP-2000;
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          AAS27819;
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2000US-0237039P.
2000US-0237040P.
2000US-0239935P.
2000US-0239937P.
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2000US-0246477P.
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2000US-0249264P.
2000US-0249265P.
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2000US-0246611P.
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2000US-0249216P.
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27-SEP-2000;
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The invention relates to novel isolated polypeptides (I), and diagnostice (II). (I), (II) and the antibody to (I) are useful for diagnosticy, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital and acquired immunodeficiencies, autoimmune confusing, properties (e.g. repeating disorders, haemoglobin abnormalities and cother blood-related disorders (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and cother blood-related disorders (e.g. disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (e.g. Alzheimer's disease, Parkinson's (e.g. stroke), renal disorders (e.g. arrythmia), respiratory disorders, dermatological disorders (e.g. Addison's epithelial cell proliferation, endocrine disorders (e.g. Addison's epithelial cell proliferation, endocrine disorders (cirrhosis), as stimulators of disease), reproductive system disorders (cirrhosis), as stimulators of theses, higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction pathway protein coding sequences and PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1479; 880pp; English
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                                                                           01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025198P.
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1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60

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0; Mismatches

Matches 101; Conservative

Search completed: July 14, 2005, 07:01:48 Job time : 142.448 secs

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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMARIES	GI	BM078095	BU963956	BU964094	FR0009140	AL597149	CC819240	BJ684174	CC819923 .	B1805285	CC818374	CC818523	CC819854	CC817752	CC817128	CC817162	CC817796	CC819067	CC819841	CC816892	CR766622	CC816905	CC819058	CC819270	CC816848
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Generation and analysis of 25 Mb of genomic DNA from the pufferfish Rugu rubripes by sequence scanning Genome Res. 9 (10), 960-971 (1999)
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Submitted (19-SEP-1997) MRC Human Genome Mapping Project Resource Centre Hintxon, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk

V_type: phagemid
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F.rupripes GSS sequence, clone 010H20aC4, genomic survey sequence.
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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Agaricales; Cortinariaceae; Hebeloma.
1 (bases 1 to 300)
Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and
Frommer, W.B.
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Site_2: XhoI"
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/tish hoste"E. coli XLI-Blue"
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library"
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                                                                                                                                                                                            Contact: Wipf D
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
Fax: 49 7071 293287
Email: daniel.wipf@zmbp.uni-tuebingen.de
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/organism="Hebeloma cylindrosporum"
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GSS, genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
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Agaricales; Cortinariaceae; Hebeloma.
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     A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis.
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library:
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homolog to Enterobacteria phage fl ; ampicillinase (le-10)
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Contact: Wipf D
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
Fax: 49 7071 291287
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Emil s. Wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 bp mRNA linear EST 04-SEP-2003 nonym: hlcc2) Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                           39 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 391)
Koehrer, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S. EST (Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hlcc2)"
Site_1: SfiIA; Site_2: SfiIB;
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No s1 sequence available.
No s1 sequence available.
This clone (DKFZp313J611) is available at the RZPD in Berlin.
Please contact.
Berlin-Charlottenburg, GERNANY; Email: clone@rzpd.de.
Location/Qualifiers
One pass dye-terminator sequencing of cosmid cloned genomic
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                                                                                                                                                                                                                Length 309;
                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                     61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                              100.0%; Score 101; DB 9;
100.0%; Pred. No. 8.2e-19;
ive 0; Mismatches 0;
                                                                      /organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="010H20aC4"
/clone=lib="cosmid 010H20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="313 (synonym:
/note="Vector: pTriplEx2;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313J1611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKFZp313J1611 rl 313 (synonym: h
DKFZp313J1611 5', mRNA sequence.
                                      Location/Qualifiers
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALS97149.1 GI:15154845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
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Best Local Similarity
Matches 101; Conserv
                    sequence.
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1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60

Matches 101; Conservative

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/done="trackloomers."
//done="trackloomers."
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone="top-color: PWD42nv; Purified macronuclear chromosomal
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gil4732114|gp|AF125072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 AGGGTTATTGTCTCATGAGGGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella.

1 (bases 1 to 414)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                             CC819240
414 bp DNA linear GSS 17-JUJ 100005D19R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC10005D19 R, genomic survey
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                                                                                                                                                 288 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sterkiella histriomuscorum"
                                                                                                          61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Plate: 0005 row: D column: 19
Sed 'primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:94289"
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Location/Qualifiers
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Fax: 801 585 7177
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Oryza sativa
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                                                                                                                                                    SM Haplochromis chilotes

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;

Labroidei; Cichlidae; Haplochromis.

E 1 (bases 1 to 417)

S Watanabe, M., Kobayshi, N., Shin-i, T., Kohara, Y. and Okada, N.

Orf sequences of cichlid in Lake Victoria are essentially same

L Unpublished (2004)

Contect: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan
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                    BJ684174 BJ684174 HCEST library Haplochromis chilotes cDNA clone no90c12,
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84112, USA
Tel: 801 585 5606
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Sterkiella histriomuscorum
Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichida; Oxytrichidae; Sterkiella.

1 (bases 1 to 491)
Dun,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax Unpublished (2003)
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100006J13R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC10006J13 R, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Haplochromis chilotes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="jaw"
/dev_stage="varied"
/clone_lib="HCEST_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:257977"
/clone="no90c12"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                              BJ684174.1 GI:46527295
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                                                                                                                                      Haplochromis chilotes
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                                                          mRNA sequence.
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Enhartoideae; Oryzae.

Enhartoideae; Oryzae.

In Chases 1 to 455;

Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Tang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.

A Gene Expression Screen in Oryza sativa

In Unpublished (2001)

Contact: Haitao Dong, Debao Li

Bioinformatics and Gene Network Research Group
Zhejiang University

Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86882051
Fax: 0086-571-86882051

Rax: 0086-571-86882051

Rax: 0086-571-86882051

Rax: O086-571-86882051

Rax: O086-571-86882051

Rax: O086-571-86882051

Rayiner: M13 forward primer.
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S035A01 Stem library from Oryza sativa (3-5 leaf stage) Oryza
sativa cDNA clone S035A01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 353
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100.0%; Score 101; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 8.4e-19;
Matches 101; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                               organism="Sterkiella histriomuscorum"
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                                             Plate: 0006 row: J column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                            High quality sequence stop: 491
Email: ddunn@genetics.utah.edu
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BI805285.1 GI:15852489
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Pred. No. 8.4e-19;

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Best Local Similarity 100.
Matches 101; Conservative
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DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gil4732114|gb|AR129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                    CC818374 17-JUL-2003 100004B07R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC100004B07 R, genomic survey
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Sterkiella histriomuscorum
Sukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichiaa; Oxytrichidae; Sterkiella.

1 (Dases 1 to 495)
Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
                                                                                                                                                                          Gaps
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                                                                                                                                     Length 495;
                                                                                                                                   Score 101; DB 4; Length 4
Pred. No. 8.4e-19;
Mismatches 0; Indels
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University of Utah Genome Center
University of Utah
University of Utah
Rm. 30 biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                 122 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 162
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Plate: 0004 row: B column: 07
Seq primer: CACACAGGAAACAGCTATGACC
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High quality sequence stop: 495.
Location/Qualifiers
  tissue_type="Stem"
                                                                                                                100.0%; Scor
100.0%; Prev
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100.0%; Score 101; DB 9; Length 495;

Query Match

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/clone="textoronous plasmid UGCIO library."
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                                                                                                     Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Bukaryota; Alvoolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 496)
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100004L13R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100004L13 R, genomic survey
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Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclar chromosomes
Unpublished (2003)
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Best Local Similarity 100.0%; Pred. No. 8.4e-19;
Matches 101; Conservative 0; Mismatches 0;
                                             Mismatches
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Plate: 0004 row: L column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends ends
High quality sequence stop: 496.
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University of Utah Genome Center
University of Utah
100.0%; F1.
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CC818523.1 GI:32897943
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Fax: 801 585 7177
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// Clone lib="Morytricha plasmid UNGC10 library"
// Clone lib="Worytricha trifallax was blunt end-repaired with DNA from Oxytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pWM42 (gi|473114|qb|AF129072.1), a copy-number inducible derivative of plasmid R1 The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Sterkiella histriomuscorum
Eukaryota, Alveolata, Ciliophora, Spirotrichea; Stichotrichia,
                                                                                                                                                                                                Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 515)
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     histriomuscorum genomic clone UUGC100003C16 R, genomic survey
                                                                                                                                                                                                                                                                               Dunn, D., Doak, T., Herrick, G. and Weiss, R. Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes Unpublished (2003)
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                                                                                                                                                 Sterkiella histriomuscorum (Oxytricha trifallax)
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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CC817128.1 GI:32896415
GSS.
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/lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Coxytricha plasmid UUGCIO library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Sterkiella histriomuscorum
Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella
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Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2002)
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/organism="Sterkiella histriomuscorum"
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61 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 101
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Plate: 0006 row: N column: 08
Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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High quality sequence stop: 503.
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Fax: 801 585 7177
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Search completed: July 14, 2005, 23:23:20
Job time : 962.667 secs
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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/clone lib="Oxytricha plasmid UUGC10 library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible
adaptors complementary to the insert adaptors and
purified The sheared, adaptored mouse DNA was annealed to
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Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichida, Stichotrichidas, Oxytrichidae, Sterkiella.
1 (Dases 1 to 519)
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Stichotrichida, Oxytrichidae, Sterkiella.
1 (bases 1 to 518)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
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Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes
Unpublished (2003)
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
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Location/Qualifiers
                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Best Local Similarity 100.
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/lab host="E. Col; strain XL10-Gold, T1-resistant, F-"
/lab host="E. Col; strain XL10-Gold, T1-resistant, F-"
/clone lib="Corytricha plasmid UUGCIO library"
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DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide Kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                             Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                     Tel: 801 585 5606
Pax: 801 585 7177
Email: ddunn@genetics.utah.edu
Plate: 0002 row: J column: 19
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Class: plasmid ends
High quality sequence scop: 519.
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84112, USA
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: July 14, 2005, 04:39:07 ; Search time 749.127 Seconds (without alignments) 6468.225 Million cell updates/sec
Title: US-09-482-682-65_COPY_1_100 Perfect score: 100 Sequence: 1 ctgctccctgcttgtgtgttcaattgcatgaagaatctgc 100
Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466
Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AR20783 Sequence
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AX6039191 Sequence Description SUMMARIES AX175195 AX775195 AX775195 AX775195 AX775195 BD107647 AX643582 AX64425 AX64426 AX64426 AX64426 AX61426 AX613038 AR698190 AR60783 AR60783 AR60783 AR122289 PCDNA3ZEO AR098191 AR207833 AX643583 a Length DB 562 633 648 648 1070 1070 2245 2427 2427 3853 3853 3853 3925 3925 4026 4026 Query Match 100.0 100.0 100.0 100.0 100.0 100.0 100.0 Score Result No.

BD009730 Tissue sp AR071324 Sequence AR078192 Sequence AR207814 Sequence BD009731 Tissue sp AR3214 Sequence 58 AX286570 Sequence AX743954 Sequence AX743954 Sequence AX060344 Sequence AX060345 Sequence AX133940 Sequence AR071323 Sequence BD23491 Sequence AN234391 Sequence AN234391 Sequence BD234590 Screening AX262621 Sequence BD19573 Cloning vec BD234590 Screening AX319664 Sequence BD195386 Compositi AX319694 Sequence BD195386 Compositi AX319694 Sequence BD195386 Compositi AX319694 Sequence	DNA linear PAT 24-FEB-2003	Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus. J. ein in cells which inducibly express in, p21 :-2002; "DNA" irus LTR promoter"	100.0%; Score 100; DB 6; Length 562; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGACGAAATTTAAGCTACA 60	VRL 28-1 LTR on 215
6 AR071324 6 AR071324 6 AR071324 6 AR071334 6 BD009731 6 AA38214 6 AX743954 6 AX743954 6 AX74394 12 SYNRSV5GPT 6 AX13394 6 AR024391 6 AR024391 6 AR024391 6 AR024391 6 AR024391 6 AR024391 6 AX13394 6 BD085110 12 SYNRSV5NEO 6 AX324391 6 BD085110 6 AX31669673 6 AX31669673 6 AX31669673 6 AX31669673 6 AX31669673 6 AX31669673 6 AX316694 12 SYNRSV5NEO 6 AX316694 12 SYNTCRC	ALIGNMENTS 562 bp Dk n Patent W002099100.	rdata, Crani entia; Sciur eworth,J. a protein; T protein; DEC-2002 fiers sp." sp." n:10095"	milarity 100.0%; Score 100; DB 6; I Conservative 0; Mismatches 0; TGCTCCCTGCTTGTGTTTGAGGGTCGCTGAGTAGTGCGGTGCCTGAGTAGTGCGCTGAGTAGTGCGCTGAGTAGTGCGCTGAGTAGTGCGTTGCGTTGAGTGCGTTGCGTTGAGTGCGTTGCGTTGAGTGCGCTGAGTGCGCTGCTGCCTGC	633 bp ss-RNA linear s (Schmidt-Ruppin), proviral, 3'
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0 000000000000000000000000000000000000	RESULT 1 AX643583 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES	ORIGIN  Query Match Best Local 8 Matches 101 Oy 1 Db 46 Oy 61 Db 106	RESULT 2 ALRPROLTB LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

ORGANISM

AUTHORS TITLE

REPERENCE

MEDLINE PUBMED

JOURNAL

AUTHORS

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FEATURES

RESULT 3 AX175190 LOCUS

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Rivera,V., Zoltick,P. and Wilson,J.M.
Methods for expression of genes in primates
Patent: WO 0142444-A 1 14-UUN-2011,
ARIAD GENE THERAPEUTICS, INC. (US) ; THE UNIVERSITY OF PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rivera, V., Zoltick, P. and Wilson, J.M. Methods for expression of genes in primates Patent: WO 0142444-A 6 14-JUN-2001; ARIAD GENE THERAPEUTICS, INC. (US); THE UNIVERSITY OF PENNSYLVANIA (US)
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    .648
    .0xganism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="vector/RSV promoter/vector"

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/db_xref="taxon:32630"
/note="Mlu1/RSV promoter/Bgll"
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AX175195 GI:14598586
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AX175190.1 GI:14598581
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[1] sites; mRNA start.
Original figure in [2] included 24 'g's on 5' end and 16 'c's on 3' end that were cDNA synthesis artifacts.

[2] also sequenced a defective clone, pSR2, with the src gene deleted (see separate entry).

[1] demonstrated the mRNA transcription initiation site shown in the Sites table using pSR1 as a template. However, this is the 3' LTR, and the functional mRNA start site would be assumed to be on the 5' LTR at the homologous site.

Location/Qualifiers
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Yamamato,T., Jay,G. and Pastan,I.
Unusual features in the nucleotide sequence of a cDNA clone derived
from the common region of avian sarcoma virus messenger RNA
Proc. Natl. Acad. Sci. U.S.A. 77 (1), 176-180 (1980)
                                                                                                                                        Yamamoto, T., de Crombrugghe, B. and Pastan, I.
Identification of a functional promoter in the long terminal repeat
of Rous sarcoma virus
Cell 22 (3), 787-797 (1980)
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                                                                                                                                                                                                                                                                                                  (amamoto, T., Tyagi, J.S., Fagan, J.B., Jay, G., deCrombrugghe, B. and
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J02025 J02022
J02025.1 GI:210255
c-myc proto-oncogene; long terminal repeat (LTR); src oncogene.
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                                                               Rous sarcoma virus
Rous sarcoma virus
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus
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/mol_type="genomic RNA"
/db_xref="taxon:11886"
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/note="3' LTR"
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Method of production of a protein in cells which inducibly express
the cell cycle inhibitor protein, p21
Patent: WO 02099100-A 1 12-DEC-2002;
Lonza Biologics plc (GB)
                                                              77 CTGCTCCCTGCTTGTGTTGTGTGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 136
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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/db_xref="taxon:10095"
/noce="RSV-LTR promotor + intron + p21 cds + TKpoly(A)
/acswitch II expression construct"
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AstraZeneca AB (SE); THE VICTORIA UNIVERSI
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AX044426
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/organism="Mus sp."
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115-JAN-2002
110-MAR-1999 UP 1998539351
11-MAR-1997 GB 9704977.9
JAMES CHARLES NEIL, MARK ALAN RIGHY, JAMES OSWALD JARRETT
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                                                                                                                                                                                                                                                                                                                              100.0%; Score 100; DB 6; Length 1070; 100.0%; Pred. No. 2.8e-25; ive 0; Mismatches 0; Indels 0
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CC CWV PROMOTER FROM DCDNA3(a Bgl II - Kpn
I restriction fragment)
CC SST I - SST I FRAGMENT IN PLASMID CMV DEL. RT CC
FROM THE t-RNA PRIMER BINDING
SITE TO THE VIRAL S8t
CC IS

    1070 / Organism='Artificial Sequence'

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other sequences; artificial sequences.

1 (bases 1 to 1070)
Neil,J.C., Rigby,M.A. and Jarrett,J.O.
Parv vaccine
Part vaccine
THE UNIVERSITY COURT OF THE UNIVERSITY OF GLASGOW
OS Artificial Sequence
                                                                                                                                                                   Patent: WO 9840493-A 6 17-SEP-1998;
RIGBY MARK ALAN (GB); JARRETT JAMES OSWALD (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                       /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Sequence 6 from Patent WO9840493.
A85308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1070 bp
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Rigby, M.A. and Jarrett, J.O.
FIV VACCINE
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                                       A85308.1 GI:6733916
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synthetic construct
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Matches 100; Conservative
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                                                                                                                                                                                                                       1. .1070
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unclassified.
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Best Local Similarity
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BD107647
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3030 CTGCTCCCTGCTTGTGTGTGGGGGTCGCTGAGTAGTGGCGGGGGAGCAAAATTTAAGCTACA 3089
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                     Long, B.O.
HLA class II-restricted presentation of cytoplasmic measles virus antigens to cytotoxic T cells
J. Virol. 63 (4), 1756-1762 (1989)
89178863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (27-FEB-1999) Zeng B.J., Gene Engineering Center,
Institute of Microbiology, Zhongguancun, Beijing, Beijing 100080,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CIGCICCCIGCTIGIGIGIGITGAGGICGCIGAGIAGIGCGCGAGCAAAATTIAAGCIACA
                                                                                                                                                                                                                                                                                                          912. .3029 - /function="ampicillin-resistance, replication origin"
   Jacobson, S., Sekaly, R.P., Jacobson, C.L., McFarland, H.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zeng,B.J.
Mammalian Expression Vector for with fuse Xanthine-guanine
phosphoribosyl transferase Tag
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 100; DB 12; Length 3557; Best Local Similarity 100.0%; Pred. No. 3.2e-25; Matches 100; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                            cloning vector"
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/organism="Expression vector pCDPT"
/mol_type="other RNA"
/db_xref="taxon:90749"
209. .863
                                                                                                                                       DNA.
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882. .984
/note="Multiple cloning site
                                                                                                                           source text: Cloning vector
Location/Qualifiers
1. ,3557
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                                                                                                                                                                                  /organism="unidentified
/mol_type="genomic DNA"
/db_xref="taxon:45196"
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/standard_name="5'LTR of
/citation=[2]
/evidence=experimental
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/function="polylinker"
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864. .882
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EVE132038
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                                                                                                      69 CTGCTCCCTGCTTGTGTGTGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 128
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                                                                            1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemical compounds
Patent: WO 0066752-A 17 09-NOV-2000;
Astrazeneca AB (SB) 7 THE VICTORIA UNIVERSITY OF MANCHESTER (GB)
Location/Qualifiers
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1...2427
1...2427
|mol_type="unassigned DNA"
|/db_xref="texon:32630"
|/note="CFG2 mutant with last exon of Thy-1 fused at 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
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High efficiency DNA-mediated transformation of primate cells
Science 221 (4610), 551-553 (1983)
83249156
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 100.0%; Score 100; DB 6; Length 2426; 100.0%; Pred. No. 3.1e-25; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                          linear
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unidentified cloning vector
unidentified cloning vector
other sequences; artificial sequences; vectors.
(sites)
                                                                                                                                                       61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
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100.0%; Pred. No. 3.1e-25;
ive 0; Mismatches 0;
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Sequence 17 from Patent WO0066752.
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New Ml3 vectors for cloning
Meth. Enzymol. 101, 20-78 (1983)
83296918
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Matches 100; Conservative
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PC
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PN J2-MAR-2001
PF 13-NOV-1997 JP 1998522958
PR 15-NOV-1996 US 08/7517,14-FEB-1997 US 08/707121/04,0775/00,A61K38/00,A61K35/12
CC 707121/04,C07K5/00,A61K38/00,A61K35/12
CC Strandedness: Single;
CC Strandedness: Single;
FH Key Loostion/Qualifiers
FT CDS 209: .862.
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Tissue specific expression of retinoblastoma protein.
BD009729
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Antelman,D., Gregory,R.J. and Wills,K.N.
Tissue specific expression of retinoblastoma.protein
Patent: JP 2001503638-A 3 21-MAR-2001;
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                                                                    141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
                                61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
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100.0%; Pred. No. 3.3e-25;
ive 0; Mismatches 0;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379297-A 5 30-APR-2002;
Location/Qualifiers
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                                                                                                                                                                                                                        AR207832 3853 bp
Sequence 5 from patent US 6379927.
AR207832
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1649. .1863
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LRSALPAGWFIADKSGAGERGSRGIIAALGPGCKSRIVVIYTGSQATMDERNRQIA
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Matches 100; Conservative 0; Mismatches 0;
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Antelman,D., Gregory,R.J. and Wills,K.N.
Retinoblastoma tusion polypeptides
Patent: US 6074850-A 5 13-JUN-2000;
Location/Qualifiers
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AR098190
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db_xref="GI:5640090"
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note="SP6"
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Matches 100; Conservative 0; Mismatches 0; Indels 0
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Patent: WO 97083334 9 06-MAR-1997,
CANCER RES CAMPAIGN TECH (GB)
Location/Qualifiers
1. .3925
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Best Local Similarity 100.0%; Pred. No. 3.3e-25; Matches 100; Conservative 0; Mismatches 0; Indels
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Sequence 9 from Patent WO9708330.
A60213.
A60213.1 GI:3715221
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July 14, 2005, 04:35:42; Search time 140.988 Seconds (without alignments) 4198.742 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Title: Perfect score: Sequence: Scoring table: Searched:	US-09-482-682-65_COPY_1_100  100  1 ctgctccctgcttgtgtgttcaattgcatgaagaatctgc 100  IDENTITY_NUC Gapop 10.0 , Gapext 1.0  4390206 segs, 2959870667 residues
Total number of	Total number of hits satisfying chosen parameters: 8780412

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

geneseqn2001bs:\* geneseqn2003bs:\* geneseqn2003cs: geneseqn2003ds: geneseqn2001as:\* geneseqn2003as:\* geneseqn2002as: N\_Geneseq\_16Dec04: geneseqn1990s:\* geneseqn2002bs: geneseqn2004bs geneseqn2000s:\* geneseqn1980s: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Abz23250 Nucleotid Aah49951 Rous sarc Aav88058 Plasmid C Adm41035 Fungus nu Adh11349 Vertebrat Adm41037 Cytomegal Abz23249 Lac repre Adm41036 Cytomegal Aad02037 Plasmid p Aat62937 3F4 human Aat62937 3F4 human Aat62937 3F4 human Aat62937 3F4 human Aat62937 3F4 plusmid p Aat90695 Plasmid p Aat90696 Plasmid p	Aag62391 Vector pV Aas17704 Vector pV
SUMMARIES	ABZ23250 AAH43951 AAV58058 AAV58058 ADH11349 ADH11349 ADH41034 ADH41034 ADD23249 AADD2036 AAT62937 AAV40006 AAT90695 AAV40007	AAQ62391 AAS17704
DB	8471741814401000000 0 70 0	9
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Abn83143 Plasmid p Add35599 Bicistron Aav69746 Nucleotid Aaf24901 Nucleotid	AATLA380 VECCOT pm AAE83146 COmplete AAQ75973 pHLA-B7/b AAD33528 Expressio AAZ38633 pEP2 expr	Adhilii Plasmid p Adfl0526 Plasmid p Acc44637 Murine rD Ad75099 Plasmid p Abk88869 Topoisome Ade83792 Plasmid p	Ado06721 Recombina Ac46692 Plasmid p Aat62933 2A2 human Abv77540 Plasmid p Abv77547 Plasmid p Abv77548 Plasmid p Abv77548 Plasmid p Abv77549 Plasmid p Abv77549 Plasmid p Abv77549 Plasmid p Abv77549 Plasmid p
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## ALIGNMENTS

p21; RSV; LTR promoter; cell cycle inhibitor protein; protein production; anchorage-independent producer cell line; ss. Nucleotide sequence of the Rous sarcoma virus (RSV)-LTR promoter. ABZ23250 standard; DNA; 562 BP. 03-JUN-2002; 2002WO-EP006054. Al-Rubeai M, Shuttleworth J; 01-JUN-2001; 2001GB-00013318. (LONZ ) LONZA BIOLOGICS PLC. (first entry) Rous sarcoma virus. WO200299100-A2. 24-MAR-2003 12-DEC-2002. ABZ23250; RESULT 1 ABZ23250 

Producing recombinant protein, particularly for maximizing or enhancing e.g. therapeutic protein production, by co-expressing protein with recombinant cell cycle inhibitor protein (p21) in producer cell line.

WPI; 2003-148669/14.

Disclosure; Page 32-33; 33pp; English.

promoter. The present sequence is used to produce vectors for use in the method of the invention. The specification describes a method for producing a protein, preferably a recombinant protein, in a mammalian anchorage-independent producer cell line. The method comprises coexpressing with the protein in the producer cell line a recombinant cell cycle inhibitor protein (preferably p21). The method is useful for producing a recombinant protein in a producer cell line. This is The present sequence represents the Rous sarcoma virus (RSV)-LTR

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Gaps

; 0

Indels

Length 648;

Score 100; DB 4; Pred. No. 8.6e-28; 0; Mismatches

100.0%;

9

1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA

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Sequence 648 BP; 163 A; 135 C; 179 G; 171 T; 0 U; 0 Other;
                                                                  Query Match
Best Local Similarity 100.
Matches 100; Conservative
     present invention
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                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for genetically engineering a primate for expression of a desired gene comprising introducing into the primate a transgene comprising an Rous Sarcoma Virus (RSV) promoter and a nucleic acid sequence heterologous to RSV promoter. Also described is a primate cell (I) containing and capable of expressing a transgene comprising an RSV promoter operably linked to a recombinant nucleic acid encoding one or more fusion proteins, where the fusion proteins bind to a ligand and in the presence of the ligand modulate(s) the expression level of a target gene. The method can be used for high level expression of genes in primates or for engineering primate cells. It is useful for increasing the efficacy of many gene therapy strategies, and for increasing the efficacy of intracellular immunisation agents, molecules
                                                                                                                                                                    1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetically engineering a primate for expression of a desired gene, comprises introducing into the primate a transgene comprising Rous Sarcoma Virus (RSV) promoter and a nucleic acid sequence heterologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rous sarcoma virus; promoter; enhancer; RSV; primate; gene expression; transgene; genetic engineering; gene therapy; immunisation; ds.
particularly useful for maximizing or enhancing the production of e.g. therapeutic proteins at an industrial scale
                                                                                                                     Gaps
                                                                                                                   ;
0
                                                                                   DB 8; Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                virus promoter nucleotide sequence SEQ ID NO:1.
                                                   Sequence 562 BP; 143 A; 109 C; 163 G; 147 T; 0 U; 0 Other;
                                                                                                                   Indels
                                                                                                                                                                                                                  61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                       106 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 145
                                                                               100.0%; Score 100; DB 8; 100.0%; Pred. No. 8.2e-28; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ARIA-) ARIAD GENE THERAPEUTICS INC. (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-2000; 2000WO-US033256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0170019P
                                                                                                                                                                                                                                                                                                                                 AAH43951 standard; DNA; 648
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zoltick P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-381673/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rous sarcoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200142444-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rous sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSV promoter
                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rivera V,
                                                                                                                                                                                                                                                                                                                                                                 AAH43951;
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This is the nucleotide sequence of a SatI fragment of plasmid CMV-delRT, in which the immediate-early promoter of human cytomegalovirus replaces the 5' long termal repeat region of feline immunodeficiency virus (FIV) clone F14-delRT (see AAV88053). FIV sequences downstream of the SatI site are identical to those in F14-delRT. Use of the CMV promoter was designed reversion to a replicating provirus, in tissues after incculation of DNA. Vaccine formulations for FIV-related diseases include a defective feline
90 CTGCTCCCTGCTTGTGTGTGTGGGGGCCCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 149
                                                                                                                                                                                                                                                                      FIV; FIPV; vaccine; reverse transcriptase; diagnosis; therapy; CMV-delRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       promoter fragment from pcDNA3 (BglII-KpnII)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protecting, e.g. cats, against feline immunodeficiency virus - by using vaccine comprising FIV pol gene containing deletion and/or insertion in reverse transcriptase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunodeficiency proviral (FIPV) polynucleotide comprising an in-frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences from primer binding site to SstI
                                              150 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 189
                           61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                     Plasmid CMV-delRT SstI fragment.
                                                                                                                                  AAV58058 standard; DNA; 1070 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jarrett JO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 4; 66pp; English.
                                                                                                                                                                                                                                                                                                                             eline immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             _ag= b
/note= "FIV s
site"
                                                                                                                                                                                                                                                                                                                                                                                       8. .896
/*tag= a
/note= "CMV p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97GB-00004977
                                                                                                                                                                                                                                                                                                                                                                                                                                  918. .1070
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rigby MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIU ) UNIV GLASGOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-520813/44.
                                                                                                                                                                                                                                                                                       promoter; cat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09840493-A1
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11-JAN-1999
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                                                                                                                                                               AAV58058;
                                                                                                                                                                                                                                                                                                                                              Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neil JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                       provirus
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like ribozymes, antisense RNA, and dominant negative proteins, that act either stoichiometrically, or by competition. The method increases the efficacy of many gene therapy strategies by substantially elevating the expression of an exogenous therapeutic gene, and allowing expression to reach therapeutically effective levels. The present sequence represents specifically claimed RSV enhancer/promoter nucleotide sequence from the

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deletion and/or insertion in the reverse transcriptase (RT) region of pol gene. Host cells comprising the FIPV are capable of producing FIV processins, except for functionally competent RT, and thus release non-infectious FIV viral particles. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                     1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                                                                                                                                                       Gaps
                                                                                                                                                                       .;
0
                                                                                                                                   Score 100; DB 2; Length 1070; Pred. No. 1e-27;
                                                                                                  Sequence 1070 BP; 275 A; 254 C; 268 G; 273 T; 0 U; 0 Other;
                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                         61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                             137 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 176
                                                                                                                   100.0%; Scor.
100.0%; Pred. No. r.
...
0; Mismatches
                                                                                                                                                                    Matches 100; Conservative
                                                                                                                                                   Local Similarity
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                                                                                                                                     Query Match
                                                                     field.)
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Fungus nucleotide sequence SEQ ID NO:3. ADM41035 standard; DNA; 1506 BP (first entry) 17-JUN-2004 ADM41035; ADM41035 RESULT 

engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; fungus; gene; ds.

Unidentified

WO2004027029-A2.

01-APR-2004.

17-SEP-2003; 2003WO-US029251.

19-SEP-2002; 2002US-0411790P.

(XIME-) XIMEREX INC

Thompson SC; Beschorner WE, Sosa CE,

WPI; 2004-295402/27.

Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.

Disclosure; SEQ ID NO 3; 48pp; English.

The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destrucying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the specification

Seguence 1506 BP; 454 A; 277 C; 361 G; 414 T; 0 U; 0 Other;

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The present invention describes a vertebrate protein homologue of an UNC-53 protein of Caenorhabditis elegans or a functional equivalent, derivative or bioprecursor of UNC-53. Also described. (1) a cDNA sequence concoling a vertebrate homologue of the C. elegans UNC-53 protein; (2) a nucleic acid which hybridises to the cDNA of (1); (3) vector comprising the cDNA as in (1); (4) a host cell containing the vector as in (3); (5) a transgenic cell; tissue or animal comprising the vector as in (3); (6) a compound identified as an enhancer or inhibitor of the regulation of cell shape, motility, or the direction of cell migration for use as a therbod for determination of whether a protein is an inhibitor or enhancer of regulation of cell behaviour, growth, shape or motility or the direction of migration by contacting a host cell computed of UNC-53 and determining a change of phenotype; (8) a method for identification of vertebrate homologues of C. elegans unc-53 gene by hybridising a probe of 15-50 by of the unc-53 sequence to a DNA library; and (9) a method for identification of a protein which is
                                        ö
                                                                                                              81 CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGGAGCAAAATTTAAGCTACA 140
                                                                            9
                                                                          1 CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.g. promoting neuronal regeneration, treating chronic neuro-degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                UNC-53 vertebrate protein homologue; UNC-53; Caenorhabditis elegans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Verhasselt P;
Vandekerckhove JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell shape regulator; cell motility regulator; cell migration; cell behaviour regulator; phenotype; signal transduction pathway; signal transduction pathway; neuronal regeneration; signal integrator protein; neuronal regeneration; revascularisation; wound healing; chronic neurodegenerative disease; acute traumatic injury;
                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrate UNC-53 protein homologue related nucleotide sequence.
                                      .
0
  Length 1506;
                                      Indels
                                                                                                                                                                          141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
                                                                                                                                                    61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
  Score 100; DB 12;
Pred. No. 1.2e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CM, Deraeymaeker M,
Luyten W, Geerts H,
                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases or acute traumatic injuries.
                                                                                                                                                                                                                                                                                         ADH11349 standard; DNA; 1600 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platteeuw CJ, Buesa Arjol CM,
Pujol NJR, Maertens LJS, Luyt
Geysen J, Bogaert TAOE;
  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibrotic disease; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                    11-MAR-2004 (first entry)
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (JANC ) JANSSEN PHARM NV.
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                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
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Query Match
Best Local Simi
Matches 100;
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active in the signal transduction pathway of a cell of which a vertebrate homologue of UNC-53 is a component comprising: (i) contacting an extract of a cell with an antibody to the UNC-53 homologue; (ii) identifying an antibody/homologue complex; and (iii) analysing such a complex to identify any non-antibody protein bound to the complex. UNC-53 is a signal transducing or signal integrator protein involved in controlling directionality of cell migration and cell shape in C. elegans. Vertebrate homologues of UNC-53 can be used to promote neuronal regeneration, revascularisation or wound healing, to treat chronic neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
                                                                                                                                                                                                                                                                                                                     CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 140
                                                                                                                                                                                                                                                                                      9
                                                                                                                                           diseases or acute traumatic injuries or fibrotic diseases. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                      1 CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA
                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                      100.0%; Score 100; DB 2; Length 1600; 100.0%; Pred. No. 1.2e-27; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                         Sequence 1600 BP; 397 A; 409 C; 398 G; 396 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                  141 ACAAGGCATGACCGACAATTGCATGAAGAATCTGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytomegalovirus nucleotide sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM41037 standard; DNA; 1782
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                                                                                                                                                                                                                                                     100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (XIME-) XIMEREX INC
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004027029-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-2004
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                                                                                                                                                                                                                                                       crecrecerecrisererefregaderescrearagreceseseaaaarrraascraca 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replacement cell; implanting foreign replacement cell;
                                                                                                                                                                                                                    9
transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.
                                                                                                                                                                                                                    CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                                                                                                                                                                 Gaps
                                                                                                                                                                               .;
0
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                                                                                                                                             Length 1782;
                                                                                                        Sequence 1782 BP; 458 A; 399 C; 451 G; 474 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2241 BP; 498 A; 630 C; 609 G; 504 T; 0 U; 0 Other;
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                 141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
                                                                                                                                                                                                                                                                                              61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                           Score 100; DB 12;
Pred. No. 1.2e-27;
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                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nucleotide sequence SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                                                                                                             ВÞ
                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-295402/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          engrafting foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004027029-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
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The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimneric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for

Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.

Thompson SC;

Sosa CE,

Beschorner WE,

WPI; 2004-295402/27.

Disclosure; SEQ ID NO 5; 48pp; English

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ADM41036;
                                     Query Match
                                                                                                                                                                                                RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a lac repressor operated p21-expression cassette comprising the Rous sarcoma virus (RSV)-LTR promoter. p21 is a cell cycle inhibitor protein. The present sequence is used to produce vectors for use in the method of the invention. The specification describes a method for producing a protein, preferably a recombinant protein, in a mammalian anchorage-independent producer cell line. The method comprises co-expressing with the protein in the producer cell line a recombinant cell cycle inhibitor protein (preferably p21). The method is useful for producing a recombinant protein in a producer cell line. This is useful for producing a recombinant protein in a producer cell line. This is useful for producing a recombinant protein in a producer cell line. The set useful for producing a recombinant protein in a producer cell line. The set use the producing or enhancing the production of e.g. therapeutic proteins at an industrial scale
                                                                      81 crecrecrecriererereresasereereaciaereceeeeeaecaaarrraageraca 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing recombinant protein, particularly for maximizing or enhancing e.g. therapeutic protein production, by co-expressing protein with recombinant cell cycle inhibitor protein (p21) in producer cell line.
                                                 GAGTAGTGCGCGAGCAAATTTTAAGCTACA
                          Gaps
                                                                                                                                                                                                                                                                                  Lac repressor; p21; RSV; LTR promoter; cell cycle inhibitor protein; protein production; anchorage-independent producer cell line; ss.
                                                                                                                                                                                                                                                           Lac repressor operated p21-expression cassette and RSV-LTR promoter.
                         .
  Length 2241;
                        Indels
                                                                                              61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                            /*tag= b
/note= "SV40 small t antigen intron"
1052. 1907
**tag= c
/note= "p21 coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "thymidine kinase polyA site"
100.0%; Score 100; DB 12;
100.0%; Pred. No. 1.3e-27;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        '*tag= a
'note= "RSV-LTR promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 15-16; 33pp; English.
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                 ABZ23249 standard; DNA; 2245 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shuttleworth J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001; 2001GB-00013318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-2002; 2002WO-EP006054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LONZ ) LONZA BIOLOGICS PLC.
                                                                                                                                                                                                                                                                                                                                                                                               564. .1051
                                                                                                                                                                                                                                 24-MAR-2003 (first entry)
                        100; Conservative
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            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Al-Rubeai M,
                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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Query Match
Best Local S:
Matches 100
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                                                                                                                                                                                                         ABZ23249;
                                                                                                                                                                                                                                                                                                                                                           promoter
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                                                                                                                                                                                                                                                                       46 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
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                                                                                                                                                                                                     1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Score 100; DB 12; Length 2294;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 100; Conservative 0; Mismatches 0; Indels 0;
                                                                     Length 2245;
Sequence 2245 BP; 532 A; 555 C; 625 G; 533 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2294 BP; 466 A; 680 C; 641 G; 507 T; 0 U; 0 Other;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                       106 ACAAGGCAAGGCTTGACCACAATTGCATGAAGAATCTGC 145
                                                                                                                                                                                                                                                                                                                                                    61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                               %; Pred. No. 1.3e-27; 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytomegalovirus nucleotide sequence SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM41036 standard; DNA; 2294 BP.
                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2003; 2003WO-US029251.
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                                                                                                      3est_Local Similarity 100.
4atches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beschorner WE, Sosa CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-295402/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (XIME-) XIMEREX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-2004
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61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100

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The present invention relates to a gene directed enzyme prodrug therapy (GDBPT) using post translational glycosylphosphatidylinositol (GPI) addition to a prodrug activating enzyme which enables anchorage of the enzyme at the cell surface. Carboxpeptidase G2 (CPG2) is a preferred prodrug activating enzyme. The invention also relates to an expression vector for expression of a GPI enzyme hybrid capable of anchorage to the surface of a mammalian cell. The expression vector comprise polynucleotide sequences encoding a signal peptide, an enzyme capable of activating a prodrug, and a post-translational GPI addition motif. The expression vector is useful in the manufacture of a medicament for cancer therapy in a mammalian host. The present DNA sequence is a plasmid exon of rat Thy I gene at its 3' end. (Updated on 11-SEP-2003 to
                  81 CTGCTCCCTGCTTGTGTGTTGTTGTTGTTGTTGTGTGCGGAGCAAATTTAAGCTACA 140
                                                                                                                                                                                                                                                                                                                                                      Carboxypeptidase G2; CPG2; gene directed enzyme prodrug therapy; GDEPT; glycosylphosphatidylinositol; GPI; cancer; therapy; rat; Thyl gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç
CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene directed enzyme prodrug therapy using post translational glycosylphosphatidylinositol addition to prodrug activating enzyme enable anchorage of enzyme at cell surface for cancer therapy.
                                                                                                                                                                                                                                                                                                                        Plasmid pNG3/RC/CPG2-Thyl comprising CPG2 DNA with rat thyl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2426;
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                                                                    61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                      141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 100; DB 4;
100.0%; Pred. No. 1.4e-27;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1e; Page 59-60; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lowenstein PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASTR ) ASTRAZENECA AB. (UYMA-) UNIV VICTORIA MANCHESTER.
                                                                                                                                                                                              AAD02037 standard; DNA; 2426 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2000; 2000WO-GB001640.
                                                                                                                                                                                                                                                                    (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-015983/02.
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Best Local Similarity
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26-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                 plasmid; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria.
                                                                                                                                                                                                                                   AAD02037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric.
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The present invention relates to a gene directed enzyme prodrug therapy (GDEPT) using post translational glycosylphosphatidylinositol (GPI) addition to a prodrug activating enzyme which enables enchorage of the enzyme at the cell surface. Carboxypeptidase G2 (CPG2) is a preferred prodrug activating enzyme. The invention also relates to an expression vector for expression of a GPI enzyme hybrid capable of anchorage to the surface of a mammalian cell. The expression vector comprise polymucleotide sequences encoding a signal peptide, an enzyme capable of activating a prodrug, and a post-translational GPI addition motif. The expression vector is useful in the manufacture of a medicament for cancer therapy in a mammalian host. The present DNA sequence is a plasmid pNG3/RC/CPG2(Q3) comprising CPG2 variant CPG2(Q3) and the last exon of rat Thy-1 at the 3' end. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pNG3/RC/CPG2(Q3)-Thy1 comprising CPG2 variant with rat thy1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                           Carboxypeptidase G2; CPG2; gene directed enzyme prodrug therapy; GD
glycosylphosphatidylinositol; GPI; cancer; therapy; rat; Thyl gene;
CPG2(Q3) variant; plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 100; DB 4; Length 2427; 100.0%; Pred. No. 1.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2427 BP; 555 A; 706 C; 670 G; 495 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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129 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1e; Page 59; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ASTR ) ASTRAZENECA AB. (UYMA-) UNIV VICTORIA MANCHESTER.
                                                                                                      AAD02036 standard; DNA; 2427 BP
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                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emery SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-015983/02.
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es 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Castro MG,
                                                                                                                                                                                             26-MAR-2001
                                                                                                                                                                                                                                                                                                                                        Rattus sp.
                                                                                                                                                                                                                                                                                                                                                         Bacteria.
Chimeric.
                                                                                                                                         AAD02036;
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                                                                   RESULT 11
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Gaps

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0; Indels

Best Local Similarity 100. Matches 100; Conservative

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CTGCTCCCTGCTTGTTGTTGTTGTTGTTGTTGTTGTGCGCGAGCAAAATTTAAGCTACA 128

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CTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGCGAGCAAAATTTAAAGCTACA

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Gaps

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Indels

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Length 3400;

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AAT62937;

AAT62937

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148 crecrecrecriererererangerecreagrandedecegageaaarrraageraca 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;
                                                                                       1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                     2A2 human G2/G4 chimeric antibody expression plasmid insert
                                                                                                                                                           61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 247
               Score 100; DB 2;
Pred. No. 1.5e-27;
100.0%; Scc. 100.0%; Pred. No. 1... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start= 1318
                                                                                                                                                                                                                                                                                        AAT62932 standard; DNA; 3400 BP.
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2566
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(first entry)
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               Query Match
Best Local Similarity 100.
Matches 100; Conservative
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286.
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567.
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984.
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P-PSDB; AAW14934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo, sapiens.
Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9711971-A1
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26-SEP-1996;
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16-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric.
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exon
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                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                     AAT62932
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                                                                                                                                                                                             원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matis LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies binding to porcine but not human cell interaction proteins useful to treat and assay for rejection of xenografted porcine organs,
                                                                                                                                                                                                                             Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis; ss.
                                                                                                                                                                                             3F4 human G2/G4 chimeric antibody expression plasmid insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rother RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mueller EE, Rollins S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 58-61; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
1286. .2055
/*tag= c
/codon_start= 1350
                                                                  AAT62937 standard; DNA; 3400 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .4. .2601
/*tag= f
2602. .2928
/*tag= 9
2929.
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/*tag= e
?484.
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3026. .3348
/*tag= i
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/*tag= a
1056. .1285
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/*tag= d
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h
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-212855/19.
P-PSDB; AAW14940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissues or cells.
                                                                                                                                                                                                                                                                                                           Homo; sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9711971-A1
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26-SEP-1996;
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                                                                                                                                        17-OCT-2003
16-JUN-1997
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Mus sp. Chimeric.

intron

intron

exon

exon

intron

exon

intron

exon

Sequence 3400 BP; 759 A; 1012 C; 909 G; 720 T; 0 U; 0 Other;

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This is the nucleotide sequence of pCTM, a plasmid which contains a CMV promoter, a tripartite adenovirus leader flanked by T7 and SP6 promoters, and a multiple cloning site with a bovine growth hormone polyA site and downstream SV40 polyA site. It has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastoma protein (BP, see AAW62465) and E2F transcription factor (see AAW62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, specifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the E2F promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Packaging-deficient construct; viral gag-pol gene; packaging cell line; moloney murine leukaemia virus; MoMLV; viral env gene; helper construct; gene therapy; humna cytomegalovirus; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA
                                                                                                                                                                                           New fusion polypeptide of, e.g. transcription factor - used to treat, e.g. hyper-proliferative disease such as cancer and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 100; DB 2; Length 3853; 100.0%; Pred. No. 1.6e-27; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3853 BP; 936 A; 986 C; 942 G; 989 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CANC-) CANCER RES CAMPAIGN TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takeuchi Y,
                                                                                                                Wills KN
                                                                                                                                                                                                                                                       Example 1; Fig 4; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid CMV10A1 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT90695 standard; DNA; 3925
                96US-00751517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%;
Matches 100; Conservative (
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                                                                                                                  RJ,
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                                                                                                                Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-179287/16
                                                                                                                                                       WPI; 1998-297858/26
                                                                           (CANJ-) CANJI
                15-NOV-1996;
14-FEB-1997;
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                                                                                                                  Antelman D,
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                                                 A DNA sequence (AAT62931) comprises a 2A2 human G2/G4 (see also AAT62931) chimeric antibody expression plasmid insert sequence. The chimeric antibody (AAW14934) is specific for porcine vascular cell adhesion molecule (VCAM) and is useful for diagnosing human rejection of porcine resortansplants and for improving xenotransplantation of porcine tissues and organs into human recipients. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                         CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 207
                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                  CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAAGCTACA
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E2F; transcription factor; human; retinoblastoma protein RB; bladder cancer; restenosis; angioplasty; diabetic retinopathy; thyroid hyperplasia; Gave's disease; psoriasis; benign prostatic hypertrophy; Li-Fraumeni syndrome; peripheral vascular disease; therapy; plasmid pCTM; ss.
                                                                                                                                                                                                                                                       Length 3400;
                                                                                                                                                                                                            Sequence 3400 BP; 776 A; 993 C; 899 G; 732 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 247
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/note= "pUC19 backbone H3 to AatII"
complement(2857, .3717)
                                                                                                                                                                                                                                                   ; Score 100; DB 2;
; Pred. No. 1.5e-27;
0; Mismatches 0;
              Disclosure; Page 44-47; 105pp; English.
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/*tag= c
/note= "SP6 promoter"
1679. .3853
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'note= "CMV promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mastadenovirus.
unidentified bacteriophage; T7.
unidentified bacteriophage; SP6.
Macaca mulatta; polyoma virus.
Bos taurus.
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/note= "AMP-ORF"
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                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                       Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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Best Local Similarity
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15-FEB-1999
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CDS

RESULT 14

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Gaps 0;

9

Selectable retroviral packaging cell lines and expression constructs - comprise selectable gene downstream of gene of interest, are selectable due to the in-efficiency associated with translation re-initiation.

Claim 23; Fig 13; 79pp; English

sequence is a packaging-deficient construct having a viral env gene (in this case from moloney murine leukaemia virus under hCMV promoter control) and a selectable marker (SM). It is an example of a recombinant expression vector (RMV) of the invention, used to create a packaging cell line. The REVS of the invention comprise a gene of interest (GOI) and a SM gene. The SM gene is arranged downstream of the GOI and a GOI associated stop codon is spaced from a start codon of the SM gene to ensure that the SM protein is expressed as a result of translation. The cell lines are transformed with two REVS, both are replication deficient, one contains the viral gap-pol gene, the other the viral env gene. By using helper constructs, such as the REV's, which are directly selectable and which provide for high expression of the viral. gene, high titre retroviral vectors may be obtained. The packaging cell lines are useful for gene therapy. Prior packaging cell lines using full length retroviral genomes as helper genomes were isolated by cotransfecting them with plasmids encoding selectable markers. However, the helper functions can be lost during the passages of the cells in culture and the current packaging systems provide limited titres of infectious retroviral vectors. Co-transfection with a plasmid encoding a SM does not directly select the best gag-pol-env-expressing cells. The new retroviral packaging cell lines overcome these problems This sequence represents the recombinant expression plasmid CMV10A. This 

Sequence 3925 BP; 963 A; 1001 C; 959 G; 998 T; 0 U; 4 Other;

Gaps o; 0; Indels Query Match
100.0%; Score 100; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.6e-27;
Matches 100; Conservative 0; Mismatches 0;

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61 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 100 130 ACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC 169 ઠે

Search completed: July 14, 2005, 07:01:48 Job time : 141.038 secs

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B67169 CpG0047A Cp
B1333630 60297459
CC62614 ABCNCOURT
CC342469 CH261-11F
CB387202 OSTF076E6
BQ110441 MR0-BT450
AQ946479 Sheared D
CC888514 SALK 1519
CK086063 RG11_C07
AL225351 Terraodon
F3272 HSPD25699 H
AA962465 0091805.8
CN386744 328755673
CB1611201 K-EST0220
CB1611201 K-EST0220
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CR537056 DKFZp459D
CN386728 170005326
BG993413 MR3-HT099
BI113747 602860946
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AW955076 EST367146
CN386730 170005316
                                                                         July 14, 2005, 05:15:57; Search time 952.146 Seconds (without alignments) 3997.736 Million cell updates/sec
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                                                                                                                                                          1 ctgctccctgcttgtgtgtt......caattgcatgaagaatctgc 100
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                          34239544 segs, 19032134700 residues
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Maximum Match 100%
Listing first 45 summaries
                                                   - nucleic search, using sw model
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AA962465
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AA984313
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CNS032VI
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9b_est2: *
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9b_est6: *
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CN386731 170005313 CN386746 17000599 CN386710 17000551 BF300573 601891808 CN386780 170005318 CD654097 AGENCOURT CN386742 170005314 CD656906 AGENCOURT BG387788 602782110 CB996419 AGENCOURT BG187788 602412672 CD643822 AGENCOURT BG187788 602412672 CD643822 AGENCOURT BG187788 COURT CC656102 AGENCOURT CC657137 RTCNT1 28 BY703355 BY703355	ALIGNMENTS  602 bp DNA linear GSS 12-MAY-2000 Cryptosporidium parvum genomic, genomic survey m m Apicomplexa; Coccidia; Eimeriida; yptosporidium. f the Cryptosporidium parvum genome: an ig and genome survey sequence analysis col. 107 (1), 1-32 (2000)	Medicine & Pharmaceutical Chemistry lisco General Hospital-University of California, San San Francisco, CA 94143-0811, USA San Francisco, CA 94143-0811, USA 206 8846 206 8845 206 8846
CN386731 CN386746 CN386717 BF309673 CN386780 CN554097 CN556906 CN556906 BG2029 BG30728 BG31728 CD643822 BG31728 CD643822 BG31738 CD643822 BG31734 CD656102 BW17450 CD656102 BW17450 CD656102 BW17450 CD656103 BW177450 CN567137	ALIGNMENTS  B67169  CpG0047A CpIOWAgDNA2 Cryptosporidivelefore.  B67169  B67169  GSS.  Cryptosporidium parvum Cryptosporidium parvum Cryptosporidium parvum Cryptosporidium parvum Cryptosporidium parvum Cryptosporididae; Cryptosporidium Sukaryota; Alveolata; Apicomplexa; Cryptosporidiidae; Cryptosporidium Lubass 1 to 602) Strong, W. B. and Nelson, R.G. Preliminary profile of the Cryptosperyressed sequence tag and genome 6 Mol. Biochem. Parasitol. 107 (1), 20183851	Medicine & Pharmaceut: Sco General Hospital-1- San Francisco, CA 941- 106 8846 60 3353 ariaditsa.ucsf.edu sequence has been edii , to correct miscalle ughout the sequence, intra  177 177 177 177 177 177 177 177 177 1
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(http://sequence-www.stanford.edu/group/techdev/shear.htm)
The randomly sheared gDNA was chromatographed on Sephacry1 S-400 to remove any small fragments and DNA eluting in the void volume was blunt-ended with T4 DNA Polymerase, treated with alkaline phosphatase to prevent the ligation of multiple fragments, ligated to Srf I-digested pCR-Script Amp (SK+) vector and transformed into E. coli strain Xil0 Gold. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 primers."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 CTGCTCCCTGCTTGTGTTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCTCCCTGCTTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAATTTAAGCTACA 60
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I (bases 1 to 829)
NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11343 row: f column: 15
High quality sequence stop: 788.
Location/Qualifiers
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/lab host="DH10B"
/clone_lib="NIH MGC_12"
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/clone="IMAGE:5139470"
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19 TIGGAGGICGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACC 78

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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2. (Date of Cancer Genomics Ph.D.

2. (Ortact: Daniela S. Gerhard, Ph.D.

3. (Serhard, Ph.D.

3. (Serhard, Ph.D.

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/clone lib="NH10B Human H1 Embryonic Stem Cell cDNA Library
(Long)"
217 TTGGGCGTCCCAGAATTGTTGGTGAGCAAACTTCAAGTTGCTGCCTGGGAAGTCCTGACT 158
                                                                                                                                                                                                                                                                                                                                CD655614
AGENCOURT 14551032 NIA Human H1 Embryonic Stem Cell cDNA Library (Long) Homo sapiens cDNA clone IMAGE:30424285 5', mRNA sequence.
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/cell line="WA01"
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/db_xref="taxon:9606"
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1 (bases 1 to 401)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Jahky, R., Moore, T.,
Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,
Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
C. elegans ORFeome version 1.1: experimental verification of the
expression
                                                                                                 свзв7202 401 bp mRNA linear EST 15-MAY-2003
OSTF076E6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB387202
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MR0-E774502-220601-202-b02 BT4502 Homo sapiens cDNA, mRNA sequence.
BQ310441. GI:20853032
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORF.come
cloning project : Contact david_hill@dfci.harvard.edu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="AD-wrmcDNA"
//note="The AD-wrmcDNA library was generated with poly(A) +
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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                                                                                                                                                                                                                 Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
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      616 AAACACTTAAACGCCAACTCCACAGAGAA 588
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/strain="N2"
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Matches 48; Conservative
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(Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC242469 1165 bp DNA linear GSS 12-MAY-2003
CHS61-11F8 RM1.1 CH261 Gallus gallus genomic clone CH261-11F8,
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                                                                                                                                                                                                                                                                                                         524 GAGCTAACTGAATTGTATGGGAGCAGCATTTAACATATTCCTAGTCAAGGACTGGATGGG 465
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                                                                                                                                                                                                                                                               /note="Vector: pTARBAC2.1; Site 1: EcoR1; Site 2: EcoR1; CH261 Female Chicken library - For library and clone ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1165)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Marren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGCTTGTGTGTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACGG
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Pred. No. 26;
0; Mismatches 37; Indels 0;
                                                                                                                                                                           Length 823;
                                                                                                                                                                                                                      28; Indels
                                                                                                                                                                       Score 30.2; DB 6;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Brror: 0.00
Seq primer: RM1 TACGACTCACTATAGGGAGA
Class: BAC ends
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/cell_line="UCD001, inbred 256"
                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 15
High quality sequence stop: 738.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'clone_lib="CH261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
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Gallus gallus
                                                                                                                                                                           30.2%;
62.7%;
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464 AAGTAAGTGAAGAAT 450
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                                                                                                                                                                                                                      47; Conservative
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Best Local Similarity
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Best Local S:
Matches 52,
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Gaps

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/close_libe_sheared DNA.
/close_libe_sheared DNA.
/note="Vector: pUC18; Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10:1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
1 (bases 1 to 754)
El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
Donelson,J., Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
Unpublished (1999)
Other GSSs: Sheared DNA-4906.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Hagnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Adorinab,C., Joske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
Man library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Reverse
Class: shotgun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 CAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.4%; Score 29.4; DB 8; Length 754; Best Local Similarity 70.9%; Pred. No. 33; Matches 39; Conservative 0; Mismatches 16; Indels (
                                                                                                                                                                                                                                                                                                                    9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREUG27/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-4906"
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Unpublished (2001)
Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC888514.1 GI:33365229
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CC888514/c
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AUTHORS
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                                                                                    Eukaryotz, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 531)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagal,M.A., deolive,P.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev stage="Adult" //dev stage="Adult" //dev stage="BT4502" //dev stage="BT4502" //dote="Drygan: breast; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707012
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-BT4502-
220601-202-b02&t3=2001-06-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 48
High quality sequence stop: 530.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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Sheared DNA-4906.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-4906, genomic survey sequence.
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Trypanosoma brucei
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
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                                    sapiens (human)
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Fisher, C.,

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Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis scale clone-end sequencing, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 207F02 of library G from Tetraodon nigroviridis, genomic survey
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                       267 gaggagriccaagaaggaaacrgaagccagaargaagaagaggcriggacrrigcaaggrcaag 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGTGTTGGAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCT 73
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                                                                                                                                                              31 GAGTAGTGCGCGAGCAAATTTAAGCTACAACAAGGCAAGGCTTGACCGACAATTGCATG
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/db_xref="taxon:99883"
/db_xref="taxon:99883"
/clone="207F02"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG207DC01SP1-end : PUC-Ori"
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                 Length 657;
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                                     DB 7;
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Pred. No. 47;
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                                 Score 29;
Pred. No. 4
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Tetraodon nigroviridis
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                                 29.0%;
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/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Cucurbitales, Cucurbitaceae, Cucumis.
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Michigan State University
Horticulture Department, Michigan State University, East Lansing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Development of genomic tools for cucumber (Cucumis sativus L.) Unpublished (2003)
Contact: Rebecca Grumet
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RG11 C07 Cucumber leaf Cucumis sativus cDNA, mRNA sequence.
CK086063
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
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'ecotype="Col-0"
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/sex="monoecious"
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/strain="Straight 8"
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Grumet, R. and McGrath, M.
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Tel: 517 353 0890
Fax: 517 355 5191 x431
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                                                                                                                                                                                                   F32722 340 bp mRNA linear EST 13-MAY-1999 HSPD25699 HM3 Homo sapiens cDNA clone 83000037G06, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 340)
1 (Dases I to 340)
2 (Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A., Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligo-dT-NotI primer (5'-biotin-AACCCGCTCGAGCGGCCGCTTTTTTTTTTTTTTTT-3'). The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="pectoral muscle (after mastectomy)"
/clone lib="HM3"
/clone="Vector: pcDNAII (Invitrogen); Site 1: BstXI;
Site 2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated
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22 GAGGTCGCTGAGTAGTGCGCGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGAC 81
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ABI Chromatograms and other information are available on WWW at
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/db_xref="taxon:9606"
/clone="s3000037G06"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
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                                                                                                                                                                                                                                                                             /tisgue_type==mbryonic stem cells, embryoid bodies derived_from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note=Toligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p22), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB161201 514 bp mRNA linear EST 30-JAN-2003
K-EST0221011 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-16-H03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 514)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Mat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 GAGCTAACTGAATTGTATGGGAGCAGCATTTAACATATTCCTAGTCAAGGACAGGATGGG 74
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Contact: Kim V3
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="L18POOL1n1-16-H03"
/cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
/lab_host="Topl0F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28.6; DB 7; Length 4
Pred. No. 57;
0; Mismatches 29; Indels
                                                                              Negeneration
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 436 Std Error: 0.00.
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21C Frontier Korean EST Project 2001
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Plate: 16 row: H column: 03
High quality sequence stop: 514.
Location/Qualifiers
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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1 Similarity 61.3%;
46; Conservative
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CDIOLIB2

K-EST0220988 L18POOLIN1 Homo sapiens CDNA clone L18POOLIN1-16-F04
5', MRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 530)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
/clone_lib="LigPoOLin1"
hote="Organ: Liver; Vector: pT773-Pac; Site_1: EcoRI;
Site_2: NoLI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell 'culture."
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Korea Research Institute of Bioscience & Biotechnology
52 Roeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                           DB 6; Length 514;
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/lab_host="Topl0F""
/clone_lib="L18POOL1n1"
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Best Local Similarity 61.3%; Pred. No. 59;
Matches 46; Conservative 0; Mismatches
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0; Mismatches
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Unpublished (2002)
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Plate: 16 row: F column: 04
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/db_xref="taxon:9606"
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ilarity 61.3%;
Conservative (
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Search completed: July 14, 2005, 23:23:20 Job time: 952.146 secs

M90520 Woodchuck AR136166 Sequence

14 OHVSURCOR 6 AR136166

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MI5954 Woodchuck hAF410859 Woodchuck AF410857 Woodchuck AF410861 Woodchuck AF410861 Woodchuck HM19183 Woodchuck hM19183 Woodchuck hM19752 Woodchuck hAX68486 Lentivira AX641835 Sequence M60766 Woodchuck hB1268253 Adenoviru AX641836 Sequence AF410855 Woodchuck AF410856 Woodchuck AF410856 Woodchuck AF410856 Woodchuck AF410856 Woodchuck AF410856 Woodchuck AF410856 Woodchuck
                                                                                   July 14, 2005, 04:39:07; Search time 756.618 Seconds (without alignments) 6468.225 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                     US-09-482-682-65_COPY_4192_4292
101
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ARIGESTS 6 ARIT7246 C CQB1826 14 AY334075 14 AY334077 14 AY628095 14 AY628096 14 AY628099 14 AY628099 14 AY628099 14 AY628099 14 AY628099 14 AY628099 16 AX328937 6 AX382148 6 AX382148 6 AX382148 6 AX382148 6 AX382148 6 AX382148 6 AX382148 6 AX382148	ALIGNMENTS  ALIGNMENTS  garons  guence 1 from Patent EP1361277. garons  mthetic construct  mthetic construct  mthetic construct  mthetic construct  her sequences; artificial sequences.  llet,J., Brun,S., Dufour,N. and Faucon-B  timization of transgene expression in man  tent: EP 1361277-A 1 12-NOV-2003;  NTRE NATIONAL DE LA RECHERCHE SCIENTIFIQ  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  Jucoganism="synthetic construct"  (mol_type="unassigned DNA"  / db xref="taxon:32630"  / db xref="taxon:32630"  / db xref="taxon:32630"  / note="Description of Artificial  / note="Description of Artificial  imilarity 100.0%; Fred. No. 1.2e-19;  conservative 0; Mismatches 0;  TGCCTTGCCCGCTGCTGCACAGGGCCTCGGCTGTTGGGCCA	CGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT [
94.6 93.7 592.94.6 93.7 3308 94.6 93	B 1 O D TEBROOM CONTRACTOR TO THE PROPERTY OF	61 T 98 T AX9 Seq AX9
1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 AX937037 LOCUS DEFINITION ACCESSION VERKORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN ORIGIN OUETY MATCH BEST LOCAL MATCHES 1 OY DD 333	Qy Db 3 RESULT 2 AX952091 LOCUS DEFINITION ACCESSION

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Woodchuck hepatitis B virus Woodchuck hepatitis B virus
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/codon_start=1
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IVOSPGLERFTTCLSSSTHNGNDSQLQTWHALCTRHYYSSLLLLFKTYGRKLHLLAHP
FIMGFRKLPWGVGLSPFLLAQFTSALLASMVRRNFPHCVVFAYMDDLVLGARTSEHLTA
IYSHLCSVFLDMGTHLANVMKTKWMGNILHFMGYVITSSGVLPQDRHYKKLSRLRSVP
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                                                                                                                   Mallet,J., Brun,S., Dufour,N. and Faucon-Biguet,N.
Optimization of transgene expression in mammalian cells
Patent: WO 03093485-A 1 13-NOV-2003;
Centre National De La Recherche Scientifique-CNRS (FR); Biovectys
(FR)
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Etiemble, J., Moroy, T., Trepo, C., Tiollais, P. and Buendia, M.A.
Nucleotide sequence of the woodchuck hepatitis virus surface
antigen mRNAs and the variability of three overlapping viral genes
Gene 500, 207-214 (1986)
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Woodchuck hepatitis virus mRNA encoding surface antigen, complete
cds, polymerase, 3' end, and cor protein, 5' end.
M15954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jul 7, 1995 this sequence version replaced gi:336154. Original source text: Woodchuck hepatitis B virus (strain W64) (clone: pWS23) cDNA to mRNA.
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Woodchuck hepatitis B virus
Woodchuck hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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'db_xref="taxon:35269"
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Pred. No. 1.2e-19;
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                                                                               other sequences; artificial sequences.
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/db xref="taxon:32630"
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/protein_id="AAA69573.1"
/db_xref="G1:336155"
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/strain="W64"
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                                                                                                                                          TITLE
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                    REFERENCE
                                                                                                                         AUTHORS
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KEYWORDS
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IPECTGONSQFQTCKHLPTSCPPTCNGFRMYLRRFIIYLLVLLLCLIFLLULDWKG
LLPVCPLQPTTETTVNCRQCTLSVQDTYTPPYCCCLKPTAGNCTCWPIPSKALGNYL
WEWALARFSWLNLLVPLLQWLGGISLIAWFLLIWMIWFWGPALLSILPPFIPIFVLFF
VNOPLDYKI CERLTGILNYVAPFTLCGYAALMPLYHAIASRTAFIFSSLYKSWLLSLY
ESBRPVVRGROVCTVFADTPTGWATTCOLLGSFPRFEDFIATABLIAACHARCW
TGARLLGTDNSVVL,GGRLTSFPWLACVAWYILRGTSFCYVPSALNPADLPSRGLLPV
LRPLPRLRLRPQTSRISLWAASPPVSPRRPVRVAWSSPVQTCEPWIPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAARLCCQLDSARDVLLIRPIGPOSSGPPFPRPAAGSAASS
PSPSDSSDLPLGRLPACFASASGPCCLVFTCADLRTMDSTVNFVSWHAKRQLGMPSKD
LWTPYIKDQLLTKWEEGSIDPRLSIFVLGGCRHKCMRLL"
                                                                                                                                                                                                                                                                                                                                                                               /translation="MKNQTFHLQGFVDGLRDLTTTERHHNAYGDPFTTLSPVVPTVST
TLSPPSTTGDPALSPEMSPSSLLGLLAGLQVVYFLWTKIPTIAQNLDWWWTSLSFPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1335 TGCCTTGCCCGCTGCTGGACAGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF410858 2649 bp DNA linear VRL 18-FEB-200 Woodchuck hepatitis B virus isolate 342 defective polymerase gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1973;
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Pred. No. 1.2e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="core protein"
/protein_id="AAA69576.1"
/db_xref="G1:555278"
/translation="MDIDPYKEFGSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                          /codon_start=1
/product="surface antigen"
/protein_id="AAA69574.1"
/db_xref="GI:336156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211. .876
/product="surface antigen'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="X protein"
/protein_id="AAA69575.1"
/db_xref="G1:893290"
                                                                                                          1. .>879
/note="S mRNA (alt.)"
                                                                                                                                                               4. .>879
/note="S mRNA (alt.)"
31. .879
/note="precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55. .>879
/note="S mRNA (alt.)"
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1418. .1843
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/note="precursor"
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FTLCGYAALMPLYHAIASRTAPIFSSLYKSWLLSLYEELWPVVRQRGVVCTVFADATP
TGWGIATTCQLLSGTFAFPLPIATAELIAACLARCWTGARLLGTDNSVVLSGKLTSFP
                                                                                                                                                                                                                                                      2 (bases 1 to 2649)
Yamamoto_T., Litwin,S., Zhou,T., Zhu,Y., Condreay,L., Furman,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALNLHLPTADLQWVHKTNAITGLYSNQAAQFNPHWIQPEFPELHLHNDLIQKLQQYFG
PLTINEKRKLQLNFPARFFPKATKYFPLIKGIKNNYPNFALEHFFATANYLWTMEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILYLRKNQTTLTFKGKPYSWEHRQLVQHYGQQHKSHLQSRQNSSMVACSGYLLHNHLP
SEPVSVSTRNLSNNISDKSQKSTRTGLCSYKQIQTDRLEHLARISCGSKITIGQQGSS
PKTSSISSNFRNQTWAYNSSRNSGHTTWFSSASNSNKSRSREKAYSSNSTSKRYSPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYEKSDFSSPGVRGRITRLDNNGTPPQCLWRSFYNTKPCGSYCTHIIVSSLDDWGPCT
VTGDVTIKSPRTPRRITGGVFLVDKNPNNSSESRLVVDFSQFSRGHTRVHWPKFAVPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQTLANLLSTNLQWLSLDVSAAFYHIPISPTAVPHLLVGSPGLERFTTCLSSSTHNGN
DSQLQTWHTLCTRHVYSSLLLLFKTYGRKLHLLAHPFIMGFRKLPMGVGLSPFLLAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MHPFSRLFRNIQSLGEEEVQELLGPPEDALPLLAGEDLNHRVAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSALASMVRRNLPHCVVFAYMDDLVLGARTSEHLTAIYSHICSVFLDLGIHLNVNKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WLLACVANWILRGTSFCYVPSALNPADLPSRGLLPVLRPLPRLRLRPQTSRISLWAAS
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                                                       Condreay, L., Furman, P.
                                                                                               Mutations of the woodchuck hepatitis virus polymerase gene that confer resistance to lamivudine and 2'-fluoro-5-methyl-beta-L-arabinofuranosyluracil J. Virol. 76 (3), 1213-1223 (2002)
                                                                                                                                                                                                                                                                                                                                                        Submitted (13-AUG-2001) Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="reverse transcriptase; contains six nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 2649)
Yamamoto,T., Litwin,S., Zhou,T., Zhu,Y., Condreay,L., Furman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:35269"
/note="isolated from serum of chronically infected
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Woodchuck hepatitis B virus"
(virion
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100.0%; Pred. No. 1.2e-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="defective polymerase"
protein id="AAL04546.1"
db_xref="G1:15637593"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPVSPRRPVRVAWSSPVQTCEPWIPP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/isolate="342"
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                                                                                                                                                                                                                                                                                                        Mason, W.S
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AUTHORS
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AF410857
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                                                     AUTHORS
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2 (bases 1 to 2655)
Yamamoto,T., Litwin,S., Zhou,T., Zhu,Y., Condreay,L., Furman,P. and
Mason,W.S.
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ALNHLIPPADLGWYHKTNHTTGLYSMOAGORPHWIQPEFERHLHUNDL GKLGQYFG
PLTINEKRKLGLNFBARFPFKATKVPPLIKGIKNNYPNFALBHFFATANYLWTIAWEA
ILYLRKNQTTLTFKGKPYSWEHRQLVQHNGQQHKSHLQSRQNSSMVACSGYLLHNHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEPVSVSTRNLSNNISDKSQKSTRTGLCSYKQIQTDRLEHLÄRISCGSKITIGQQGSS
PKYSYKSISSOBNRNOTWANNSRNGSHTTWFSSANSNKSKSRSRRKAYSRNSTRXYSP
PLAYEKSDSSSPGWGKITRLDNNGTPPQCLWRSFYNTKPCGSYCHHIVSSLDDWGP
CTVTGDVIIKSPRTPRRIIGGVFLVDKNPNNSSESRLVVDFSQFSRGHTRVHWPKRAV
                                                     Condreay, L., Furman, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APFTLCGYAALMPLYHATASRTAFTFSSLYKSWLLSLYEBLWPVVRQRGVVCTVFADA
TPTGWGTATTCQLLSGTFAFPLPTATAELTAACLARCWTGARLLGTDNSVVLSGKLTS
FPWLLACVANWTLRGTSFCYVPSALNPADLPSRGLLPVLRPLPRLRLRPQTSRTCLWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNLQTLANLLSTNLQWLSLDVSAAFYHIPISPDAVPHLLVGSPGLERFTTCLSSSTHN
GNDSQLQTWHTLCTRHIYSSLLLLFKTYGRKLHLLAHPFIMGFRKLPMGVGLSPFLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OFTSALASMVRRNFPHCVVFAYMDDLVLGARTSEHLTAIYSHICSVFLDLGIHLNVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKWWGNHLHFMGYVI TSSGVLPQDKHVKKLSRYLRSVPVNQPLDYKI CERLTGI LNYV
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Woodchuck hepatitis B virus isolate 335 polymerase gene, complete
                                                                                                   gene that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated from serum of chronically infected woodchuck"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCTTGCCCGCTGCTGGACAGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG
                                                                                                                                                                                                                                                                                                                                                              Cancer Center, 7701 Burholme
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Woodchuck hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                                                                                 Mutations of the woodchuck hepatitis virus polymerase confer resistance to lamivudine and 2.fluoro-5-methyl-beta-L-arabinofuranosyluracil J. Virol. 76 (3), 1213-1223 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Woodchuck hepatitis B virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="type I mutant polymerase"
                             1 (bases 1 to 2655)
Yamamoto,T., Litwin,S., Zhou,T., Zhu,Y.,

    2655
    note="reverse transcriptase"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:35269"
/note="lamivudine resistant
                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (13-AUG-2001) Fox Chase Ca
Avenue, Philadelphia, PA 19111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAL04545.1"
/db_xref="GI:15637591"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/isolate="335"
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/db_xref="G1:15637595"

/db_xref="G1:15637595"

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/translation="MHPFSRLPRNIQSLGEEGVQELLGPPEDALPLIAGEDIAHRVAD
ALMLHLPTADLQWVHKTNAITGLYSNQAAQFNPHWIQPEFPELHLHNDLIQKLQQYFG
PLTINERRKLQLNFPRRFPRAFYFPLIKGIKNYPNFALEHFFATANYLWTLWEAG
ILYLRKNQTTLTFKGKPYSWEHRQLVQHNGQQHKSHLQSRQNSSWVACSGYLLHNHLP
SEPVSYGTRNISNNISDNSGKSTRTGLCSYRQVQTDRLEHLARISCGSKITTGQQGSS
PKTSYKSISSNPRNQTWASRNSGHTTWFSSASNSNKSRSREKAYSSNSTSKRYSP
PLNYSKSDFSSPGVRRITLDNNGFPPQCIMRSFYNTRPCGSYCIHHIVSSLDDWGF
CTVTGDVTIKSPRTPRRITGGVFLVDKNPNNSSESRLVVDFSQFSRGHTRVHWPKFAV
                     and
                                                                                                                                                                                   2 (bases 1 to 2655)
Yamamoto_T., Litwin,S., Zhou,T., Zhu,Y., Condreay,L., Furman,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNLQTLANLLSTNLQWLSLDVSAAFYHIPISPAAVPHLLVGSPGLERFTTCLSSSTHN
GNDSQLQTWHTLCTRHIYSSLLLLFKTYGRKLHLLAHPFIMGFRKLPMGVGLSPFLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QFTSALASMVRRNFPHCVVPAYMDDLVLGARTSEHLTAIYSHICSVFLDLGIHLNVNK
TKWWGNHLHFMGYVITSSGVLPQDKHVKKLSRYLRSVPVNQPLDYKICERLTGILNYV
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TPTGWGIATTCQLLSGTFAFPLPIATAELIAACLARCWTGARLLGTDNSVVLSGKLTS
FPWLLACVANWILRGTSFCYVPSALNPADLPSRGLLPVLRPLPRLRLRPQTSRISLWA
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1 (bases 1 to 2655)
Yamamoto,T., Litwin,S., Zhou,T., Zhu,Y., Condreay,L., Furman,P.
                                       Mason,W.S.
Mutations of the woodchuck hepatitis virus polymerase gene that
                                                                                                                                                                                                                                                                      Submitted (13-AUG-2001) Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA Location/Qualifiers
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Woodchuck hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases I to 2655)
                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:35269"
/note="isolated from serum of chronically infected
woodchuck"
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                                                                           confer resistance to lamivudine and 2'-fluoro-5-methyl-beta-L-arabinofuranosyluracil J. Virol. 76 (3), 1213-1223 (2002)
                                                                                                                                                                                                                                                                                                                                                        organism="Woodchuck hepatitis B virus"
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100.0%; Pred. No. 1.2e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/isolate="335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="polymerase"
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Submitted (13-AUG-
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Matches 101
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UNDSQLQTHWITCTRHIYSLLLLEFYTGRKCHLLAHPTINGFKLLPWOYGLSPPLAA
QFTSALLASWYRRNPHPUVVRYRYDLYJCJARTSEHLTAIYSHTCHLAHVINT
TKWWGNHLHFMGYVITSSGVLPQDKHVKKLSRYLRSVPVNQPLDYKICERLTGILNYV
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TPTGWGIATTCQLLSGTFAFPLPIATAELIAACLARCWTGARLLGTDNSVVLSGKLTS
FPWLLACVANWIMRGTSFCYVPSALNPADLPSRGLLPVLRPLPRLRLRPQTSRISLWA
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Yamamoto,T., Litwin,S., Zhou,T., Zhu,Y., Condreay,L., Furman,P. and
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Yamamoto, T., Litwin, S., Zhou, T., Zhu, Y., Condreay, L., Furman, P. and
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                                                                                               Mutations of the woodchuck hepatitis virus polymerase gene that confer resistance to lamivudine and 2' filuoro-5-methyl-beta-L-arabinofuranosyluracil J. Virol. 76 (3), 1213-1223 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (13-AUG-2001) Fox Chase Cancer Center, 7701 Burholme
Avenue, Philadelphia, PA 19111, USA
1. Cocation/Qualifiers
1. .2655
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Woodchuck hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (Dases 1 to 2655)
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iive 0; Mismatches 0;
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/mol_type="genomic DNA"
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Yamamoto, T., Litwin, S., Zhou, T., Zhu, Y., Condreay, L., Furman, P. and
                                                                                                                                                                                                                                                                                                                                                         Yamamoto, T., Litwin, S., Zhou, T., Zhu, Y., Condreay, L., Furman, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALNLHLPTADLQWVHKTNAITGLYSNQAAQFNPHWIQPEFPELHLHNDLIQKLQQYFG
PLTINEKRKLQLNFPARFFPKATKYFPLIKGIKNNYPNFALEHFFATANYLWTIWEAG
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GNDSQLQTMHTLCTRHVYSSLLLLFKTYGRKCHLLAHPFIMGFRKLPMGVGLSPFLLA
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Woodchuck hepatitis B virus
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                                                                         Mutations of the woodchuck hepatitis virus polymerase gene that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-AUG-2001) Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                       confer resistance to lamivudine and
2.fluoro-5-methyl-beta-L-arabinofuranosyluracil
J. Vicol. 76 (3), 1213-1223 (2002)
21635500
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Woodchuck hepatitis virus 2, complete genome.
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(protein_id="AAL04549.1"
(db_xref="GI:15637599"
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Best Local Similarity 100.
Matches 101; Conservative
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Direct Submission
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AUTHORS
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MEDLINE
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LYLRKNQTTLTFKGKPYSWEHRQLVQHNGQQHKSHLQSRQNSSMVACSGHLLHNHLSS
BSVSVSTRNLSNNISDKSQKSTRTGLCSYKQ1QTDRLEHLARISCGSKIFIGQQGSSP
KTLYKSISSNFRNQTWAYNSSRNSGHTTWFSSASNSNKSRSREKAYSSNSTSKRYSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNYEKSDFSSPGVRRITRLDNNGTPTQCLSRSFYNTKPCGSYCIHHIVSLLDDMGPC
TVTGDVTIKSPRTPRRITGGVFLVDKNPNNSSESRLVVHFSQFSRGHTRVHWPKFAVP
NLQTLANLLSTNLQMLSLDVSAAFYHIPISPAAVPHLLVGSPGLERFNTCLSSSTHNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNSQLQTMENLCTRHVYSSLLLLFKTYGRKLHLLAHPFIMGFRKLPMGVGLSSSLLAQ
FTSALASMVRRNFPHCVVFAYMDDLVLGARTSEHLTAIYSHICSVFLDLGIHLNVNKT
KWWGNHLHFWGYVITSSGVLPQDKHVKKISRYLLSVPVNQPLDYKISERLTGILNYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDGLRDLTTTERQHNAYRDPFTTLSPAVPTVSTILSPPSTTGDPALSPEMŠPSSLĪGL
LAGLQVVYBHTRILITIAQNDBWWTCSLSPRGGTPECTGOMSQPGYCKHLPTSCPPTC
NGFRWMYLRRFITLTLILGLIFLVLLLCLIFLVLLDWKGLIPVCPLQPTTETYNGCTISAQ
DMYTPPYCCCLKPTAGNCTCWPIPSSWALGNYLWEWALARLSWINLLVPLLQWHLGGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="G1:501836"
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PSPSDDSDLPLGRLPACFAGSGGPCCLVFTCADLRTWDSTVNFVSWHANRQLGMPSKD
LWTPYIKDQLLTKWBEGSIDPRLSIFLLGGCRHKCMRLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFTLCGYAALMPLYHAIASRMAFIFSSLYKSWLLSLYEELWPVVRQRGVVCTVFADAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTGWGIATTCQLLSGTYAFPLPIATAELIAACLARCWTGARLLGTDNSVVLSGKLTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPGPIIVPGIRDIPRGLVPPQTPTNRDQGRKPTPPTPPLRDTHPHLTMKNQTFHLQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homology to WHV1, GHSV, and HBV(adr). The X open reading frame is remarkably conserved and may also encode a protein, but no protein has yet been isolated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MHPFSRLFRNIQSLEEEVQELLGPPEDALPLLAGEDLNHRVAD#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTINEKRKLQLNFPARFFPKATKYFPLIKGIKNHYPNFALEHFFATANYLWTLWEAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PWLLACVATWILRGTSFCYVPSALNPADLPSRGLLPALRPLPRLRLRPQTTRISLWAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MGNNIKVTFNPDKIAAWWPAVGTYYTTYPONQSVFQPGIYQTT
SLINPKNQQELDSVLINRYKQIDWNTWQGFPVDQKFSLVSRDPPPFPYINQSAQTFEI
                                                                                                                                                                                                                                                                                                                                                                                                         The sequence shown is the complemented and inverted L-strand, and thus has the polarity of the S-strand.
Kodama, K., Ogasawara, N., Yoshikawa, H. and Murakami, S.
Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
evolutional relationship between hepadnaviruses
J. Virol. 56 (3), 978-916 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNLHLPTADLOWVHKTNAITGLYSNOAAOFNPNWIOPEFPELHLHNDLIOKLOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The peptides in the features table were assigned primarily by
                                                                                                                                                                                                                                                             (Marmota monax) plasm DNA, clone WH81. of sequence for [1] kindly provided by S.Murakami,
                                                                                                                                                                                                                      Original source text: WHV (woodchuck hepatitis virus) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIAWFLLIWMIWFWGPALLSILPPFIPIFVLFFLIWVYI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Woodchuck hepatitis ]
/mol_type="unassigned DNA"
/db_xref="taxon:35269"
join[2427, .3320,1. 1758]
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/product="envelope protein".
1503. .1928
/note="X ORF; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="envelope protein"
/protein_id="AAA19182.1"
/db_xref="GI:336133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(2989. .3320,1. .964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAA19183.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'codon_start=1
'protein_id="AAA19184.1"
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/db_xref="GI:336135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db xref="GI:336134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2021. .2584
/note="core protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                         woodchuck (Marmota monax)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon start=1
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ORIGIN

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DNA polymerase; coat protein; complete genome; core protein; envelope-associated protein; origin of replication; polymerase. Woodchuck hepatitis B virus Woodchuck hepatitis B virus Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus. 1 (bases I to 3123) Cohen, J. I., Miller, R. H., Rosenblum, B., Denniston, K., Gerin, J. L. and Purcell, R. H.
                                                                                                                                                                                                                                                                                                                                                                                   /translation="waarlccoldsardvlllrpfgpossgppprpagsaasstss
pspsdsblplgrlpacfasasgpcclvftcadlrtwdstvnfvswhakrqlgmpskd
lwtpyikdqlltkweegsidprlsifvlggcrhkcwrll"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MDIDPYKEFGSSYQLINFLPLDFFPDLNALVDTATALYEEELTG
FERCSPHTARQALVCWBELTKLINAMSSNITSEQVRTIIVHTVNDTWGLKVRQSLW
FHLSCLIFGGHTEGPELVSFGVWIRTPAPYRPPNAPILSTLFEHTVIRRGGARASRS
PRRRTPSPRRRRSQSPRRRRSGSPSANC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1420 TGCCTTGCCCGCTGCTGGACAGGGCTCGTGGGCACTGATGCAATTCCGTGGTGTTG 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OHVCGD 3323 bp ms-DNA circular VRL 04-MAY-1994 Woodchuck hepatitis virus (WHV), complete genome, clone WHV 7.
/translation="mgnnIkvTfnPDKIAAWWPAVGTYYTTTYPQNQSVFQPGIYQTT
SLINPKNQQELDSVLINRYKQIDWNTWQGFPVDQKLPLVSRDPPLKPHINQSAQTFEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence comparison of woodchuck hepatitis virus replicative forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Original source text: Woodchuck hepatitis virus DNA, clone WHV 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TGCCTTGCCCGCTGCTGGACAGGGCCTCGTGGGCCACTGACAATTCCGTGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1480 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 1520
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/mol_type="genomic DNA"
/db_xref="taxon:35269"
join[02477. .3323,1. .1758)
/codon_start=1
/product="DNA_polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCTGTGT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 14;
100.0%; Pred. No. 1.2e-19;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                    /product="surface protein"
1503. .1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from a carrier trapped in Maryland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="core protein"
/protein_id="AAA46765.1"
/db_xref="GI:336145"
                                                                                                                                                                                                                                                                                                                     /product="X protein"
/protein_id="AAA46764.1"
/db_xref="GI:336144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shows conservation of the genome Virology 162 (1), 12-20 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2021. .2587
/codon_start=1
/product="core p
                                                                                                                                                                                                                                                                                                  /codon start=1
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                                                                                                                                                                                                                               .961
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Matches 101; Conserv
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                                                                                                                                                                                                                               mat_peptide
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OHVCGD
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PUBMED
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KEYWORDS
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ENECSHHFTATRQALVCWBELTKLIAMMSSNITSEQVRTIIVNHVNDTWGLKVRQSLW
FHLSCLTFGATVQDFELVSFVVWIRTPAPXTRPPNAPILSTLPEHTVIRRGGARASRSP
RRRTPSPRRRSQSPRRRSQSPANC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3323 bp ms-DNA circular VRL 04-MAV-1994
Woodchuck hepatitis virus (WHV), complete genome, clone WHV 59.
M19183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cohen, J. I., Miller, R., Rosenblum, B., Denniston, K., Gerin, J.L. and Purcell, R.H.
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Plinekrkiolnpparpppatkypplikgiknnypnpalehppatanylmtumeag
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SPPVSPRRPVRVAMSSPVQTCEPWIPP"
join(2992. . .3323.1. . .964)
note="precursor"
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                                                                                                                                                                                                                                                                        1420 TGCCTTGCCCGCTGCTGGACAGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA polymerase; WHC protein, WHeAg protein, coat protein, complete genome; core protein; envelope-associated protein; origin of replication; polymerase.
Woodchuck hepatitis B virus
Woodchuck hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence comparison of woodchuck hepatitis virus replicative forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Original source text: Woodchuck hepatitis virus DNA, clone WHV 59, from a carrier woodchuck trapped in Pennsylvania.
Location/Qualifiers
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                                                                                                                                                                                                                               1 TGCCTTGCCCGCTGCTGGACAGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG
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                                                                                                                                     100.0%; Score 101; DB 14; Length 3320;
100.0%; Pred. No. 1.2e-19;
ive 0; Mismatches 0; Indels 0;
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/protein_id="AAA46762.1"
/db_xref="GI:336142"
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/codon_start=1
/product="DNA polymerase"
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/db_xref="GI:336143"
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Virology 162 (1), 12-20 (1988)
88101359
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/db_xref="taxon:35269"
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                                                                                                                                                                                    Conservative
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Matches 101; Conserv
                                                                                            EcoRI site.
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                                                                                                                                          Query Match
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Original source text: Woodchuck hepatitis B virus (strain WHV8), cDNA to viral DNA, clone pWHV8.

Draft entry and computer-readable sequence for [1] kindly submitted by R.Girones, 24 MAY-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="MSPSSLLGLLAGLQVVYPLWTKILTIAQNLDWWWTSLSFPGGIP
STGONSOGOTCKHLDTSCPPTCNGFRWWIARFIIYLLLVLLLGLFLFLULDWKGLI
PVCPLQPTTETTVMKGTTI SAGDMYTPPFXCCLKFPAGNCTCWPIBSSWALGANYLWB
WALARFSWINLLVPLLQWLGGISLIAWFLLIWMIWFWGPALLSILPPFIPIFVLFFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="Waarlcchldsardvillerpegossgpsppraagsaass
pspsdbsdlplgrlpacfasasgpcclvftcadlrtwdstvnpvswhanrqlgmpskd
Lwtpyikdqlltkwbbgsidprlsifvlggcrhkcwrll"
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FHLSCLTFGQHTVQEFLVSFGVWIRTPAPYRPPNAPILSTLPEHTVIRRRGGARASRS
PRRRTPSPRRRRSQSPRRRRSQSPSANC"
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                                                                                                               Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
1 (bases 1 to 3323)
Girones,R., Cote,P.J., Hornbuckle,W.E., Tennant,B.C., Gerin,J.L.,
Purcell,R.H. and Miller,R.H.
Complete nucleotide sequence of a molecular clone of woodchuck
hepatitis virus that is infectious in the natural host
Proc. Matl. Acad. Sci. U.S.A. 86 (6), 1846-1849 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTTG
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Lentiviral transfer vector pHsCXW, complete sequence.
AY468486
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100.0%; Pred. No. 1.2e-19;
iive 0; Mismatches 0;
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/db_xref="GI:336147"
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/db_xref="GI:336149"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296. 964
/note="surface protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:35269"
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/note="direct repeat"
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/note="direct repeat"
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/note="core protein"
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Woodchuck hepatitis B virus
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           GI:336146
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Best Local Simi
Matches 101;
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DEFINITION
ACCESSION
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                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
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/product="x protein"
/product="x protein"
/protein_id="AA46766.1"
/db_xref="G1:336139"
/db_xref="G1
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FHLSCLTFGQHTVQEFLVSFGVWIRTPAPYRPPNAPILSTLPEHTVIRRRGGARASRS
PRRRTPSPRRRRSGSPRRRRSQSPSANC"
                                                                                                                                                                                                                       SESVSVSTRNLSNNISDKSQKSTRTGLCSYKQIQTDRLEHLARISCGSKITIGQQGSS
PKTLYKSISSNFRNQTWAYNSSRNSGHTTWFSSASNSNKSRSREKAYSSNSTSKRYSP
PLNYEKSDFSSPGVRRRITRLDNNGTPTQCLWRSFYNTKPCGSYCIHHIVSSLDDWGP
                                                                                                                                                                                                                                                                                                                               CTVTGDVTIKSPRTPRRITGGVFLVDKNPNNSSESRLVVDFSQFSRGHTRVHWPKFAV
BUNGTLANLLATNLQMLSLDVSAAFYHIPISPAVPHLLVGSPGLERFRYTGLSSSTHN
RNNSQLQTHAHLCTPHYVSSLLIFKTYGRKLHLLAHPINGFRKLPROYGLSPFLLA
QFTSALASMVRRNFPHCVVFAYMDLVLGARTSEHLFAISINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKWWGNHLHFMGYVITSSGVLPQDKHVKKISRYLRSVPVNQPLDYKICERLTGILNYV
APFTLCGYAALMPLYHAITSRTAFIFSSLYKSWLLSLYEELWPVVRQRGVVCTVFADA
TPTGWGIATTYQLLSGTFAFPLPIATAELIAACLARCWTGARLLGTDNSVVLSGKLTS
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LAGLQVVYSPEMTKILTIAGNLDWWHSLSRPGGSTBECTGONSGPGTCKHLDFSCPPTC
NGFRWWYLRR PILLVILLICLI PLIVLLLOCH PLIVLLDWKGLI PVCPLQPTTTVNCRQCTISAO
DMYTPPYCCCLKPTAGNCTCWPIPSSWALGNYLWEWALARFSWI.NILVPLLQWLGGIS
                                                                            translation="MHPPSRLFRNIQSLGEEEVQELLGPPEDALPLLAGEDLNHRVAD"
                                                                                                               ALNLHLPTADLOWVHKTNAITGLYSNQAAQFNPHWIQPEFPELHLHNDLIOKLOQYFG
PLTINEKRKLQLNFPARFFFPKATKYFPLIKGIKONYFNFALEHFFATANYLWTAWEAG
                                                                                                                                                                                            1LYLRKNQTTLTFKGKPYSWEHRQLVQHNGQQHKSHLQSRQNSSMVACSGHLLHNHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPWLLACVANWILRGISFCYVDSALNPADLPSRGLLPVLRPLPRLRLRPQTSRISLWA
ASPPVSPRRFVRVAWSSPVQNCEPWIPP"
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KPGPIIVPGIRDIPRGLVPPQTPTNRDQGRKPTPPTRDPTHDHLTMKNQTFHLQGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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100.0%; Pred. No. 1.2e-19;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="surface protein"
protein_id="AAA46766.1"
db_xref="GI:336137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296. .961
/product="surface protein"
1503. .1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(2992. .3323,1. .964)
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db_xref="GI:336140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oin(2992. .3323,1. .295
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product="core protein"
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LOCUS DEFINITION ACCESSION

RESULT 12

OHVHEPBA

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ORIGIN

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AX663053.1 GI:29163598
                                  synthetic construct
synthetic construct
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AUTHORS
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JOURNAL
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AUTHORS
TITLE
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/drotein_id="Mar24091.1"
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DRWEPELNEAIPNGMSTTWPVFAATTLRKLITGELLTLAGROQLIDWMEAVRAGEL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATWDERNRQIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="3' LTR; self-inactivating 3' LTR version; distal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                          2 (bases 1 to 7207)
Kusk, P. and Johansen, J.
Direct Submission
Submitted (19-NOV-2003) NsGene A/S, Baltorpvej 154, Ballerup
                       Lentiviral transfer vector phsCXW
Lentiviral transfer vector phsCXW
other sequences; artificial sequences; vectors.

1 (bases 1 to 720)
Johaneen J., Pornoe, J., Rosenblad, C., Dago, L. and Kusk, P.
Improved lentiviral transfer vector
Outpublished
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'note="Woodchuck post-regulatory element; WPRE"
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                                                                                                                                                                                                                                                                                     'organism="Lentiviral transfer vector pHsCXW'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                          686. .823
/note="packaging signal; psi"
1310. .1514
/note="Rev_responsive element; RRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omplement (2674. .2693)
note="T7 recognition/binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="ampicillin resistance gene"
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0
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/note="CMV promoter"
2618. .2671
/note="multiple cloning site"
complement (2674. .2693)
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                                                                                                                                                                                                                                                                                                /mol_type="other DNA"
/db_xref="taxon:256321"
1. _634
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                                                                                                                                                                                                                                                                                                                                                           'note="5' HIV-1 LTR"
                                                                                                                                                                                                                                           Location/Qualifiers
1. .7207
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 GI:38565537
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   AY468486.1
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                                                     ORGANISM
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TITLE
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AX663053
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PAT 22-MAR-2003

linear

DNA

AX663053 7515 bp Sequence 4 from Patent WO02086132. AX663053

LOCUS DEFINITION ACCESSION

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/translation="GLLPVCPLQPTTETTVNCRQCTLSVQDTYTPPYCCCLKPTAGNC
TCWPIPSSWALGNYLWEWALARFSWLNLLVPLLQWLGGISLIAWFLLIWMIWFWGPAL
LSILPPFIPIFVLFFLIWVYI"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinoma
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Woodchuck hepatitis virus surface antigen (preS) and X protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="protein coding region crossing over viral/host
boundary"
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source text: Woodchuck hepatitis virus DNA, clone Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 7808)
Yamazoe,M., Nakai,S., Ogasawara,N. and Yoshikawa,H.
Integration of woodchuck hepatitis virus (WHV) DNA at two
Chromosomal sites (Vk and gag-like) in a hepatocellular ca
Gene 100, 139-146 (1991)
                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                    Length 7515;
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                                               Kingsman, S.A., Mitrophanous, K. and Ellard, F.M.
                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 6;
ilarity 100.0%; Pred. No. 1.2e-19;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                             /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="pSmart2 MCS 5prime cppt"
                                                                                                                                                                 1. .7515
/organism="synthetic construct"
other sequences; artificial sequences.
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4123. .4496
/note="viral coding region"
                                                                  Vector system
Patent: WO 02086132-A 4 31-OCT-2002;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="surface antigen"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Marmota monax'
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M60766.1 GI:191471
X protein; surface protei:
Marmota monax (woodchuck)
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les 101; Conserv
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| CDS | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER | LATER
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AAD28308
AAD28269
ADM68969
                                                  AAD32075
ADL35206
AAD32076
                                                                                                  ADL35211
ADL35210
                                                                   ADL35208
                                                                             7033
7248
July 14, 2005, 04:35:42 ; Search time 142.398 Seconds
(without alignments)
4198.742 Million cell updates/sec
                                                                1 tgccttgcccgctgctggac......ccatggctgctcgcctgtgt 101
                                                                                                       8780412
   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                           4390206 seqs, 2959870667 residues
                                                      US-09-482-682-65_COPY_4192_4292
                        nucleic search, using sw model
                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

Add28274 Alpha-lac Add88974 Alpha-lac Add88971 Alpha-lac Add82070 Alpha-lac Add22078 Human alp Add22078 Human alp Add32076 Human alb Add32076 Human alb Add32076 Plasmid p Add32070 Plasmid p Add35207 Plasmid p Add35207 Plasmid p Add35207 Plasmid p Add35212 Plasmid p Add35212 Plasmid p Add35212 Plasmid p Add35210 Plasmid p Add35210 Plasmid p Add35210 Plasmid p Add35210 Plasmid p Add35210 Plasmid p Add35210 Plasmid p Add28309 Alpha-lac Add28309 Alpha-lac Adm68970 Alpha-lac

## ALIGNMENTS

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

seq length: 0 seq length: 200000000

88

Minimum

N\_Geneseq\_16Dec04:\*

Database

genesegn1980s:

ADM68970 ACH00963

woodchuck hepatitis virus; postranscriptional regulatory element; ds; New trans-lenti viral vector systems with cis-acting sequences, polypurine tract-central terminators, etc., useful for gene transfer, e.g. delivering genes encoding therapeutic or viral inhibitory polypeptides to cells. integrase; gag; gag-pol precursor; polypurine tract-central terminator sequence; PPT-CTS; gene transfer; gene expression; transduction; replication competent retrovirus; RCR. trans-lenti viral vector system; Vpr; Vpx; reverse transcriptase; Woodchuck hepatitis virus postranscriptional regulatory element. BP 24-JUL-2002; 2002US-00202457. 98US-00089900. 14-DEC-1999; 99US-00460548. 13-NOV-2000; 2000US-00709501. Woodchuck hepatitis B virus. ADA38373 standard; DNA; 592 20-NOV-2003 (first entry) WPI; 2003-625514/59. (KAPP/) KAPPES J C. (WUXX/) WU X. Wu X; US2003072938-A1. 03-JUN-1998; 17-APR-2003 Kappes JC, ADA38373; ADA38373 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:\* geneseqn2004as:\* geneseqn2004bs:\* geneseqn2003cs:

geneseqn2001bs:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\*

geneseqn2001as:\* geneseqn2002as:

geneseqn1990s:\*

	Description	Ada38373 Woodchu			Add67513 WPRE	Ado25310 Woodch	Aad55114 HflapUr	Acc45098 HIV-1 f		Adm47497 Lysosc	Adm47498 Lysosc	Aaa59091 Nucleot	Adf48775 fibre	Adm82791 DNA re	Adm82791 DNA re	Adm82792 DNA re	Acd27899 pdmT2 v	Aax32299 Nucleot	Ado01085 Woodch	Ade24111 Provir	Aad28271 Alpha-1
SUMMARIES	a	ADA38373	AAD55110	ACC45094	ADD67513	AD025310	AAD55114	ACC45098	ABV77010	ADM47497	ADM47498	AAA59091	ADF48775	ADM82791	ADM82791	ADM82792	ACD27899	AAX32299	AD001085	ADE24111	AAD28271
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	* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	93.7	93.7	93.7	90.5
	Score	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	94.6	94.6	94.6	91.4
	Result No.		7	e	4	Ŋ	9	7	80	σ	10	11	12	13	c 14	c 15	16	17	18	19	20

Ada38173 Woodchuck Add55110 Woodchuck Add57513 WPRE elem Ado25310 Woodchuck Add55114 HflapUbig Acc4508 HIV-1 fla Abv77010 Nucleotid Adm47498 Lysosomal Adm47498 Lysosomal Adm47498 Lysosomal Adm87791 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82792 DNA repai Adm82792 DNA repai Adm82792 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82791 DNA repai Adm82791 DNA repai 10 ADE24111 6 AAD28271 3671 90.5 94.b 91.4

The invention describes a trans-lenti viral vector system. The new trans-

Example 5; Page 7; 19pp; English

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conciding at least one fusion protein comprising a functional portion of a perceiving at least one fusion protein comprising a functional portion of a Reverse Transcriptase polypeptide fused in frame to a functional portion of a Reverse Transcriptase polypeptide fused in frame to a functional portion of the verse polypeptide fused in frame to a functional portion of a paintegrase polypeptide, where the first nucleic acid segment is capable of expression in a mammalian cell, and where the functional portion of the very properties and protein into a viral particle; a second nucleic acid segment comprising a nucleotide sequence encoding a proteins of a Gag polypeptide and functional portion of a Gag polypeptide and functional portion of a protease polypeptide, where the second nucleic acid does not concode a functional Reverse Transcriptase polypeptide or a functional concoderation of a capable of concoderation and sequence encoding a functional envelope polypeptide or a functional concoderation and entry of the viral particle into a target cell, where the third nucleic acid segment does not encode a functional equivalent of a polypurine tract-central terminator sequence and at least on nucleotide sequence and at least on nucleotide sequence and at least on nucleotide sequence and at least on nucleotide sequence and at least on nucleotide sequence and at least on nucleotide sequence and at least on nucleotide sequence and at least on nucleotide sequence and at least on nucleotide sequence on system proteir system proteir system produces a viral particle capable of introducing the concoderation of the genome of the target cell. The trans-lent viral vector system is configurable of introducing heterologous nucleotide sequences of the target cell. The trans-lent viral vector system is particles capable of introducing heterologous nucleotide sequences (which encode viral inhibitory polypeptides or a therapeutic of particles particles particles particles particles particles particles particles particles particles parti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           creation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retrovirus (RCR) events. This sequence represents woodchuck hepatitis
virus postranscriptional regulatory element (WPRE) used in the creatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the trans-lenti viral vector system.
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1 TGCCTTGCCCGCTGCTGGACAGGGCTCGGCTGTTGGGCCACTGACAATTCCGTGGTGTTG 60
                                                            Gaps
                                                           ö
                             Length 592;
Sequence 592 BP; 77 A; 188 C; 148 G; 179 T; 0 U; 0 Other;
                                                         0; Indels
                                                                                                                                                                  TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 428
                                                                                                                                                 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 101
                             100.0%; Score 101; DB 9; 100.0%; Pred. No. 4.8e-22;
                                                            Mismatches
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                            Query Match
Best Local Similarity
                                           Best Local Sim:
Matches 101;
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Transgenic; biotechnology; Woodchuck hepatitis virus regulator element;
                                                                        Woodchuck hepatitis virus regulator element (WRE) DNA.
        BP.
        AAD55110 standard; DNA; 604
                                                                                                                     Woodchuck hepatitis B virus.
                                                      (first entry)
                                           (revised)
                                           27-OCT-2003
07-AUG-2003
                           AAD55110;
AAD55110
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WO2003022040-A2.

20-MAR-2003

(CALY ) CALIFORNIA INST OF TECHNOLOGY.

13-SEP-2001; 2001US-0322031P. 09-JAN-2002; 2002US-0347782P.

12-SEP-2002; 2002WO-US029157

20-MAR-2003

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Transgenic animal; transgenic bird; transgenic fish; transgene; retroviral construct; lentiviral; long terminal repeat; LTR; WRE; biotechnology; agriculture; woodchuck hepatitis virus; regulator element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                commercial use, which comprises transfecting a packaging cell line with retroviral construct, recovering recombinant retrovirus from the cell line and infecting embryonic cell with the recombinant virus. The method is useful in producing transgenic animals using retroviral constructs engineered to carry a transgene of interest. The transgenic animals may find use in commercial applications like biotechnology and agriculture. The present sequence is Woodchuck hepatitis virus regulator element (WRE) DNA used to illustrate the method of the invention. (Updated on 27-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                   Producing a transgenic animal for commercial use, comprises transfecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 604 BP; 81 A; 190 C; 150 G; 183 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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11 Similarity 100.0%; Pred. No. 4.8e-22;
101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                 Lois-Caballe C,
                                                                                                                                                                                              (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 18B; 76pp; English.
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                            12-SEP-2002; 2002WO-US029130
                                                                                           13-SEP-2001; 2001US-0322031P.
09-JAN-2002; 2002US-0347782P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to
                                                                                                                                                                                                                                                             Baltimore D, Hong EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant virus.
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use in commercial applications like biotechnology and agriculture. The present sequence represents a woodchuck hepatitis virus regulator element (WRB) nucleotide sequence, which is used in an example from the present invention. (Updated on 27-ocr-2003 to standardise OS field)
                                                                                                                                                                                                                The present invention describes a method for producing a transgenic bird or fish. The method comprises transfecting a packaging cell line with a retroviral onstruct, recovering recombinant retroviral particles from the packaging cell line, and infecting a bird or a fish egg with the recombinant retroviral particles. The retroviral construct comprises the R and US sequences from a 5' lentiviral long terminal repeat (LTR) and a self-inactivating 3' lentiviral LTR. Also described is a transgenic bird or fish made by the above method whose genome comprises a proviral DNA that has a self-inactivating 3' lentiviral LTR. The method is useful using retroviral constructs engineered to carry a transgene of interest. The method is used to introduce the gene of choice into animals in order to confer upon them desired attributes. The transgenic animals may find
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing a transgenic bird or fish for commercial use, comprises transfecting a packaging cell line with retroviral construct, recovering recombinant retrovirus from the cell and infecting bird or fish egg with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuroprotective; antiparkinsonian; nootropic; anticonvulsant; transgene delivery; WPRE element; APPS'UTR; tau3'UTR; TH3'UTR; vector; neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCTTGCCCGCTGCTGGACAGGGGCTCCGCTGTTGGGCACTGACAATTCCGTGGTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 604;
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                       Pease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                     Lois-Caballe C,
                                                                                                                                                                                   Example 1; Fig 18; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.'
Matches 101; Conservative
                     Hong EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPRE element #SEQ ID 1.
                                                                                                                                             the recombinant virus
                                                      WPI; 2003-301005/29.
                   Baltimore D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3P1361277-A1
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Gaps

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The invention relates to a vector for transgene delivery into mammalian cells. The vector comprises a chimeric genetic construct with a transgene operably linked to at least two distinct posttranscriptional regulatory elements. e.g. WPRE element, APPS'UTR, tau3'UTR or TH3'UTR region. The transfer comprises the nuclectide sequence of 609, 95, 237 and 91 bp, respectively ADD67513-ADD67516. The vector comprises a promoter controlling transcription of the transgene in the mammalian cells, a marker gene and a polyadenylation signal operably linked to the controlling transcription of the transgene in the mammalian cells, a marker gene and a polyadenylation signal operably linked to the cransgene. The vector is a plasmid or a recombinant virus. The vector or recombinant cell is used for the manufacture of a medicament for treating a disease. The vector, recombinant cell or composition is useful for treating a human disease, e.g. neurodegenerative diseases selected from Parkinson's disease or retinal degenerative diseases. They can also be used in experiments research or prophylactic areas. The current sequence correpresents the WPRE element nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 recentecececrecidedededececrecidentesecretarentesecretaren 397
                                                                                     New vector, for transgene delivery into mammalian cells, comprising a chimeric genetic construct with a transgene linked to a WPRE element, APP5'UTR, tau3'UTR or TH3'UTR region, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGCCTTGCCCGCTGCTGGACAGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; porcine; uroplakin II gene; promoter; expression vector; surrogate mother animal; transgenic animal; urine; bladder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 609 BP; 83 A; 191 C; 151 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.8e-22;
                 Dufour N, Faucon-Biguet N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 101;
                                                                                                                                                                                   Claim 9; SEQ ID NO 1; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08; PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AD025310 standard; DNA; 632 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-2002; 2002KR-00067856.
03-NOV-2003; 2003KR-00077256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-2003; 2003WO-KR002339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Woodchuck hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHO-A PHARM CO LID.
                                                                                                                                            neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 101; Conservative
                                                    WPI; 2003-879907/82.
                 Mallet J, Brun S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004042062-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD025310
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WPI; 2003-300976/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                    The invention relates to a novel porcine uroplakin II gene promoter (I).

An expression vector containing the promoter is useful in a method of producing useful proteins which involves implanting the vector into a surrogate mother animal, obtaining transgenic animals from the surrogate mother animal. Detaining transgenic animals from the unine of the transgenic animals. The promoter, the expression vector, and the transgenic animals. The promoter, the expression vector, and the transgenic animal can be used in the producion field of useful proteins that are medicinally valuable. The promoter promotes the bladder-specific expression of a target protein at high efficiency. An animal which was transformed using the promoter, so as to express the target protein content in its urine at high concentration, and the protein thus produced shows a superior physiological activity to that of the same kind of the existing protein. This sequence represents the administration of the concentranslation and the produced shows a superior physiological activity to that of the same kind of the existing protein. This sequence represents the administration and the produced shows a superior physiological activity to that of the same kind of the existing protein. This sequence represents the administration and the produced shows a superior physiological activity to that of the same kind of the existing protein. This sequence represents the same confirming the same kind of the same confirming the same kind of the same confirming the same kind of the same confirming the same kind of the same confirming the same kind of same confirming the same kind of the same confirming the same kind of same confirming the same kind of same confirming the same kind of the same confirming the same kind of same confirming the same kind of the same confirming the same kind of the same confirming the same kind of same confirming the same kind of same confirming the same kind of same confirming the same kind of same confirming the same confirming the same co
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                                                                                                                                                                                                                                                                                                                                                                                    sequence which is used as a marker gene for cloning of genes of interest and linking to the porcine uroplakin II gene promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGCCTTGCCCGCTGCTGGACAGGGGCTCGCTGTTGGGCACTGACAATTCCGTGTGTTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic; biotechnology; agriculture; green fluorescent protein; GFP; Woodchuck hepatitis virus regulator element; WRE; human; ubiquitin; Human immunodeficiency virus type 1; HIV-1; chimeric; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                   Novel porcine uroplakin II gene promoter, useful for promoting the bladder-specific expression of a specific target protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 12; Length 632; 100.0%; Pred. No. 4.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 632 BP; 80 A; 201 C; 158 G; 193 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                       Claim 7; SEQ ID NO 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HflapUbiGWRE chimeric construct DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD55114 standard; DNA; 2853 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2001; 2001US-0322031P.
09-JAN-2002; 2002US-0347782P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2002; 2002WO-US029130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
Woodchuck hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baltimore D, Hong EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003022040-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                 The invention relates to a method for producing a transgenic animal for commercial use, which comprises transfecting a packaging cell line with retroviral construct, recovering recombinant retrovirus from the cell line and infecting embryonic cell with the recombinant virus. The method is useful in producing transgenic animals using retroviral constructs engineered to carry a transgene of interest. The transgenic animals may find use in commercial applications like biotechnology and agriculture. The present sequence is Hilaphicomes chimneric construct DNA comprising Human immunodeficiency virus type 1 (HIV-1) NL4.3 flap sequence, green fluorescent protein (GFP) variant encoding sequence, human ubiquitin promoter sequence and Woodchuck hepatitis virus regulator element (WRE). This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Producing a transgenic animal for commercial use, comprises transfecting
                                a packaging cell line with retroviral construct, recovering recombinant retrovirus from the cell line and infecting embryonic cell with the recombinant virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV-1 flap + ubiquitin + GFP + WRE construct DNA sequence SEQ ID NO:8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 101; DB 8; Length 2853; 100.0%; Pred. No. 6.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2853 BP; 564 A; 774 C; 858 G; 657 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                            Example 1; Fig 21; 76pp; English.
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09-JAN-2002; 2002US-0347782P.
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Woodchuck hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC45098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The present invention describes a method for producing a transgenic bird or fish. The method comprises transfecting a packaging cell line with a retroviral construct, recovering recombinant retroviral particles from the packaging cell line, and infecting a bird or a fish egg with the recombinant retroviral particles. The retroviral construct comprises the recombinant retroviral particles. The retroviral construct comprises the self-inactivating 3' lentiviral LTR. Also described is a transgenic bird or fish made by the above method and whose genome comprises a proviral DNA that has a self-inactivating 3' lentiviral LTR. The method is useful in producing transgenic animals, particularly transgenic birds and fish, using retroviral constructs engineered to carry a transgene of interest. The method is used to introduce the gene of choice into animals in order to confer upon them desired attributes. The transgenic animals may find use in commercial applications like biotechnology and agriculture. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents a construct nucleotide sequence comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-1 sequence, a green fluorescent protein (GFP) variant sequence, a human ubiquitin promoter sequence and a woodchuck hepatitis regulator element sequence, which is used in an example from the present invention
recombinant retrovirus from the cell and infecting bird or fish egg with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2853 BP; 564 A; 774 C; 858 G; 657 T; 0 U; 0 Other;
                                                                                           Example 1; Fig 21; 68pp; English.
                                   the recombinant virus
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2559 TGCCTTGCCCGCTGCTGGACAGGGGCTCGGTGGTGTGGGCACTGACAATTCCGTGGTGTTG 2618 ö 1 TGCCTTGCCCGCTGCTGGACAGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG 60 Gaps ő Length 2853; 0; Indels 2619 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCTGTGT 2659 61 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 101 100.0%; Score 101; DB 8; 100.0%; Pred. No. 6.5e-22; 0; Mismatches Matches 101; Conservative Local Similarity Query Match 셤 8 8 셤

ABV77010 standard; DNA; 7515 BP (first entry) 03-MAR-2003 ABV77010; œ RESULT

Nucleotide sequence of plasmid pSmart2 5'cppt.

Viral vector; adipose tissue; adipose tissue metabolism; obesity; diabetes; blood disorder; vascular disease; ss.

Synthetic

WO200286132-A2.

31-0CT-2002

19-APR-2002; 2002WO-GB001830

20-APR-2001; 2001GB-0009781

Ellard FM; Mitrophanous K, Kingsman SA,

(OXFO-) OXFORD BIOMEDICA UK LTD

WPI; 2003-093139/08.

Use of viral vector system for transducing a target adipose tissue site, and for treating and/or preventing vascular diseases or diseases associated with death or impaired function of adipose tissue cells, such as obesity and diabetes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid molecule capable of expressing a lysosomal enzyme. The nucleic acid molecule comprises at least a sequence coding for the lysosomal enzyme and a promoter highly active in the brain inserted upstream from the sequence. Compositions and methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases e.g. Gaucher type I disease, Hurler disease (MPSI) or Sanfilippo disease (MPSIII) in humans. The invention is also useful in gene therapy. The present sequence is a DNA related to the invention.
                              The specification describes the use of a viral vector system for transducing a target adipose tissue site. The viral vector system is useful for transducing a target adipose tissue site, in the manufacture of a pharmaceutical composition for treating and/or preventing a disease associated with a derangement in the metabolism of adipose tissue, such as obesity and diabetes. The viral vector system is also useful for treating and preventing a disease associated with death or impaired function of adipose tissue cells, a disease associated with hereditary blood disorders, and vascular diseases. The present sequence represents plasmid pSmart 5'cppt, which is used to construct vectors for use in the
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                                                                                                                                                                                                                                                                                                                                                   Gaps
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Hurler disease; Sanfilippo disease; gene therapy; ds.
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                                                                                                                                                                                                                                                                     Sequence 7515 BP; 1978 A; 1733 C; 1829 G; 1975 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                           100.0%; Score 101; DB 8;
100.0%; Pred. No. 7.8e-22;
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Example; Page 65-67; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                   invention
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RESULT 10 ADM47498

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4192 TGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG 4251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL exons. The nucleic acid is used to produce an adenovirus vector particle, deliver an exogenous gene to a target cell, pseudotype recombinant viral vectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a gutless adenoviral vector particle. The present sequence represents plasmid pDV90, which contains a TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid comprising an adenovirus tripartite leader nucleotide for producing high-capacity and targeted vectors for adenovirus-based
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3807 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 3847
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
(SCRI ) SCRIPPS RES INST.
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                                                                                                                                                                                                                                                                                                                                                  sequence of plasmid pDV90.
                                                                                                                                                         BP
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                                                                                                                                                         AAA59091 standard; DNA; 8484
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Hurler disease; Sanfilippo disease; gene therapy; ds.
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                             Sequence 7648 BP; 1546 A; 2244 C; 2052 G; 1806 T; 0 U; 0 Other;
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                                                                                       Score 101; DB 12;
Pred. No. 7.8e-22;
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                                                                                       100.0%;
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                                                                                                                     Similarity
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                                                                                                                     Best Local Sim:
Matches 101;
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                                                                                    Query Match
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(first entry)

12-FEB-2004

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cytostatic; anti-HIV; gene therapy; HIV gene expression inhibitor expression construct pDV90.

HIV gene expression activation; adenovirus tripartite leader; TPL; gutless adenoviral vector particle; helper-independent fiberless recombinant adenovirus vector; packaging cell line; pseudotrping; adenovirus vector; gene therapy; hereditary disorder; tumour; HIV infection; fibre expression construct;

ds; circular; cyclic.

Human adenovirus type 5. Synthetic

US2003157688-A1.

21-AUG-2003

14-JAN-2000; 2000US-00482682

26-JUN-2000; 2000US-00423783. 99US-0115920P 14-JAN-1999;

(VSEG/) VON SEGGERN D J. NEMEROW G R. NEME/)

HALLENBECK E (HALL/) I (STEV/) ! (SKRI/) !

SKRIPCHENKO Y

Hallenbeck P, Stevenson S; Von Seggern DJ, Nemerow GR, Skripchenko Y; Skripchenko

WPI; 2003-843463/78.

Novel isolated nucleic acid molecule useful for delivering heterologous gene to human or any animal, or for producing gutless adenoviral vector particle.

Claim 10, SEQ ID NO 65; 157pp; English.

The invention describes an isolated nucleic acid molecule (I) comprising an adenovirus tripartite leader (TPL) nuclectide, the TPL nuclectide an adenovirus tripartite leader (TPL) nuclectide, the TPL nuclectide comprising a first and second different TPL exons chosen first, second and third same or different TPL exons, the TPL exons chosen from complete or partial TPL exon, complete TPL exon 2 and complete TPL exon 3. (I) is useful for delivery of an animal, or for producing a gutless adenoviral vector particle. A recombinant adenovirus particle (II) is useful for delivery of an amount of (II) sufficient to infect the cell. A helper-independent complements recombinant adenovirus vector genome (III) is useful for producing an adenovirus vector particle containing (III) which involves providing a packaging cell line which complements replication and packaging of the genome and (III) which is deficient in expressing packaging of the genome and (III) which is deficient in expressing containing particles and harvesting the particle produced by the cell containing particles and harvesting the particle produced by the cell containing particles and harvesting the particle produced by the cell containing particles and harvesting the particle produced by the cell containing particles and harvesting the particle produced by the cell containing particles and harvesting the demovirus vector. (III) is also useful for specifically calpendent adenovirus vector to a cell of choice. (I) is useful for readucing proliferation of tumour cells in a subject, or capture, and for reducing proliferation of tumour cells in a subject, or containing particles and particles represents a fibre expression containing a particle or cell seaful cor represents a fibre expression containing particles and particles or expression containing particles and particles or expression containing particles and particles and particles and particles are particles and particles are particles and particles and particles are particles and particles are particles construct containing a post-transcriptional regulatory element

Sequence 8484 BP; 1996 A; 2238 C; 2125 G; 2125 T; 0 U; 0 Other;

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                                                 Gaps
  100.0%; Score 101; DB 10; Length 8484; 100.0%; Pred. No. 8e-22; cive 0; Mismatches 0; Indels 0;
Query Match 100.
Best Local Similarity 100.
Matches 101; Conservative
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4192 TGCCTTGCCCGCTGCTGGACAGGGGTTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG 4251 inducer; inhibitor; DNA repair pathway; anti-HIV; cytostatic; virucide; antidiabetic; neuroprotective; retroviral infection; AIDS; HIV infection; cancer; human adult T-cell leukaemia; lymphoma; feline immunodeficiency virus; Type I diabetes; multiple sclerosis; gene therapy; human; cyclic; circular; CMV promoter; ss. 9 Screening for compounds that modulate a DNA repair pathway and/or retroviral integration, useful for treating retroviral infection, comprises determining the amount of a retroviral cDNA circularization in TGCCTTGCCCGCTGCTGGACAGGGGCTCGCTGTTGGGCACTGACAATTCCGTGGTGTTG DNA repair pathway related retroviral vector cDNA with CMV promoter. 4252 rcegegaagcreacercerrecarescrececerers 4292 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 101 Claim 73; SEQ ID NO 5; 89pp; English. the presence of the test compound. 뮴 ADM82791 standard; cDNA; 9731 04-APR-2003; 2003WO-US010302. 05-APR-2002; 2002US-0370376P. 03-JUN-2004 (first entry) Yoder KE; WPI; 2003-854096/79. (FISH/) FISHEL R A. (YODE/) YODER K E. WO2003089573-A2 Unidentified. 30-OCT-2003. Fishel RA, ADM82791; -61 RESULT 13 ADM82791 a 셤 ð

The invention relates to a novel method for screening for inducers or inhibitors of a DNA repair pathway by contacting at least one component of a DNA repair pathway with a non-circularized retroviral cDNA in the presence and absence of a test compound, and determining whether circularization of the cDNA is increased or decreased in the presence of the test compound. The DNA repair pathway components have the following activities: anti-HIV, cytostatio, virucide, antidiabetic, and neuroprotective. The method is useful for identifying compounds that used in manufacturing a pharmaceutical composition for the treatment of a retroviral infection (e.g. AIDS, HIV infection, cancer, human adult Tection (e.g. AIDS, HIV infection, cancer, human adult Tection or for inereasing the efficiency virus, Type I diabetes or multiple sclerosis) or for increasing the efficiency of gene delivery in a gene therapy. This polymucleotide represents a retroviral cDNA Sequence 9731 BP; 2444 A; 2412 C; 2548 G; 2327 T; 0 U; 0 Other; Length 9731; Query Match 100.0%; Score 101; DB 11; Best Local Similarity 100.0%; Pred. No. 8.2e-22; Matches 101; Conservative 0; Mismatches 0; sequence of the invention

1 TGCCTTGCCCGCTGCTGGACAGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG

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6513 TGCCTTGCCCGCTGCTGGACAGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG 6572
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                                                                                                                                                                                                                                      inducer; inhibitor; DNA repair pathway; anti-HIV; cytostatic; virucide; antidiabetic; neuroprotective; retroviral infection; AIDS; HIV infection; cancer; human adult T-cell leukaemia; lymphoma; feline immunodeficiency virus; Type I diabetes; multiple sclerosis; gene therapy; human; cyclic; circular; CMV promoter; ss.
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                                                      6573 rcgggaagcrgacgrccrrrccarggcrgcrcccrgrgr 6613
                           TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 101
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                                                                                                                          ADM82791 standard; cDNA; 9731 BP
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Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fishel RA, Yoder KE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inducer; inhibitor; DNA repair pathway; anti-HIV; cytostatic; virucide; antidiabetic; neuroprotective; retroviral infection; AIDS; HIV infection; cancer; human adult T-cell leukaemia; lymphoma; feline immunodeficiency virus; Type I diabetes; multiple sclerosis; gene therapy; human; cyclic; circular; MSH2 promoter; ss.
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                                  7228 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 7188
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61 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT
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; Pred. No. 8.2e-22;
0; Mismatches 0;
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7288 TGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGGCACTGACAATTCCGTGGTGTTG 7229

TGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTG 60

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1280 TCGGGGAAGCTGACGTCCTTTCCATGGCTGCTCGCCTGTGT 1240

Search completed: July 14, 2005, 07:01:51 Job time: 145.448 secs

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AY538700 Serratia AY538701 Serratia AY538699 Serratia AY538699 Serratia AY394610 Klabsiell AJ08558 Escherich AY392531 Streptoco AY42562 Streptoco AY42562 Streptoco AY426262 Streptoco

AY394610 ECO308558

AY452662 AF104441 AF104442

AY538698 AY589493

103356 Sequence 4 AY628199 Escherich AF535127 Klebsiell AY243512 Klebsiell AY628175 Escherich AY101764 Klebsiell AR371489 Sequence

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1 (bases 1 to 142)
Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 AGGGTTATTGTCTCATGAGGGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus polynucleotides and sequences Patent: US 6593114-A 2608 15-JUL-2003; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 101; DB 6;
100.0%; Pred. No. 8.7e-20;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR538046 142 bp DNA
Sequence 2608 from patent US 6737248.
AR538046
                                                                                                                                                                                                                                                                AR356490 142 bp DNN
Sequence 2608 from patent US 6593114.
AR356490

    142
    /organism="unknown"
    /mol_type="genomic DNA"

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                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
              1072
                                                                                                                                                                                                                                                                                                                       Unclassified.
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Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                Rosen, C.A.
Unknown.
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AR356490/c
LOCUS
DEFINITION
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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AR538046/c
                                                                                                                                                                                                                                                                                                                ORGANISM
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VERSION
KEYWORDS
SOURCE
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E00019 DNA coding
M10199 Plasmid pMM
E00018 DNA coding
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E01156 DNA fragmen
E01274 DNA encodin
E01302 DNA encodin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX260098 Sequence
AX260150 Sequence
A43886 Sequence 11
AR116755 Sequence
AX553171 Pseudomon
X97254 S. marcescen
Z92776 Caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101644 Sequence 1
L18624 Human chrom
BD195256 Nucleotid
                                                    July 14, 2005, 04:39:07; Search time 756.618 Seconds (without alignments) 6468.225 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                      AR356490 Sequence
                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                   1 agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101
                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                           9416466
       version 5.1.6
- 2005 Compugen Ltd.
                                                                                                                                           4708233 segs, 24227607955 residues
                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                    US-09-482-682-65_COPY_8384_8484
101
                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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HUMUT5345
BD195256
E010892
E01156
E01156
E01274
E01302
AX260098
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Maximum Match 100%
Listing first 45 summaries
                                     nucleic search, using sw model
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AR116755
AYS59171
SMTEMAQGE
CEC11F10
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E00019
PMMOENDO
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                                                                                                                          Gapop 10.0 , Gapext 1.0
       GenCore (c) 1993
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seq length: 2000000000
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11
6
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251
251
344
400
456
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              Copyright
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Maximum DB
                                     OM nucleic
                                                                                                    Sequence:
                                                                                                                                           Searched:
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No.
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PAT 17-AUG-2003

linear

AX195443 Sequence AY729027 Proteus m X54606 Pseudomonas

K54607 Pseudomonas K54604 Pseudomonas

PATN2PN1B PATN3PN1A

AY101764 AR371489 AY243512

AX195443 PATN1 PN2 AF027199

ALIGNMENTS

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Gaps

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0; Indels

Length 142;

9 48 PAT 08-OCT-2004

linear

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Query Match
                                                        RESULT 4
PMMOENDO/c
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                                                                                                  DEFINITION
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Matches
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VERSION
KEYWORDS
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PUBMED
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JOURNAL
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KEYWORDS
SOURCE
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E00018/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 AGGCTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 116
       Unclassified.

1 (bases 1 to 142)

Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriacea; Escherichia.

1 (Dases 1 to 228)

Uorutaa, G. and Karen, T.

VSYNTHERIS OF SELECTIVE AGED PROTEIN OR POLYPEPTIDE IN BACTERIA DINIV HARVARD
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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11-APR-1980 US 80 139225
UORUTAA PREUBAAD, KAREN TARWAATSUJI
C12P21/00,C07H21/00,C12N1/00,C12N15/00//C12R1/19; CC
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0
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Best Local Similarity 100.0%; Pred. No. 8.7e-20;
Matches 101; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 228;
                                                  Rosen, C.A.
Staphylococcus aureus polynucleotides and sequences
Patent: US 6737248-A 2608 18-MAY-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210. .>228
/product='E.coli penicilinase'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                   61 GGGTTCCGCCCCACATTCCCCCGAAAGTGCCACCTGACGTC 101
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DNA coding for Escherichia coli penicillinase.
E00019
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100.0%; Pred. No. 8.7e-20;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:562"
                                                                                                                                          /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .228
/organism="Escherichia
                                                                                                              1. .142
/organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *source: clone=pKT218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OS Escherichia coli
PN 1981154999-A/2
PD 30-NOV-1981 JP 198
PR 09-APR-1981 JP 198
PR 11-APR-1980 US 80
PI UNUTPA GIRUBAATO,
PC C12P21/00, C07711/0
Strandedness: Double;
CC topology: Linear;
CC antl-sense: No;
CC *Source: clone=pKT
FH Key
FT CDS 21
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP 1981154999-A/2
30-NOV-1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         topology: Linear;
anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                              E00019.1 GI:2168327
JP 1981154999-A/2.
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Escherichia coli
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Best Local S
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ACCESSION
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ORGANISM
ORGANISM
                         REFERENCE
AUTHORS
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AUTHORS
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KEYWORDS
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E00019/c
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                                                                                                                                                                                                                                                                                                                                                                                                    Borgmeyer, U. and Mizuroth, K.
Borgmeyer, U. and Mizuroth, K.
Resolution of Holliday structures by endonuclease VII as observed in interactions with cruciform DNA
Cold Spring Harb. Symp. Quant. Biol. 49, 815-825 (1984)
85153063
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Enterobacteriaceae; Escherichia.
                                                                                                                                             PMMOENDO 240 bp DNA linear BCT 26-APR-1
Plasmid pMM110 region of endo VII cleavage sites near cruciform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (Dases 1 to 251)
Uorutaa,G. and Karen,T.
SYNTHESIS OF SELECTIVE AGED PROTEIN OR POLYPEPTIDE IN BACTERIA
PPATENT: JP 1981154999-A 1 30-NOV-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ON BECKETCHIA COLI

PN JP 198115499-A/1

PD 30-NOV-1981

PP 09-APR-1981 UP 1981052488

PR 11-APR-1980 US 80 139225

PC C12P21/00,C07H21/00,C12N1/00,C12N15/00//C12R1/19; CC

Strandedness: Double;

CC topology: Linear;

CC anti-sense: No;

CC anti-sense: No;

CC fragment type: N-Terminal Fragment;

CC *Source: Clone=PKT241;
                                                                                                                                                                                                                                                                                                                                             other sequences; plasmids.
1 (bases 1 to 240)
Kemper,B., Jensch,F., von Depka-Prondzynski,M., Fritz,H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E00018 251 bp DNA linear
DNA coding for Escherichia coli penicillinase.
E00018
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115 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source text: Plasmid pMM110 DNA. Location/Qualifiers
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anti-sense: No;
fragment type: N'Terminal Fragment;
*source:_clone=pKT241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .240
/organism="Plasmid pMM110"
/mol_type="genomic DNA"
/db_xref="texon:2599"
/plasmid="Plasmid pMM110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E00018.1 GI:2168326
JP 1981154999-A/1.
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Escherichia coli
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Plasmid pMM110
                                                                                                                                                                                                  structures.
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OS Unidentified
PN JP 2002513277-A/43
PD 08-MAY-2002
PP 08-MAY-2004
PF 21-NOV-1997 JP 1998523916
PR 22-NOV-1996 US 60/031626,14-OCT-1997 US 60/061953 PI
PATRICK J DILLOM, GIL H CHOI, RODNEY A WELCH
PC C12N15/11,C12N15/63,C07K16/12,G01N33/569,G06F17/30,G11B7/00 CC
Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
CC Nucleotide sequence of Escherichia coli pathogenicity islands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 400)
Dillon, P.J., Choi, G.H. and Welch, R.A.
Nucleotide sequence of Escherichia coli pathogenicity islands
Patent: JP 2002513277-A 43 08-MAY-2002;
HUMAN GENOME SCIENCES INC, WISCONSIN ALUMNI RESEARCH FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ылуэгэб 400 bp DNA linear PAT 17-JUL
Nucleotide sequence of Bscherichia coli pathogenicity islands.
BD195256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 101; DB 11; Length 344; 100.0%; Pred. No. 8.7e-20; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                      Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 .224
/standard_name="STS UT5345"
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/map="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36. .60
complement(202. .224)
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Extension: 72C 20sec
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unidentified
unclassified.
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primer_bind
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BD195256/c
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VERSION
KEYWORDS
SOURCE
ORGANISM
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COMMENT
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                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 344)
Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L18624.1 GI:308338
STS; PCR primer; STS sequence; microsatellite marker; .
microsatellite repeat; repeat polymorphism; sequence tagged site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mature protein synthegis
Patent: US 4338397-A 1 06-UUL-1982;
President and Fellows of Harvard College; Cambridge, MA
                                      210. .>252
/product='E.coli penicilinase' FT
                                                                                                                                                                                                 Query Match

100.0%; Score 101; DB 6; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.7e-20;
Matches 101; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                      61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 bp ss-DNA
Sequence 1 from Patent US 4338397.
101644

    .251
    ^organism="Escherichia coli"
    mol type="genomic DNA"
    /db_xref="taxon:562"

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/organism="unknown"
/mol_type="unassigned DNA"
                                                                    al 190. 196.
Location/Qualifiers
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Gilbert, W. and Talmadge, K:
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Homo sapiens
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Best Local Similarity 100.
Matches 101; Conservative
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Unclassified.
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HUMUT5345
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PAT 17-JUL-2003

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61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCCACCTGACGTC 101
 /db_xref="taxon:32630"
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hypothetical: No;
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JP 1987083890-A/1.
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E 1 (bases 1 to 456)
S Okai, H., Momota, Y., Kumakura, T., Tochifusa, N., Kitazawa, T., Ojida, K. and Matsushiro, A.
POLYPEPTIDE SECRETION DEVELOPMENT VECTOR, MICROORGANISM TRANSFORMED WITH SAME, AND PRODUCTION OF POLYPEPTIDE WITH MICROORGANISM Patent: JP 1986140089-A 1 07-JUL-1986;
EARTH CHEM CORP LID
OS Artificial sequence; Genes.
PN JP 1986149089-A/1
PD 07-JUL-1986
PP 21-DEC-1986
PP 21-DEC-1986
PP 21-DEC-1986
PP 21-DEC-1986
PP 21-DEC-1986
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                                                                                                                                                                                                                                                                                                                                              E00892 456 bp DNA linear PAT 29-SEP-1997 Synthetic DNA encoding fused polypeptide between E coli beta-lactamase and human beta-urogastrone.
                                                                                                                                                                                                              1 AGGGTTATTGTCTCATGAGGGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 60
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TOCHIFUSA NORIYUKI,
KITDAMA TOSHIKI, OJIDA KAZUHIDE, MATSUSHIRO AIZO PC
5/00,C12N1/20,C12P21/00,(C12N1/20,C12R1:19),(C12P21/00, PC
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                                                                                                                                     100.0%; Score 101; DB 6; Length 400; 100.0%; Pred. No. 8.7e-20; cive 0; Mismatches 0; Indels
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    .400
    /organism='Unidentified'.

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*source: clone=pVG201;
Feature is identified by experimental;
Key
Location/Qualifiers
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/mol_type="genomic DNA"
Location/Qualifiers
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of beta-lactamase
200. .203
209. .438

    .400
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

                                        Location/Qualifiers
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topology: Linear;
hypothetical: No;
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JP 1986149089-A/1.
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Best Local Similarity 100.
Matches 101; Conservative
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E00892/c
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synthetic construct
1 (bases 1 to 456)
Yoshikawa, K., Momota, Y., Kajifusa, N., Koide, T. and Okai, H.
POLYPEPTIDE SECRETION EXPRESSION VECTOR, MICROORGANISM TRANSFORMED
BY SAID VECTOR AND PRODUCTION OF POLYPEPTIDE USING SAID
Patent: JP 1987083890-A 1 17-APR-1987;
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Length 456;
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/note='beta lactamase promoter'
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/product='beta urogastrone'
209. .277
278. .436
/product='beta urogastrone'
                                                                                                                                                                                               61 GGGTTCCGCGCACATTTCCCCGGAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                B01156 which secrets beta urogastrone.
Query Match 100.0%; Score 101; DB 6; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 101; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/do_xref="taxon:32630"
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Artificial sequence; Genes.
JP 1987083890-A/1
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synthetic construct
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                                                                                                      456 bp DNA linear PAT 29-SEP-1997
Signal peptide of beta-lactamase.
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31-JAN-1986 JP 1986021032
OKAI HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, ADACHI SHOJI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATSUBARA AKIMASA, OJIDA KAZUHIDE, YANO MAKI, MIHARA SHIGERU,
MATSUSHIRO AIZO, YANAIHARA NOBORU
C12P21/00,C12N15/00,(C12P21/00,C12R1:91);
                                                                                                                                                                                                             Delight GI:2169533

JP 1987179398-A/1.

Spitchetic construct

Synthetic 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide 278. .436
/product='beta-urogastron'
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113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
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/db_xref="taxon:32630"
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200. .203
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hypothetical: No;
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E01302.1 GI:2169561
JP 1987190083-A/1.
synthetic construct
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Homo sapiens
JP 1987190083-A/1
20-Aug-1987
14-FEB-1986 JP 1986031415
OKAI HIDBO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, KOIDE TAKAO,
MOMOTA YUTAKA
CI2N15/00,C07H21/04,C12N1/00,C12P21/02,(C12N1/00,C12R1:19), PC
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                                           Okai,H., Kumakura,T., Kawamoto,S., Koide,T. and Momota,Y.
POLYPPETIDE-EXPRESSION VECTOR, HOST TRANSFORMED WITH SAID VECTOR
AND PRODUCTION OF POLYPETIDE USING SAID HOST
PATENT: JP 1987190083-A 1 20-AUG-1987;
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Bukaryota, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
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other sequences, artificial sequences.
1 (bases 1 to 456)
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Patent: WO 0172774—A 60 04-OCT-2001;
Cyclacel Limited (GB)
Location/Qualifiers
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                                                                                                                                                        Artificial gene
Artificial sequence; Genes.
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200. .203
209. .277
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topology: Linear;
hypothetical: No;
anti-sense: No;
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Matches 101; Conservative
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Cuphea lanceolate

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Myrtales; Lythraceec Cuphea.

1 (bases 1 to 693)

1 (bases 1 to 693)

Hoericke-Grandpierre, C., Bothmann, H., Filsak, E.,
Hoericke-Grandpierre, C., Klein, B., Martini, N., Mueller, A.,
Schulte, W., Voetz, M., Walek, J. and Schell, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
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Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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100.0%; Pred. No. 8.7e-20;
iive 0; Mismatches 0;
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Patent: WO 0172774-A 112 04-OCT-2001;
Cyclacel Limited (GB)
Location/Qualifiers
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MAX PLANCK GESELLSCHAFT (DE)
Other publication CA 2169093 950316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (fruit fly)
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Sequence 11 from Patent W09507357.
A43586
A43586.1 GI:2298779
/db_xref="taxon:7227"
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AX260150.1 GI:16509172
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Best Local Similarity 100.
Matches 101; Conservative
                                                                                     Conservative
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                                                                   Similarity
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AX260150/c
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A43586
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version 5.1.6
- 2005 Compugen Ltd.
  GenCore (c) 1993 -
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July 14, 2005, Run on:

04:35:42; Search time 142.398 Seconds (without alignments) 4198.742 Million cell updates/sec

US-09-482-682-65\_COPY\_8384\_8484 Title:

Perfect score:

1 agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101

Scoring table:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003ds:\* geneseqn2003cs: geneseqn2001bs:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2004as: geneseqn2004bs: geneseqn2002as:\* geneseqn2001as: N\_Geneseq\_16Dec04: geneseqn1990s:\* geneseqn2000s:\* geneseqn1980s: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

						SUMMAKIES	
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Re	Result		Query				
,	No.	Score	Match	Match Length DB	DB	ID	Description
υ	н	101	100.0	142	7	AAV76919	Aav76919 Staphyloc
U	7	101	100.0	228	-	AAN10032	
O	m	101	100.0	251	н	AAN10031	Aan10031 Sequence
U	4	101	100.0	400	7	AAV31229	Aav31229 E. coli J
U	ŝ	101	100.0	456	н	AAN60624	Aan60624 Plasmid p
U	9	101	100.0	456	ч	AAN71080	Aan71080 Sequence
U	7	101	100.0	456	7	AAN70833	Aan70833 Beta-uroq
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U	ъ ъ	101	100.0	466	9	ABA90413	Aba90413 Drosophil
U	10	101	100.0	487	7	AAX21173	Aax21173 Polynucle
U	11	101	100.0	535	7	AAX21149	Aax21149 Polynucle
U	12	101	100.0	573	9	ABA90456	Aba90456 Drosophil
	13	101	100.0	605	12	ADH58311	Adh58311 Blectroph
U	14	101	100.0	116	4	AAS30560	Aas30560 DNA encod
U	15	101	100.0	176	4	AAS27819	Aas27819 DNA encod
٠.	16	101	100.0	116	4	ABK42984	Abk42984 Genomic s
U	17	101	100.0	176	4	AAL07344	Aal07344 Human rep
U	18	101	100.0	176	4	AAL03229	Aal03229 Human rep
U	13	101	100.0	176	4	AAL06588	Aal06588 Human rep
U	20	101	100.0	176	4	AAL07340	Aal07340 Human rep

Abal4573 Human ner	Aas34681 Human DNA	Ada41574 Human sec	Acc50905 Human sec	Abz71508 Secreted	Adb91869 Human sec	Adb61140 Connectiv	Adb94622 Novel hum	Adc74663 Human sec	Ada57709 BAC fragm	Adn41551 Novel hum	Aas30559 DNA encod	Aas27818 DNA encod	Abk42983 Genomic B	Aas41807 Genomic s	Aas41855 Genomic s	Aak85485 Human imm	Aak85434 Human imm	Aal07343 Human rep	Aal06587 Human rep	Aal07339 Human rep	Aal03228 Human rep	Abal4572 Human ner	Aas34680 Human DNA	Adb61139 Connectiv
ABA14573	AAS34681	ADA41574	ACC50905	AB271508	ADB91869	ADB61140	ADB94622	ADC74663	ADA57709	ADN41551	AAS30559	AAS27818	ABK42983	AAS41807	AAS41855	AAK85485	AAK85434	AAL07343	AAL06587	AAL07339	AAL03228	ABA14572	AAS34680	ADB61139
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776	176	176	176	776	116	176	176	176	116	176	845	845	845	845	845	845	845	845	845	845	845	845	845	845
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	.100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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c 21	c 55	c 23	c 24	c 25	c 26	C 27	c 28	c 29	c 30	c 31	c 32	c 33	G 34	c 35	c 36	c 37	c 38	c 39	c 40	c 41	c 42	c 43	C 44	c 45

## ALIGNMENTS

AAV76919 standard; DNA; 142 BP. (first entry) 16-MAR-1999 AAV76919; AAV76919/c 

Staphylococcus aureus contig SEQ ID #2608.

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds

Staphylococcus aureus.

EP786519-A2.

30-JUL-1997

97EP-00100117. 07-JAN-1997;

96US-0009861P. 05-JAN-1996;

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA; Fannon MR, Dillon PJ, Barash SC, Choi GH, WPI; 1997-374922/35. Kunsch CA,

Staphylococcus aureus -in the production of anti-Polynucleotide(s) and proteins derived from stored on computer readable medium and used S.aureus vaccines.

Claim 1; Page 2287; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or

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P-PSDB; AAP10038.
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                 likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulities, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, acalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                                                                                                                                     107 AGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 48
                                                                                                                                                                                                                                                                                                                                                                                         AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAAATAAACAAATAG
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  sequences which
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  Specifically,
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100.0%; Pred. No. 2.1e-21;
ive 0; Mismatches 0;
  industrial importance can be obtained.
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AAN10032 standard; DNA; 228 BP
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translational start signal. In the examples, the 3' end of pKT241 was attached to the signal DNA sequence of the DNA fragment (19) for rat preproinaulin (see AAN10033). The closest identifiable promoter for the penicillinase gene in pKT218 (AAN10032) is located in the region 14 to 2 mucleotides before its translational start signal. In the examples, the fragment (CB6) for rat preproinaulin (see AAN10034)
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                                                                                                                                                                                                                                                                                                                             Sequence 228 BP; 72 A; 37 C; 46 G; 73 T; 0 U; 0 Other;
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                                                                                                                                                New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to elicit an immune response to pathogenic E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                      PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; vaccine; protective immune response; ds.
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3' end of pKT218 was attached to the signal DNA sequence of the DNA fragment (CB6) for rat preproinsulin (see AAN10034)
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                                                                       100.0%; Score 101; DB 1; Length 251; 100.0%; Pred. No. 2.3e-21;
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                                                                                                                                                                                          61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                         Sequence 251 BP; 74 A; 45 C; 50 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                              115 GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC 75
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                                                                                                   0; Mismatches
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97US-0061953P.
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                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant vector for polypeptide secretion - contains signal peptide sequence directly bonded to peptide-coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oshiden K;
1 AGGGTTATTGTCTCATGAGCGGATACATATTTGGATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kajifusa N, Kitazawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                        GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                    GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pUG201 sequence encoding beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3eta-lactamase signal peptide; pGH54; pGH55; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= d
/label= Beta-lactamase signal
278. .436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Table 4; 79pp, Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuwakura T,
                                                                                                                                                                                                                                                                   AAN60624/c
ID AAN60624 standard; DNA; 456 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85WO-JP000696
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209. .439
/*tag= c
209. .277
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 100.0
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3= a
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BP.

(revised) revised)

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AAN70833/c
ID AAN70833 standard; DNA; 456
                                     25-MAR-2003
                                             .0-MAR-2003
                      AAN70833;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                        promoter
                                                                                                                                       RBS
                                                                                                                                                      CDS
                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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        Sequence encodes beta-urogastrone under the control of a tac promoter. The peptide may be expressed from plasmid pUGT 150s in a transformed E.coli host. The plasmid may carry several separately expressing sequences comprising a tac promoter, SD site, signal peptide, and coding sequence, to produce beta-UG in high yield. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                  Expression vector contg. multiple information units is used to transform host all for increased prodn. of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 101; DB 1; Length 456; 100.0%; Pred. No. 2.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                             GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                /*tag= b
/transl_except= (pos:434. .436,aa:Arg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                      GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 553; 34pp; Japanese.
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                              Sequence encoding beta-urogastrone.
                                                                       Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
                             61
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                                                                   RESULT
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An example of a sequence detected by a probe consisting of polyinosine, polydeoxyinosine, oligoinosine and/or oligodeoxyinosine is labeled. The sens man probe are hybridized and the existence of DNA in the product is detected. It can be used to detect the presence of malignant tumour. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of DNA and/or RNA - by converting to single strand form and using probe contg. labelled inosine deriv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 101; DB 1;
100.0%; Pred. No. 2.6e-21;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 11; 11pp; Japanese.
                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SEKI ) SEKISUI CHEM IND CO LID
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                                                                                Tumour; inosine; DNA probe;
                                                                                                                                                                                                                                                     /*tag= c
209. .439
/*tag= a
209. .277
/*tag= d
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(first entry)
(first entry)
                                         Beta-urogastrone sequence.
                                                                                                                                                                                                                               . 204
                                                                                                                                                                                      125. .170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 101; Conservative
                                                                                                                                                                                                                                                   /*tag=
209. .4
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                                                                                                                                                                                                                               200.
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P-PSDB; AAP70505.
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                                                                                                                                                                                                                                                                                                                                                                              JP62244398-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
13-DEC-1990
                                                                                                                         Unidentified
18-JAN-1991
                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-1987
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ID AAN8:
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AC AAN8:
XX
DT 25-M
DT 13-D
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RESULT 7

Synthetic

(23)

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280 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 221
                                                                                                                                                                                                                                                                                                                                                               The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90366-ABA90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting mitosis and/or meiosis. They can also be used in a method for treating a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as (glomerulonephritis and rheumatoid arthritis), dermatological disorders (such as speriesis), anticinflammatory, antifungal and antiparasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 466 BP; 135 A; 87 C; 93 G; 150 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 101; DB 6;
; Pred. No. 2.6e-21;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               Claim 1; Page 99; 213pp; English.
                                                                                                                                                                                           Glover DM, Midgley C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                           23-MAR-2001; 2001WO-GB001297
                                                                                                               24-MAR-2000; 2000GB-00007268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX21173 standard; DNA; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders (such as malaria)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
1es 101; Conservative
                                                                                                                                                                                                                                 WPI; 2002-055132/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum
                                                                                                                                                      CYCLACEL
WO200172774-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1999
                                    04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                             Deak P,
                                                                                                                                                      (CXCI-)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAAAAAAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    action. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of HB101 (pGH201) encoding new beta-urogastrone deriv. Met(21),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New beta-urogastrone deriv. - has gastric acid secretion inhibition and proliferation promotion activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tic enzymes such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The deriv. has various biological activities such as gastric acid secretion inhibiting action, or cell proliferation promoting action. If deriv. has the same biological or pharmacological activities as betaurogastrone. It is not susceptible to denaturation by oxidn. and is chemically stable. Deriv. has resistance to proteolytic enzymes such protease. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antiproliferative; cytostatic; cardiant; immunosuppressive; meiosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila cell cycle progression protein coding sequence #48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 101; DB 1; Length 456; 100.0%; Pred. No. 2.6e-21; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                           secretion; cell proliferation; hormone; ds
                                                                                                                                                                                                                                                     "New beta-urogastrone deriv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 685; 76pp; Japanese.
                                                                                                                                                    cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            86JP-00153783
                                                                                                                                                                                                                                                                                                                                                                     86JP-00153783
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ABA90413 standard; DNA; 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EART ) EARTH SEIYAKU KK.
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P-PSDB; AAP81349.
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                                                                           Gastric acid
                                                                                                                                                                                                                                                                                          JP63012298-A
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                                                                                                                                                                                                                                                                                                                               19-JAN-1988
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ABA90413/

Query Match

Local

9

Gaps

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Length 466; Indels 9

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Gaps

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Indels

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ВР

Length 535;

Score 101; DB 2; Pred. No. 2.7e-21; 0; Mismatches

100.0%;

9

WPI; 1999-081273/07

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antiînflammatory, antipsoriatic; dermatological; antifungal; mitosis; antiparastic; antimalarizal; antirheumatic; antiarthritic; cell division; cell cycle progression protein; tumour; proliferative disorder; cardiovascular; autoimmune; dermatological disorder; ds.
                                                                                                                 Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                            Antiproliferative; cytostatic; cardiant; immunosuppressive; meiosis;
                                                                                                                                                                                                                                                                                                                                                                                        Drosophila cell cycle progression protein coding sequence #91
                                                                                                                                                       GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                         GGGTTCCGCGCATTTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-GB001297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-2000; 2000GB-00007268
                                                                                                                                                                                                                                                                              ABA90456 standard; DNA; 573
Query Match
Best Local Similarity 100.0
Marches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glover DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-055132/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                     12-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2001
                                                                                                                   158
                                                                                                                                                       61
                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                   ABA90456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deak P,
                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                 ABA90456,
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                           lated Treponema pallidum nucleic acids - used to develop products detection, diagnosis, characterisation, prevention and therapy of
                                                                                                                                                                                                                                                                                                                                                                                            AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAAACAAATAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                              AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of
                                                                                                                                                                                                                                                                                                                                                                      1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                          develop
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                               Length 487;
                                                                                                                                                                                                                                                             Sequence 487 BP; 125 A; 127 C; 113 G; 121 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                 100.0%; Score 101; DB 2; 100.0%; Pred. No. 2.6e-21;
                           New isolated Treponema pallidum nucleic acids -
                                                             pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                          biosynthetic products such as enzymes
                                                                                               Claim 1; Page 1106; 1150pp; English.
                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US013041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX21149 standard; DNA; 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                               Local Similatry
nes 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9859034-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                       323
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                                                                                                                                                                                                                                                                                                 Query Match
                                            the
                                                                                                                                                                                                                                                                                                                                    Matches
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ID AAX2
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                                           The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90366-ABA90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting mitosis and/or meiosis. They can also be used in a method for treating a tumour or proliferative disorder, cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                (Buch as restenosis and cardiomyopathy), autoimmune disorders such as
(glomerulonephritis and rheumatoid arthritis), dermatological disorders
(such as psoriasis), antiinflammatory, antifungal and antiparasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 573 BP; 154 A; 118 C; 116 G; 184 T; 0 U; 1 Other;
Claim 1; Page 144; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                          (such as psoriasis), antiin
disorders (such as malaria)
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%
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AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of

Claim 1; Page 1093; 1150pp; English.

Sequence 535 BP; 145 A; 108 C; 122 G; 155 T; 0 U; 5 Other;

biosynthetic products such as enzymes

Midgley C;

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AAS30560;
 RESULT 14
AAS30560/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel method for the optimisation of primer libraries. Specifically, it refers to increasing the affinity of short oligonucleotide primers, also known as extendable oligos (EOS), for their template sequences. The present invention describes improved methods for sequencing and the linear and exponential amplification of DNA that can be useful for PCR, RT-PCR, ligation chain reaction (LCR), rolling circle amplification, strand displacement amplification and isothermal DNA amplification. Accordingly, these extendable oligos with improved specificity and affinity are particularly important in fields ranging from biotechnology and agriculture to medical research. This polynucleotide sequence is the electropherogram of a DNA sequencing reaction that used the pUG19 plasmid and BIS4/T422 oligos, used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 AGGGTTAFTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAAATAAACAAATAG 318
                                                                                                                                                                                                                                                                           ds; primer library; extendable oligos; EO; ligation chain reaction; LCR; rolling circle amplification; strand displacement amplification; isochermal DNA amplification; biotechnology; agriculture; medical research; pUC19 plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing the affinity of an extendable oligonucleotide (EO) for a target nucleic acid, for providing primers having improved specificity, comprises hybridization of the EO to a template oligonucleotide (TO) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                        Electropherogram of a DNA sequencing reaction using E154 & T422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                   295 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 255
GGGTTCCGCGCACATTCCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 101; DB 12; 100.0%; Pred. No. 2.8e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Fig 23; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-2002; 2002WO-AU001763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2002; 2002AU-00002045.
                                                                                                                             ADHS8311 standard; DNA; 605
                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NUCL-) NUCLEICS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tillett D, Thomas T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       extension of the EO.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003093500-A1.
                                                                                                                                                                                                   25-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                  ADH58311;
61
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                                                                                         RESULT 13
                                                                                                              ADH5831.
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GGGTTCCGCGCACATTCCCCCGAAAGTGCCACCTGACGTC 101

61

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GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 359

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osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blod-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; respiratory; liver disorder; wound healing; food preservative; ds.
                                                                                               antianaemic, dermatological, immunosuppressive, antiinflammatory, antiarthritic, antirheumatic, virucide, hepatotropic, nephrotropic,
                                                                                      Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
                                                               DNA encoding novel prostate gland antigen, Seq ID No 418.
AAS30560 standard; DNA; 776 BP.
                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US001330.
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2000US-0216647P
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                                         21-NOV-2001 (first entry)
                                                                                                                                                                                                                                            WO200155447-A1.
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05-SEP-2000;
06-SEP-2000;
                                                                                                                                                                                                                       Homo sapiens.
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2000US-0232401P
2000US-0233063P
2000US-0233064P
2000US-0233065P
2000US-0234223P
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2000US-0231244P.
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2000US-0231414P.
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2000US-0232081P.
2000US-0231968P.
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2000US-0232398P.
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2000US-0232400P.
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2000US-0235484P.
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2000US-0235836P.
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2000US-0240960P.
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2000US-0241786P.
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2000US-0241808P.
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2000US-0246523P.
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2000US-0246527P.
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2000US-0246611P.
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2000US-0249207P,
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2000US-0249211P.
    2000US-0230438P
2000US-0231242P
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2000US-0249218P
06-SEP-2000, 2
08-SEP-2000, 2
08-SEP-2000, 2
08-SEP-2000, 2
08-SEP-2000, 2
08-SEP-2000, 2
08-SEP-2000, 2
12-SEP-2000, 2
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14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
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21-SEP-2000; 2
21-SEP-2000; 2
25-SEP-2000; 2
26-SEP-2000; 2
27-SEP-2000; 2
27-SEP-2000; 2
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The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prevention, and/or treatment of diseases and/or disorders of the prostatite such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, prostaticis, prostatic on-bacterial prostatitis, prostaticis,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
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                                                                                                                                                                                                                                                                                         2000US-0251856P.
2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
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2000US-0249299P-
2000US-0249300P-
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7819/c AAS27819 standard; DNA; 776

RESULT 15 AAS27819/ ID AAS2

2000US-0234223P. 2000US-0234274P. 2000US-0234997P. 2000US-0234998P.

2000US-0235484P. 2000US-0235834P. 2000US-0235836P. 2000US-0236327P.

2000US-0236367P. 2000US-0236368P. 2000US-0236369P.

2000US-0236370P

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                                                                    Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; ammune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; carddiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ds; acquired immune deficiency syndrome.
                                                  DNA encoding novel signal transduction pathway protein, Seq ID 1479
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2000US-0190076P.
2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
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                              07-NOV-2001 (first entry)
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17-MAR-2000;
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14-AUG-2000;
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          AAS27819;
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2000US-0241808P. 2000US-0241809P. 2000US-0241826P.

2000US-0244617P. 2000US-0246474P. 2000US-0246475P.

2000US-0240960P. 2000US-0241221P. 2000US-0241785P. 2000US-0241786P.

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2000US-0249212P. 2000US-0249213P. 2000US-0249214P. 2000US-0249245P 2000US-0249264P 2000US-0249265P

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The invention relates to novel isolated polypeptides (I), and diagnosting preventing and treating diseases including immune system diagnosting, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rongenital and acquired immunodeficiencies, autoimmune conferences (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and storders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders (e.g. deucher's disease, parkinson's disease, haemoglobin abnormalities (e.g. Alzheimer's disease, Parkinson's (e.g. stroke), renal disorders (e.g. Alzheimer's disease, parkinson's (e.g. stroke), renal disorders (e.g. anthythmia), readiovascular disorders (e.g. anthythmia), readiovascular disorders (e.g. Anthythmia), respiratory disorders, dermatological disorders (e.g. Addison's epithelial cell proliferation, endocrine disorders (e.g. Addison's collesase), reproductive system disorders, gastroointestinal disorders (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce (in pathologies e.g. acquired immune deficiency syndrome (AIDS), AASS6976-AASZ7850 represent novel signal transduction pathway protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders and neuronal disorders.
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                                  17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250190P.
05-DEC-2000; 2000US-025198P.
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11-DEC-2000; 2000US-0254097P.
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100003G03

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Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB : Maximum DB :

Database

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SM Hebeloma cylindrosporum

Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Cortinariaceae; Hebeloma.

E 1 (bases 1 to 300)
S Wipf, D., Benjdia, M., Tegeder, M. and Frommer, W.B.
Construction of a functional cDNA library from the ectomycorrhizal fungus Hebeloma cylindrosporum
L Unpublished (2001)
Contact: Wipf D.
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstealle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM078095 300 bp mRNA linear EST 30-NOV-2001
83374 Hebeloma cylindrosporum functional CDNA library Hebeloma
cylindrosporum cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
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'organism="Hebeloma cylindrosporum"
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Generation and analysis of 25 Mb of genomic DNA from the pufferfish
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Direct Submission
Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource Centre Hintron, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
V_type: phagemid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 111
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F.rubripes GSS sequence, clone 010H20aC4, genomic survey sequence.
AL000426
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                                                                                                     A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis
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Agaricales; Cortinariaceae; Hebeloma.
1 (bases 1 to 300)
Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and
Frommer, W.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tisue_type="Mycelia"
/lab_host="E. coli XL1-Blue"
/clone_lib="Hebeloma cylindrosporum functional cDNA
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                                                                                                                                                                                                   Contact: Wipf D
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
Fax: 49 7071 29287
Email: daniel.wipf@zmbp.uni-tuebingen.de
no homology below 1e-10.
Location/Qualifiers
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Genome Res. 9 (10), 960-971 (1999)
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GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="H1"
/db_xref="taxon:76867"
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1 (Dases 1 to 300)

Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and
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Hebeloma cylindrosporum
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
Contact: Wipf D
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Auf der Morgenstelle 1, 72076 Tuebingen, Germany
Fax: 49 7071 2976160
Fax: 49 7071 297816
Fax: 49 7001 291287
Email: daniel.wipf@zmbp.uni.tuebingen.de
homolog to Enterobacteria phage f1; ampicillinase (1e-10).
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                                                                              61 GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                          110 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACTGACGTC 70
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/mol_type="mRNA"
/strain="H1"
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/tissue_type="Mycelia"
/lab_host="E. coli_XL1-Blue"
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ACCESSION VERSION KEYWORDS SOURCE

RESULT 3

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Class: plasmid ends
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Fax: 801 585 7177
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (NFZ); Email s.wiemann@dkfz- heidelberg.de;
Berquenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
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391 bp mRNA linear EST 04-SEP-2003
DKFZp313J1611_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp313J1611_5', mRNA sequence.
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Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S. EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S. Unpublished (1999)
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Site_1: SfiIA; Site_2: SfiIB;
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6, 14059
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                                      One pass dye-terminator sequencing of cosmid cloned genomic
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This clone (DKEZp313J1611) is available at the RZPD in lates contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 101; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 8.3e-19;
Matches 101; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                            Length 309;
                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 139
                                                                                                                                                                                                                                                                                                                                                                                          GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                          100.0%; Score 101; DB 9;
100.0%; Pred. No. 8.2e-19;
                                                                                                           organism="Takifugu rubripes"
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="010H20aC4"
/clone_lib="cosmid 010H20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="313 (synonym:
/note="Vector: pTriplEx2;
cDNA-collection"
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/mol_type="mRNA"
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|clone="DKFZp313J1611"
|dev_stage="adult"
|lab_host="DH108"
                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                           Similarity
   PRIMER: KS
                                                         sequence.
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AL597149
                                                                        FEATURES
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/lab host="E. Col; strain XL10-Gold, T1-resistant, F-"
/lab host="E. Col; strain XL10-Gold, T1-resistant, F-"
/clone lib="Coxytricha plasmid UUGCIO library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Coxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligomucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWH42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Bukaryota, Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 414)
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414 bp DNA linear GSS 17-JUI 100005D19R Oxytricha plasmid UUGC1O library Sterkiella histriomuscorum genomic clone UUGC100005D19 R, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn,D., Doak,T., Herrick,G. and Weiss,R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2002)
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                                             288 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 328
61 GGGTTCCGCGCACATTTCCCCGGAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Plate: 0005 row: D column: 19
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/db_xref="taxon:94289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 414.
Location/Qualifiers
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                                                                                                                                                                                                                                              Haplochromis chilotes
Haplochromis chilotes
Haplochromis chilotes
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Labroidei; Cichlidae; Haplochromis.

Labroidei; Cichlidae; Haplochromis.

Labroidei; Cichlidae; Haplochromis.

Natanabe,M., Kobayashi,N., Shin-i,T., Kohara,Y. and Okada,N.

Orf sequences of cichlid in Lake Victoria are essentially same
Unpublished (2004)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Fax: 1. Labroided State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State Sta
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University of Utah Genome Center
University of Utah
Genome Center
Wan 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                               BJ684174 11brary Haplochromis chilotes CDNA clone no90c12,
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Sterkiella histriomuscorum
Eukaryota; Alvoclata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 491)
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Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2003)
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/dev_stage="varied"
/clone_lib="HCEST_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:257977"
/clone="no90c12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                           BJ684174.1 GI:46527295
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Matches 101; Conservative
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Tel: 801 585 5606
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BJ684174
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BI805285
S035A01 Stem library from Oryza sativa (3-5 leaf stage) Oryza
Sativa cDNA clone S035A01, mRNA sequence.
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (basea Lo 495)
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X.,
Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
Oppublished (2001)
Contact: Haitao Dong, Debao Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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Email: webmaster@estarray.org, URL: http://www.estarray.org
Seg primer: M13 forward primer.
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100.0%; Score 101; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 8.4e-19;
Matches 101; Conservative 0; Mismatches 0; Indels 0
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Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Plate: 0006 row: J column: 13
Seq primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
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BI805285.1 GI:15852489
                                                                                          Class: plasmid ends
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Pred. No. 8.4e-19; 0; Mismatches 0;
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High quality sequence stop: 496.
Location/Qualifiers
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CC818523.1 GI:32897943
GSS.
Best Local Similarity 100.0%;
Matches 101; Conservative 0
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Fax: 801 585 7177
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CC818523/c
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/clone lib="Oxytricha plasmid UUGCIO library"
/note="Vector: PWD4Dvy Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pwD42 (gi|4732114|gb|AR129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC818374 17-JUL-2003 100004807R Oxytricha plasmid UUGCIO library Sterkiella histriomuscorum genomic clone UUGCIO0004807 R, genomic survey
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                                                                                                                                                                                                                                                           62 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAAAAAA 121
                                                                                                                                                                                                                               Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Bukaryota; Alvoclata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
      /dev_stage="3-5 leaf stage"
/clone_lib="Stem library from Oryza sativa (3-5 leaf
stage)"
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2003)
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                                                                                                                                           100.0%; Score 101; DB 4; Length 495;
.larity 100.0%; Pred. No. 8.4e-19;
Conservative 0; Mismatches 0; Indels (
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University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                                          122 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 162
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                                                                                                                                                                                                                                                                                                                  61 GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 101
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Plate: 0004 row: B column: 07
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                   /note="Vector: pSport2"
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Location/Qualifiers
  /tissue_type="Stem"
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CC818374.1 GI:32897661
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Fax: 801 585 7177
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Matches 10
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100.0%; Score 101; DB 9; Length 495;

Query Match

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Stichotrichida, Oxytrichidae, Sterkiella.
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100004L13R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100004L13 R, genomic survey
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Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclar chromosomes
Unpublished (2003)
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Indels
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Plate: 0004 row: L column: 13
Seg primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
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histriomuscorum genomic clone UUGC100003C16 R, genomic survey
                                                                                                                              Sterkiella histriomuscorum
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CC817128/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /urganism="Sterkiella histriomuscorum"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_txef="reaxon:94289"
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/note="Vector: PWD42nv; Purified macronuclear chromosomal DNA from Oxytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                GSS 17-JUL-2003
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DEFINITION 100003C16R Oxytricha plasmid UUGC10 library Sterkiella
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                                                                                                                                                                                                                                                                        Sterkiella histriomuscorum (Oxytricha trifallax)
Sterkiella histriomuscorum
Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichia; Oxytrichidae; Sterkiella.
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                                                                                                                            CC819854 linear GSS 17-JUI 100006N08R Oxytricha plasmid UUGC10 library Sterkiella histriomuscorum genomic clone UUGC10006N08 R, genomic survey
                                                                                                                                                                                                                                                                                                                                                                          Dun, D., Doak, T., T., Herrick, G. and Weiss, R. Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 101; DB 9; Length 503; 100.0%; Pred. No. 8.4e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Plate: 0006 row: N column: 08
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 503.
Location/Qualifiers
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Fax: 801 585 7177
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Best Local Similarity
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84112, USA
                                                                                                                                                                                           sequence.
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CC819854/c
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/Mol type="genomic DNA"
// (Ab xref="taxon:94289"
// (Clone="UUGC100003C16"
// (Lab hose="E. Col; strain XL10-Gold, T1-resistant, F-"
// (Lone lib="Coytricha plasmid UUGC10 library"
// (Lone lib="Coytricha plasmid UUGC10 library"
// (Lone lib="Coytricha trifallax was blunt end-repaired with DNA from Coytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pwpdz (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. Coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Sterkiella histriomuscorum
Eukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
                                                          Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 515)
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                                                                                                                                                                       Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macromuclear chromosomes
Unpublished (2003)
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Sterkiella histriomuscorum (Oxytricha trifallax)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##112, UST
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Plate: 0003 row: C column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 515.
Location/Qualifiers
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University of Utah Genome Center
University of Utah
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completed: July 14, 2005, 23:23:29
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Job time : 962.667 secs
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// (db xref="taxon:94289"
// (clone="UGGC100002D21"
// (lab host="E. Coli strain Xi10-Gold, T1-resistant, F-"
// (clone="UGGC100002D21"
// (lab host="E. Coli strain Xi10-Gold, T1-resistant, F-"
// (clone lib="Oxytricha plasmid UGGC10 library"
// (note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AR129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. Coli XL10-Gold (stratagene) cells
and selected for ampicillin resistance."
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Sterkiella histriomuscorum
Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
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                                              Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
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Paired end reads from plasmid inserts of Oxytricha trifallax
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Stichotrichida; Oxytrichidae; Sterkiella.
1 (bases 1 to 518)
                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Plate: 0002 row: D column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 518.
Location/Qualifiers
                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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University of Utah Genome Center
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Unpublished (2003)
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Matches 101; Conserv
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DNA from Oxytricha trifical ax was blunt end-repaired with a ligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with addrivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptors complement and transformed into chemically-competent E. Coli X10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="UUGC100002J19"
Jab hoge="E. Coli strain XI10-Gold, T1-resistant, F-"
/clone lib="Oxytricha plasmid UUGC10 library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
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                                                                                                                                                                                                                                                                                                                                                       /organism="Sterkiella histriomuscorum"
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                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@enetics.utah.edu
Plate: 0002 row: J column: 19
Seq primer: ACACAGGAAACAGCTAATGACC
Class: plasmid ends
High quality sequence scop: 519.
                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Best Local Similarity 100.0
Matches 101; Conservative
University of Utah
                               Rm. 308, B
84112, USA
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1

Title: Perfect score:

Sequence:

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Scoring table:

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AX05821 Screening
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AX1171 Sequence
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AX11121 Sequence
AX11127 Sequence
AX41366 Sequence
AX4437643 Sequence
AX44366 Sequence
AX24336 Sequence
15677 Sequence
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AX21287 Sequence
AX21317 Sequence
AX20478 Sequence
AX73107 Sequence
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Unclassified.
1 (bases 1 to 3853)
Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 5 13-UW-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 100; DB 6; ilarity 100.0%; Pred. No. 9.4e-24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                  ALIGNMENTS
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                                                                 AR411127
AY437643
AX211282
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AX202478
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I56772
I95540
 CVU89673
                            AX319694
A44171
AR116416
AR222266
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AX342685
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AX349365
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BD009729 Tissue sp
X90639 Cloning vec
AR098191 Sequence
AR20783 Sequence
AR20783 Tissue sp
AR098192 Sequence
BD009731 Tissue sp
AR20784 Sequence
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AX36570 Sequence
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                                                                 July 14, 2005, 04:39:07; Search time 749:127 Seconds (without alignments) 6468.225 Million cell updates/sec
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                                                                                                                              1 gacggatcgggagatctcc.......ctgctccctgcttgtgtgtt 100
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                               4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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PAT 14-FEB-2001

PAT 20-JUN-2002

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Score

Result

source

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Matches

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JOURNAL FEATURES

TITLE

REFERENCE AUTHORS

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cloning vector; expression vector; multiple cloning site; Plasmid. synthetic construct synthetic construct
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                                                                                                                                              Peters,H., Hundhausen,T., Kroenke,M. and Marget,M.
A new small sized high-level eukaryotic expression vector
Unpublished
                                                                                                                                                                                                                                       Direct Submission
Submitted (07-AUG-1995) H. Peters, Inst. f. Immunologie,
Michaelisstr.5, D- 24105 Kiel, PRG
Related sequences: M1295 and K03104.
Location/Qualifiers
1. 3986
/organism="synthetic construct"
/mol type="cther DNA"
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1.396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3986;
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/note="cloning vector (PZeoSV) (Invitrogen)"
2797. .3986 /
/note="cloning vector (pcDNA3)"

    .2125
/note="cloning vector (pcDNA3) (Invitrogen)"

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/note="multiple cloning site (MCS)"
2126. .2796
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1 (bases 1 to 4026)
Antelman, D., Gregory, R.J. and Wills, K.N. Retinoblastoma fusion polypeptides
Patent: US 6074850-A 19 13-JDN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                              other sequences; artificial sequences.
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/wol_type="unassigned DNA"
Cloning vector pcDNA3ZEO DNA
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X90639.1 GI:949972
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Tissue specific expression of retinoblastoma protein.
BD009729
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Antelman, D., Gregory, R.J. and Wills, K.N.
Tissue specific expression of retinoblastoma protein
Parent: JP 2001503638-A 3 21-MAR-2001;
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               1 (bases 1 to 3853)
Antelman,D., Gregory,R.J. and Wills,K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 5 30-APR-2002;
Location/Qualifiers
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JP 2001503638-A/3.
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Unclassified.
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1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
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iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 9.3e-24;
Matches 100; Conservative 0; Mismatches 0;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379297-A 33 30-APR-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 4249)
Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 33 13-JUN-2000;
Location/Qualifiers
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Sequence 33 from patent US 6379927.
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                  al Similarity 100.
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PN JP 2015038-A/4
PD 21-MAR-20190638-A/4
PD 21-MAR-201907 JP 1998522958
PR 13-NOV-1996 US 08/751517,14-FEB-1997 US 08/1
PR 15-NOV-1996 US 08/751517,14-FEB-1997 US 08/1
CO7H21/04,CO7K5/00,A61K38/00,A61K35/12
CC Strandedness Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source /organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4026;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Tissue specific expression of retinoblastoma protein
Patent: JP 2001503638-A 4 21-MAR-2001;
CANJI INC
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                  CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
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Location/Qualifiers
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100.0%; Pred. No. 9.3e-24;
ive 0; Mismatches 0;
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion proteins
Patent: US 6379927-A 19 30-APR-2002;
Location/Qualifiers
1. .4026
/organism="unknown"
                                                                                                                                             AR207833 4026 bp
Sequence 19 from patent US 6379927.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Matches 100; Conservative
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Matches 100; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon.32630"
/note="Vector pVAC1"
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Cancer Research Ventures Limited (GB)
Location/Qualifiers
/organism="unidentified"
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AX286570
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PN JP 2001503638-A/5

PP 13-NOV-1996 US 08/751517,14-FEB-1997 US 08/801092 PI

DOUGLEAS ANTELMAN, RICHARD J GREGORY, KENNETH N WILLS PC

COTH21/04, COTKS/00,A61K38/00,A61K35/12

CC Strandedness Single;

FH Key

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MEDICAL RES COUNCIL (GB)
Other publication CA 2145064 940414
Other publication AU 4822493 940426
Other publication AU 4822493 940426
Other publication JP 8501699T 960227.
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              61 CCGCATAGTTAAGCCAGTATCTGCTCCTGCTTGTGTGTT 100
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100.0%; Pred. No. 9.3e-24;
tive 0; Mismatches 0;
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/organism="unidentified"
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JP 2001503638-A/5.
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PAT 21-NOV-2001
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100.0%; Pred. No. 9.3e-24;
iive 0; Mismatches 0; Indels 0.
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="This gradence is artificial and is based on well
setablished comm ercially available vectors that are cited
with their vendor within the patent applicatio"
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1 (bases 1 to 5053)
Fikes,J.D., Hermanson,G.G., Sette,A., Ishioka,G.Y., Livingston,B.
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="pCDNA3.1/GS vector by Invitrogen Corporation"
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                                                                                      100.0%; Score 100; DB 6; 100.0%; Pred. No. 9.2e-24;
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Patent: JP 2002520000-A 18 09-JUL-2002;
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synthetic construct
other sequences; artificial sequences.
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Cell transfection
Patent: WO 0119853-A 1 22-MAR-2001,
THE UNIVERSITY OF SHEFFIELD (GB)
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OS Artificial Sequence
PN 472-1091
PN 17-2002
PP 13-MAY-1999 UP 200548449
PR 13-MAY-1999 UP 2000548449
PC CINNIS/OB ARTAIL/ABSANDRO
SETTE, CLENN Y ISHIOKA,
PC A61P31/14, A61K31/711, A61K39/00, A61K39/12, A61K39/29,
PC A61P31/16, A61P31/20, A61P37/02, C12N15/00
PC Vector PEP2
C Vector PEP2
PF Source
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    5053
    forganism="synthetic construct"
|mol type="genomic DNA"
|db_xref="taxon:32630"

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Best Local Similarity
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July 14, 2005, 04:35:42 ; Search time 140.988 Seconds
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Copyright (c) 1993 - 2005 Compugen Ltd.
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(without alignments) 4198.742 Million cell updates/sec	US-09-482-682-8_COPY_1_100 100
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100 1 gacggatcgggagatctccc......ctgctccctgcttgtgtgtt 100 score: Scoring table: Sequence:

4390206 seqs, 2959870667 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0

8780412 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 8 0 0 0 Minimum Maximum

geneseqn2003ds: geneseqn2004as: N\_Geneseq\_16Dec04:\* geneseqn2001bs:\* geneseqn2003cs: geneseqn1990s:\* geneseqn2001as: geneseqn2003as: geneseqn2000s:\* genesegn1980s:\* geneseqn2002as: genesegn2002bs: geneseqn2003bs: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:

	Description	Adm41035 Fungus nu	Adh11349 Vertebrat	Adm41037 Cytomegal	Adm41034 Human nuc	Adm41036 Cytomegal	Aav40006 Plasmid p	Aav40007 Plasmid p	Aav63466 Plasmid p	Aag62391 Vector pv	Aas17704 Vector pV	Abn83143 Plasmid p	Aaf24901 Nucleotid	Aad39652 Human sma	Aaf83146 Complete	Adb33528 Expressio	Aaz38633 pEP2 expr	Aas12839 DNA seque	Adh11417 Plasmid p	Adf10526 Plasmid p	Acc44637 Murine rD
SUMMARIES	G.	ADM41035	ADH11349	ADM41037	ADM41034	ADM41036	AAV40006	AAV40007	AAV63466	AAQ62391	AAS17704	ABN83143	AAF24901	AAD39652	AAF83146	ADB33528	AAZ38633	AAS12839	ADH11417	ADF10526	ACC44637
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	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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## ALIGNMENTS

engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; fungus; gene; ds. Fungus nucleotide sequence SEQ ID NO:3. ADM41035 standard; DNA; 1506 BP. 17-SEP-2003; 2003WO-US029251. 17-JUN-2004 (first entry) WO2004027029-A2. Unidentified. 01-APR-2004. ADM41035; 

19-SEP-2002; 2002US-0411790P. (XIME-) XIMEREX INC.

Beschorner WE, Sosa CE, Thompson SC;

WPI; 2004-295402/27.

Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host.

Disclosure; SEQ ID NO 3; 48pp; English.

replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replacement cells replacement and implanting foreign replacement cells in the tissue of the fetal non-human mammal host. The present invention describes a method for engrafting foreign

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35 protein of Caenorhabditis elegans or a functional equivalent,
derivative or bioprecursor of UNC-53. Also described: (1) a DDNA e-
encoding a vertebrate homologue of the C. elegans UNC-53 protein; (2) a
nucleic acid which hybridises to the CDNA of (1); (3) vector comprising
the CDNA as in (1); (4) a homologue of the CDNA of (1); (3) vector comprising
a transgenic cell, tissue or animal comprising the vector as in (3); (6)
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                                                                                                                                                                                                                                                                                                     GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
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                                                                                                                                                                                                                                 Gaps
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Vandekerckhove JS;
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                                                                                                                                                                                          DB 12; Length 1506;
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100.0%; Pred. No. 4e-26;
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Luyten W,
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Pujol NJR, Maertens LJS,
Geysen J, Bogaert TAOE;
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                                                                                                                  specification
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                                                                                                                                                                                          Query Match
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Matches
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cell shape, motility, or the direction of cell migration of the regulation of cell shape, motility, or the direction of cell migration for use as a inhibitor or enhancer of regulation of cell behaviour, growth, shape or motility or the direction of migration by contacting a host cell ceresising a homologue of UNC-53 and determining a change of phenotype; (8) a method for identification of vertebrate homologues of C. elegans unc-53 gene by hybridising a probe of 15-50 bp of the unc-53 sequence to a DNA library; and (9) a method for identification of a protein which is active in the signal transduction pathway of a cell of which a vertebrate homologue of UNC-53 is a component comprising; (i) contacting an extract of a cell with an antibody to the UNC-53 homologue; (ii) identifying an antibody/homologue complex; and (iii) analysing such a complex to a cell migration and cell shape in C. elegans. Vertebrate homologues of UNC-53 can be used to promote neuronal regeneration, revascularisation or wound healing, to treat chronic neurodegenerative diseases or acute traumatic injuries or fibrotic diseases. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 100; DB 2; Length 1600; 100.0%; Pred. No. 4.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1600 BP; 397 A; 409 C; 398 G; 396 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytomegalovirus nucleotide sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 5; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells in the cells resplace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
                   \begin{array}{c} \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{C}} \\ \mathcal{C}_{\mathcal{C}} & \mathcal{C}_{\mathcal{
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GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG Gaps ö Length 1782; Sequence 1782 BP; 458 A; 399 C; 451 G; 474 T; 0 U; 0 Other; Indels 61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100 CGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100 100.0%; Score 100; DB 12; 100.0%; Pred. No. 4.2e-26; iive 0; Mismatches 0; 100.08; Matches 100; Conservative Similarity Н Query Match Local

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RESULT 5 ADM41036

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ADM41034 standard; DNA; 2241 BP ADM41034; RESULT 4 ADM41034

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Human nucleotide sequence SEQ ID NO:2. (first entry) 17-JUN-2004 

engrafting foreign replacement cell; implanting foreign replacement cell; growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; human; gene; ds.

WO2004027029-A2. Homo sapiens

01-APR-2004.

17-SEP-2003; 2003WO-US029251

19-SEP-2002; 2002US-0411790P

(XIME-) XIMEREX INC

Thompson Sosa CE, Beschorner WE,

SC;

WPI; 2004-295402/27.

Engrafting foreign replacement cells within a fetal non-human mammal, useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host. Disclosure; SEQ ID NO 2; 48pp; English.

replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a The present invention describes a method for engrafting foreign

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                                                  sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the
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mammalian host, and for producing chimeric mammals that can be used develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present
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                                                                                                                                                      Length 2241;
                                                                                                                    Sequence 2241 BP; 498 A; 630 C; 609 G; 504 T; 0 U; 0 Other;
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                                                                                                                                                      , DB 12;
4.5e-26;
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engrafting foreign replacement cell; implanting foreign replacement growth; differentiation; drug development; vaccine development; tissue transplantation; human disease study; cytomegalovirus; gene; Cytomegalovirus nucleotide sequence SEQ ID NO:4. BP. ADM41036 standard; DNA; 2294 17-JUN-2004 (first entry) Cytomegalovirus ADM41036; 

17-SEP-2003; 2003WO-US029251. WO2004027029-A2 01-APR-2004

19-SEP-2002; 2002US-0411790P

(XIME-) XIMEREX INC

Thompson SC; Beschorner WE, Sosa CE,

WPI; 2004-295402/27

useful in producing chimeric mammals, comprises selectively destroying native cells in a tissue of a fetal non-human mammal host. Engrafting foreign replacement cells within a fetal non-human mammal

Disclosure; SEQ ID NO 4; 48pp; English.

The present invention describes a method for engrafting foreign replacement cells within a foetal non-human mammal, which comprises selectively destroying native cells in a tissue of a foetal non-human mammal host, where the number of maternal cells of the same tissue is not substantially reduced, and implanting foreign replacement cells in the tissue of the fetal non-human mammal host, where the foreign replacement cells replacement cells replace destroyed cells of the tissue. The method is useful for facilitating growth and differentiation of foreign cells within a mammalian host, and for producing chimeric mammals that can be used to develop new drugs and vaccine, factors, drugs and tissues for transplantation, also useful to study human diseases. The present sequence represents a nucleotide sequence given in the Sequence Listing of the present invention but not mentioned further within the of the present specification.

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e.g. hyper-proliferative disease such as cancer and restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta; polyoma virus.
                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 100; Conservative 0
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1851. .4026
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cytomegalovirus.
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                                                                                                                                                                                                                                                                                                                                                                   Plasmid pCTMI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc feature
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15-FEB-1999
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promoter
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                                                              1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion polypeptide of, e.g. transcription factor - used to treat,
                                    Gaps
                                    ö
                                                                                                                                                                                                                                E2F; transcription factor; human; retinoblastoma protein RB; bladder cancer; restenosis; angioplasty; diabetic retinopathy; thyroid hyperplasta; Grave's disease; psoriasis;
                 100.0%; Score 100; DB 12; Length 2294; 100.0%; Pred. No. 4.5e-26;
Sequence 2294 BP; 466 A; 680 C; 641 G; 507 T; 0 U; 0 Other;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                      *tag= b
function= "tripartite leader sequence"
                                                                                                                                                                                                                                                           benign prostatic hypertrophy; Li-Fraumeni syndrome; peripheral vascular disease; therapy; plasmid pCTM; ss
                                                                                       61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
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/note= "pUC19 backbone H3 to AatII"
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                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (2857. .3717)
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note= "CMV promoter"
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/note= "SP6 promoter"
1679. .3853
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209. .864
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/note= "AMP-ORF"
                                                                                                                                                                                                                                                                                              mastadenovirus.
unidentified bacteriophage, T7.
unidentified bacteriophage, SPG.
Macaca mulatta, polyoma virus.
                                                                                                                                                   AAV40006 standard; DNA; 3853 BP.
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97US-00801092,
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                                                                                                                                                                                               (first entry)
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                         Best Local Similarity 100.
Matches 100; Conservative
                                                                                                                                                                                                                                                                                      Human cytomegalovirus.
                                                                                                                                                                                       (revised)
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                                                                                                                                                                                                               Plasmid pCTM
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15-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antelman D,
                                                                                                                                                                                                                                                                                                                                Bos taurus.
                                                                                                                                                                    AAV40006;
                  Query Match
                                                                                                                                                                                                                                                                                                                                          Chimeric
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                                                         This is the nucleotide sequence of pCTM, a plasmid which contains a CMV promoter, a tripartite adenovirus leader flanked by T7 and SP6 promoters, and a multiple cloning site with a bovine growth hormone polyA site and downstream SV40 polyA site. It has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastoma protein (BP, see AAW62465) and E2F transcription factor (see AAW62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, specifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the E2F promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E2F; transcription factor; human; retinoblastoma protein RB; bladder cancer; restenosis; angioplasty; diabetic retinopathy; thyroid hyperplasia; Grave's disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3853 BP; 936 A; 986 C; 942 G; 989 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function= "tripartite leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            benign prostatic hypertrophy, Li-Fraumeni syndrome;
peripheral vascular disease; therapy; plasmid pCTMI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= e
/note= "pUC19 backbone H3 to AatII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100; DB 2;
Pred. No. 5.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "hybrid SV40 late intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "CMV promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mastadenovirus.
unidentified bacteriophage; T7.
unidentified bacteriophage; SP6.
Example 1; Fig 4; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV40007 standard; DNA; 4026 BP
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"tripartite leader sequence"

antigen binding site"

us-09-482-682-8\_copy\_1\_100.rng

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This is the nucleotide sequence of pCTMIE, a plasmid that was constructed by amplifying the SV40 enhancer from SV40 viral DNA by PCK, digesting the amplified product with Bg11I and insertino BamHI-digested plasmid pCTMIE was been used as a vector for the expression of fusion proteins of the invention that comprise expression of fusion proteins of the invention that comprise testinoblashcoma protein (BP, see AAM62465) and ESF transcription factor (see AAM62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, specifically cancer (particularly of the bladder) or resenosis. They are more effective in repressing transcription of the ESF promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion polypeptide of, e.g. transcription factor - used to treat, e.g. hyper-proliferative disease such as cancer and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 4249 BP; 1020 A; 1074 C; 1048 G; 1107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         *tag= e
'note= "72 bp tandem repeat enhancer"
                                                                                                                                                                                                                                                                                                                 'note= "72 bp tandem repeat enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "pUC19 backbone H3 to AatII"
                                                                                                                                                                                                                                                                                                                                                                                                    'note= "hybrid SV40 late intron"
                                                                                                                                                                                note= "hybrid SV40 late intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (3255. .4113)
                                                                                    /*tag= a
/note= "CMV promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "SP6 promoter"
2075. .4249
                                                         cocation/Qualifiers
209. .864
                                                                                                                                                                                                                             note= "early mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antelman D, Gregory RJ, Wills KN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "AMP-ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 8; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUG-2003 to correct OS field.)
 Macaca mulatta; polyoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US021821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00751517.
97US-00801092.
                                                                                                                                                       081. .1145
                                                                                                                                                                                                                                             .1332
                                                                                                                                                                                                                                                                                       .1404
                                                                                                                                                                                                                                                                                                                                                                           .1478
                                                                                                                                           function=
                                                                                                             .1074
                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                              *tag=
                                                                                                                                                                       *tag=
                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                       333.
                                                                                                                                                                                                  164.
                                                                                                                                                                                                                                             261.
                                                                                                                                                                                                                                                                                                                                  1366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CANJ-) CANJI INC.
                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9821228-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-1997;
                Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-1998
                             Chimeric
                                                                       promoter
                                                                                                                                                                                                                                             enhancer
                                                                                                                                                                                                                                                                                       enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                        intron
                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOS
                                                         Key
 ö
                                                                                                                                                                                                                                                                                                                                        This is the nucleotide sequence of pCTMI, a plasmid that was constructed from pCTM (see AAV40006) by digesting pCTM with XhoI and NotI and subcloning a 180 bp introm XhoI-NoII fragment from a pCMW-beta-gal vector. Plasmid pCTMI has been used as a vector for the expression of fusion proteins of the invention that comprise retinoblastoma protein (BP, see AAW62465) and B2F transcription factor (see AAW62464). Such fusion proteins, particularly expressed from gene therapy vectors, are used to treat hyperproliferative conditions, specifically cancer (particularly of the bladder) or restenosis. They are more effective in repressing transcription of the B2F promoter than RB alone and cause cell-cycle arrest in a variety of cells. (Updated on 27-AUG-2003 to correct os field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACGGAICGGGAGAICTCCCCGAICCCCTAIGGTCGACTCTCAGTACAATCTGCTCTGAIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                      New fusion polypeptide of, e.g. transcription factor - used to treat, e.g. hyper-proliferative disease such as cancer and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E2F; transcription factor; human; retinoblastoma protein RB; bladder cancer; restenosis; angioplasty; diabetic retinopathy; thyroid hyperplasia; Gavev's disease; psoriasis; benign prostatic hypertrophy; Li-Fraumeni syndrome; peripheral vascular disease; therapy; plasmid pCTMIE; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4026 BP; 978 A; 1021 C; 982 G; 1045 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccecaragraagccagrarcrecrecrecrrererr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 100; DB 2;
100.0%; Pred. No. 5.3e-26;
iive 0; Mismatches 0;
complement (3032. .3890) /*tag= f
                                                                                                                                                                                                               Wills KN;
                            /note= "AMP-ORF
                                                                                                                                                                                                                                                                                                                 Example 1; Fig 6; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mastadenovirus.
unidentified bacteriophage; T7.
unidentified bacteriophage; SP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV63466 standard; DNA; 4249 BP
                                                                                                               97WO-US021821
                                                                                                                                        96US-00751517.
97US-00801092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                               Gregory RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity 100.
100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                            WPI; 1998-297858/26.
                                                                                                                                                                                   (CANJ-) CANJI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pCTMIE.
                                                                                                                                        15-NOV-1996;
14-FEB-1997;
                                                        WO9821228-A1
                                                                                                             13-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-2003
15-FEB-1999
                                                                                 22-MAY-1998
                                                                                                                                                                                                               Antelman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Si
Matches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV63466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV63466
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antibody/retroviral envelope fusion protein can be used as a plasmid vaccine and it induces a strong humoral response to the antibody moiety in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 4341 BP; 1032 A; 1099 C; 1091 G; 1119 T; 0 U; 0 Other;

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Gaps

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DB 2; Length 4341; Indels

; Score 100; DB 2; ; Pred. No. 5.4e-26; 0; Mismatches 0;

100.001 100.0%;

Conservative

Best Local Similarity Matches 100; Conserv

Query Match

61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100

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                                             1 GACGGATCGGGAGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                        1 GACGGATCGGGAGATCTCCCCGATCCCCTTGGTCGACTCTCAGTACATCTGCTCTGATG 60
                                                                                                                                                                                                                                    Vector; pVAC1; pRc/RSV; leader sequence; termination signal; fusion protein; pSfi/Not.Tag1; pelB leader; human; immunoglobulin; VH1; single chain; Fv; murine antibody; retroviral; envelope; plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating immune response to a disease marker - by administering a vector which expresses the disease marker to interact with the immune
                            Gaps
                           ö
       Length 4249;
                          0; Indels
                                                                                  61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                           CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Russell SJ, Stevenson FK, Winter GP,
      ; Score 100; DB 2;
; Pred. No. 5.4e-26;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 complement (1. .775)
                                                                                                                                                                                                                                                                                                                                                     *tag= b
note= "Claim 8"
106. .716
                                                                                                                                                                                                                                                                                                                          *tag= c
note= "Claim 9"
                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "Claim 7"
                                                                                                                                                  AAQ62391 standard; DNA; 4341 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Fig 7; 77pp; English.
      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 93WO-GB002054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92GB-00020808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                            .780
                         Matches 100; Conservative
                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                             606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-135575/16.
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            WO9408008-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hawkins RE,
                                                                                                                                                                                       25-MAR-2003
18-NOV-1994
                                                                                                                                                                                                                   Vector pVAC1
                                                                                                                                                                                                                                                                   vaccine; sa
                                                                                                                                                                                                                                                                                                                                                                                                                              14-APR-1994
                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                     AAQ62391;
                                                                                                    61
                                                                                                                                                                                                                                                                                                              misc RNA
                                                                                                                                                                                                                                                                                                                                           misc_RNA
                                                                                                                                                                                                                                                                                                                                                                      misc_RNA
        Query Match
                Best Local
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The invention relates to a nucleic acid construct for delivery into living cells in vivo, to induce an immune response to a disease peptide antigen, where the construct directs expression of a fusion protein comprising the peptide antigen and the first domain of FrC. Also included are a nucleic acid vector comprising the above construct or vector and a method of producing a nucleic acid construct for inducing an immune response. The method comprises identifying a nucleic acid sequence encoding a disease peptide comprises identifying a nucleic acid sequence encoding a disease peptide nucleic acid sequence, introducing the cloned nucleic acid into a vector which allows the antigen to be expressed as a fusion with a first domain FrC from tetanus toxin, and optionally isolating the construct from the vector. The construct or vector is used as a vaccine to induce an immune response, particularly to tumour antigens. The present sequence is vector
                                                                                                                                                                                                                                                  Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTL; PCR primer; pVAC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid construct, useful to immunize against various diseases including cancer, expresses the first domain of tetanus toxin FrC fused to a disease peptide antigen to provide a vaccine.
CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                                                               Vector pVAC1 encoding a DNA vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 4; 71pp; English.
                                                                                                     AAS17704 standard; DNA; 4341 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CANC-) CANCER RES VENTURES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-APR-2001; 2001WO-GB001719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2000; 2000GB-00009470.
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                         Cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stevenson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-066370/09.
                                                                                                                                                                                                                                                                                                    Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                           WO200179510-A1
                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                            12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2001
              61
                                                                                                                                       AAS17704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice J,
                                                                    RESULT 10
                                                                                 AAS17704
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commercially available vector pRC/RSV. Leader sequences and termination signals were introduced into the vector to allow for production of fusion proteins. The vector, pSIG/Not.Tagl, was modified to replace the pelb leader with the human immunoglobulin VH1 leader sequence that permits the encoding of an SfiI cloning site without modification of the amino acid sequence. This fragment was then cloned as an EcoRI/Blunt-HindIII fragment into NotI/Blunt-HindIII cut vector pRC/RSV to give pVACI. The single chain Fv for an individual patient can be inserted within the VH1 leader sequence. This plasmid when encoding a single chain murine

This sequence represents the vector pVAC1. This vector is based on the

9

1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG

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AAF24901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel nucleic acid construct for inducing an immune response in vivo to an antigen, capable of directing the expression of a fusion protein that comprises an antigen and an adjuvant sequence derived from a plant viral coat protein. The construct of the invention has cytostatic and virucide activity. The nucleic acid construct is useful for inducing an immune response in a patient, for construct is useful for inducing an infectious disease caused by an antigen vaccinating a patient against an infectious disease caused by an antigen derived from a pathogen e.g. a virus, for treating a cancer patient or a patient with a predisposition to cancer and for treating a patient having a B cell malignancy, where the construct is encapsidated, and optionally, a second nucleic acid sequence encoding a further immunomodulatory undicated to the patient. The construct is also useful in medical treatment, and in the preparation of a vaccine for treating or preventing a disease state associated with the antigen. The sequence
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                                                                               9
                                                                                             GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGCCTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                                                                Immune response; plant viral coat protein; pVAC1; cytostatic; virucide;
cancer; B cell malignancy; ds.
                                                                           1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid construct for delivery into living cells as a vaccine, useful for treating e.g. cancer, directs the expression of a fusion protein comprising an antigen and an adjuvant sequence derived from a
                                                    Gaps
Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
                                                    ö
                                                   0; Indels
                                                                                                                                 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                                                                                                                                   CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                           Score 100; DB 6;
Pred. No. 5.4e-26;
               100.0%; Scc. 100.0%; Pred. No. - 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shows the complete sequence of vector pVAC1
                                                                                                                                                                                                                                                                                                           Plasmid pVAC1 complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CANC-) CANCER RES VENTURES LTD.
                                                                                                                                                                                                                             ABN83143 standard; DNA; 4341 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 7; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2000; 2000GB-00028319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2001; 2001WO-GB005142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Savelyeva N, Stevenson F;
                                                                                                                                                                                                                                                                                  (first entry)
                                     al Similarity 100.
100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant viral coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-500202/53.
                                                                                                                                                                                                                                                                                                                                                                                                       WO200240513-A2
                                                                                                                                                                                                                                                                                  10-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                 61
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                                                                                                                                                                                                                                                        ABN83143;
                         Query Match
Best Local 3
                                                   Matches
                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                 ABN83143
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The specification describes a microsphere comprising dihydrazide derivatised hyaluronic acid crosslinked to a nucleic acid (NA). The microspheres cause reduced inflammatory responses, and have increased safety and biodegradability. The microspheres are useful for transfecting a cell of a subject and for treating a subject having myocardial ischemia, by increasing cardiac angiogenesis. They are also useful for treating hemophilia. The present sequence represents the plasmid pCDNA3.1/Gs, into which is inserted a polynucleotide sequence which is crosslinked to hyaluronic acid. The polynucleotide sequence encodes a vascular endothelial growth factor (VEGF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyaluronic acid micro spheres for use in gene therapy of myocardial ischemia and hemophilia, comprising dihydrazide derivatized hyaluronic acids crosslinked to nucleic acids.
GACGGATCGGGAGATCTCCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microsphere; dihydrazide; hyaluronic acid; inflammatory response; myocardial ischemia; cardiac angiogenesis; haemophilia; vascular endothelial growth factor; VEGF; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4597 BP; 1062 A; 1214 C; 1206 G; 1115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                         CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the plasmid pCDNA3.1/GS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 36-38; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COLL-) COLLABORATIVE GROUP LTD.
                                                                                                                                                                                                                                                                                                                                     ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-2000; 2000WO-US016837.
                                                                                                                                                                                                                                                                                                                                 AAF24901 standard; DNA; 4597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-071363/08.
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les 100; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                       AAF24901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W;
                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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RESULT 13 AAD39652

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Gaps

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100.0%; Score 100; DB 6; Length 4341; 100.0%; Pred. No. 5.4e-26; 1ve 0; Mismatches 0; Indels 0;

Query Match 100. Best Local Similarity 100. Matches 100; Conservative

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The invention provides a nucleic acid molecule (I) comprising at least the functional part of blasticidin resistance (BS) gene, or its homolog, linked through a recognition sequence to at least one selected gene. (I) is useful in treatment comprising: (I) providing cells/tissues transfected with (I); (2) surgical administration of the cells/tissues to the patient to be treated; and optionally (3) monitoring the status of the cells/tissues by the patient. Therapeutic compositions comprising cells/tissues transformed with (I) is useful in identifying the role of genes in healthy and diseased tissue, in tissue engineering and in cosmetic surgery. Tissue engineering can be used to treat arthritis, joint replacement, skin grafts for burn victims, and replacement coronary arteries. Cosmetic tissue surgery includes rhinoplasty. The present sequence represents the nucleotide sequence of the vector pIRES/BS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion protein; amyloid precursor protein; APP; transcription factor; noucropic; neuroprotective; APP inhibitor; amyloid precursor protein inhibitor; Alzheimer's disease; beta-secretase; gamma-secretase; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                                                                                                                                        Novel nucleic acid molecule useful for therapeutic and cosmetic tissue engineering, comprising at least a functional part of blasticidin resistance gene linked through a recognition sequence, to a selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4840 BP; 1154 A; 1227 C; 1236 G; 1223 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression vector nucleotide sequence SEQ ID NO:27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 100; DB 4;
Pred. No. 5.6e-26;
0; Mismatches 0;
                                                                                                                                                                                                   Kafienah W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB33528 standard; DNA; 5015 BP
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Fig C; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 100; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-2003; 2003WO-US005458.
                                                                    2000WO-GB003462
                                                                                                              99GB-00021418
                                                                                                                                                                                                     Barker MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           containing the BS gene
                                                                                                                                                          SHEFFIELD
                                                                                                                                                                                                                                                 WPI; 2001-290354/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003072041-A2
                                                                                                                                                                                                   Hollander AP,
                                                                11-SEP-2000;
                                                                                                                                                          VINU (-HSYU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                              11-SEP-1999;
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                         22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB33528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a recombinant vector which comprises DNA, consisting of an insertion cassette contained between at least two insertion sites, that encodes a small nuclear (sn) RNA. The invention is used to identify snRNA modifications that inhibit expression of transcription products (and the identified snRNA are used to suppresse expression) for delivering antisense sequences to the nucleus and to create transgenic animals. The present DNA sequence is human snRNA, UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blasticidin resistance, BS gene, gene therapy, tissue engineering, cosmetic surgery, arthritis, joint replacement, skin graft; rhinoplasty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60
                                                                                                                                                                            recombinant vector; insertion cassette; small nuclear RNA; snRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant vector containing sequence for small nuclear RNA, e.g. for identifying variant snRNA that suppresses expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4639 BP; 1067 A; 1198 C; 1243 G; 1131 T; 0 U; 0 Other;
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100.0%; Pred. No. 5.5e-26;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete seguence of vector pIRES/BS.
                                                                                                                                Human small nuclear RNA (snRNA) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 18pp; English
  BP.
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AAD39652 standard; DNA; 4639
                                                                                                                                                                                                                                                                                                                                                                             12-MAR-2001; 2001US-00804481
                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAR-2000; 2000US-0188304P
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hes 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lander ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-499510/53.
                                                                                                                                                                                                   transgenic animal;
                                                                                                                                                                                                                                                                                        US2002058287-A1
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                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                     22-OCT-2002
                                                                                                                                                                                                                                                                                                                                    16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Graaf DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                           AAD39652
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Best Loca Matches

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Gaps ;

Length 4840; Indels 9

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The present invention describes a DNA molecule (I) that encodes a fusion protein (FP) comprising: (i) an amino acid sequence of amyloid precursor protein (FP), either the wild type, Swedish or NREV versaions; and (ii) a transcription factor (TF), fused in frame to the C-terminus of (i). Also described: (1) an expression vector containing (I); (2) a eukaryotic cell inhibits processing of APP, using the cells of (2). (I) has nootropic and neuroprotective activities. (I) can be used to produce eukaryotic cells that express FP and are useful in screening for agents that inhibit processing of APP. The agents are potentially useful for the treatment or prevention of Alzheimer's disease. Cells that express FP can screen for inhibitors of: (a) beta- and gamma secretases; and (b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytoplasmic/extracellular APP signaling in a single assay. Cell-based assays may be free of interference from alpha-secretase activity and are homogeneous (no chromatography, immunoprecipitation or washing required) so well suited to high-throughput screening. The present sequence represents a plasmid nucleotide sequence from the present invention.
                                                                                                                                                                                                                                      DNA encoding a fusion protein of amyloid precursor protein, useful in screening for anti-Alzheimer agents, comprises a fused transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5015 BP; 1167 A; 1297 C; 1279 G; 1272 T; 0 U; 0 Other;
                                                                                                                   Flores OA, Hazuda DJ, Inglese J;
Shi X, Simon AJ, Zuck PD;
                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 32B-F; 193pp; English
                         27-FEB-2002; 2002US-0360274P.
                                                                                                                   Espeseth AS, Ferrer M,
Miller MD, Register B,
                                                                   (MERI ) MERCK & CO INC
                                                                                                                                                                                         WPI; 2003-689968/65.
                                                                                                                                                                                                                                                                                     factor
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1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATG 60 Gaps ; 0 Length 5015; Indels 100.0%; Score 100; DB 10; 100.0%; Pred. No. 5.6e-26; tive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 100; Conservative

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61 CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100 δ

1 GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACATCTGCTCTGATG 60

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Search completed: July 14, 2005, 07:01:24 Job time : 147.038 secs

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100004J13 100004J13 100006E20 100005001 100002J14 100002K13

100003G07 100005D19 100004C11 100003A24 100003M12

1000001 100003F16

.00006M24

CC818492 CC81761 CC818511 CC818511 CC819049 CC81704 CC81704 CC81762 CC81762 CC81763 CC817682 CC817682 CC817682 CC817784 CC818384 CC817834 CC817834 CC817834 CC817834 CC817834 CC818384 CC818384 CC818384 CC818384 CC81837

OM nucleic

on:

Run

Sequence:

Searched:

Database

Result No.

an

/note="Vector: PR-Script Amp SK+; Site\_1: SrfI; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yronne Thorstenson of the Stanford DNA Sequencing and Technology Center

nbeb0022E CIT-HSP-2

jnr21d02

AQ075099 BZ049113

AQ863966 AQ075099

52.8 52.6 52.4

BZ049113

BZ053587

nr56b03

BZ050646 BZ054793

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264 GCATAGTTAAGCCAGCCCGACACCC 239
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BZ054067/c
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                             SOURCE
                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
COMMENT
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AUTHORS
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AUTHORS
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KEYWORDS
                                                                 RESULT 3
BZ050328
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jnr13g03.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
(http://sequence-www.stanford.edu/group/techdev/shear.htm)
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(bases 1 to 694)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Mash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: portal; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                             41 CAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 cegarcearaderecerecaerrarrarderecaerecaeracaarerecererearee
                The randomly sheared gDNA was chromatographed on Sephacryl S-400 to remove any small fragments and DNA eluting in the void volume was blunt-ended with T4 DNA Polymerase, treated with alkaline phosphatase to prevent the ligation of multiple fragments, ligated to Srf 1-digested pCR-Script Amp (SK+) vector and transformed into E. coll strain Xilo Gold. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7 primers."
                                                                                                                                                                                                                                                                                                                                                                                  1 CAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTT 60
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                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                60.0%; Score 60; DB 8; Length 602; 100.0%; Pred. No. 2.4e-10; ive 0; Mismatches 0; Indels
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
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/mol_type="genomic DNA"
/db xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3712"
/clone_lib="B.oleracea001"
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Seg primer: -28RPpOT reverse
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High quality sequence stop: 551.
Location/Qualifiers
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Best Local Similarity
Matches 60; Conserva
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BZO50328 696 bp DNA linear GSS 09-OCT-2002 jnr42c12.b1 B.oleracea001 Brassica oleracea genomic, genomic survey
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jnr38b09.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
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                                                                                                                                                                            Brassica oleracea
Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="b.olerasca001"
/note="Vector: pOTW13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thosmas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
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Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Sequencing Center
Washington University School of Medicine
Bail: submissions@watson.wustl.edu
Plate: jnr42 row: c column: 12
Seq primer: -21UPpOT forward
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High quality sequence stop: 180.
Location/Qualifiers
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Gaps

70

COMMENT

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AL714571 Danio rerio embryonic inner ear subtracted cDNA Danio rerio cDNA clone BNOAA007ZC02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                           AL715724 343 bp mRNA linear EST 18-APR-2002
AL715724 Danio rerio embryonic inner ear subtracted cDNA Danio
rerio cDNA clone BNOAA018ZF12 5', mRNA sequence.
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                                                                                                                           65 GCGGTATACACACCGCATATGGTGCACTCTCAGTACAATCTGCNCTGATGCCGCATAGTT 124
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( bases I to 343)

Coimbra, R., Well, D., Brottier, P., Blanchard, S., Levi, M., Hardelin, J. P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //issue_type="inner" ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 TCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA
                                                                                                11 GAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Locatelon/Qualifiers
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Pred. No. 4.8e-08;
0; Mismatches 11; Indels C
    Length 348;
                                                 Indels
53.6%; Score 53.6; DB 2; ilarity 80.5%; Pred. No. 4.1e-08; Conservative 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="subtracted cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BNOAA018ZF12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL715724.1 GI:20180327
                                                                                                                                                                                                                                         125 AAGCCAGTATACACTCC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio rerio (zebrafish)
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Best Local Similarity 84.5%;
Matches 60; Conservative
                                                                                                                                                                                           71 AAGCCAGTATCTGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                embryonic inner ear
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  Query Match
Best Local Similarity
Matches 62; Conserv
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AL715724/c
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AL714571/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW409112 348 bp mRNA linear EST 31-DEC-2000 sall0h5 Salivary Gland Library Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="B.oleracea001"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica elecae TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 CGGATCGATAGGTCCCTGGACTAGTTATGGTGCACTCTCAGTACAATCTGCTCTGATGCC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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South African Institute For Medical Research
P.O.Box 1038, Johannesburg, Gauteng, 2000, South Africa
Fax: 2711 489 9226
Email: micheler@mail.saimr.wits.ac.za.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 55.6%; Score 55.6; DB 8; Length 7: Best Local Similarity 77.9%; Pred. No. 9.1e-09; Matches 67; Conservative 0; Mismatches 19; Indels
                        Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="Salivary Gland"
/clone_lib="Salivary Gland Library"
/note="Vector: pAMP10"
                                                                                        Genome Sequencing Center
Washington University, School of Medicine
Mashington University, School of Medicine
Platall: submissions@watson.wustl.edu
Plate: jnr38 row: b column: 09
Seq primer: -28RPpOT reverse
Class: shocyun
High quality sequence start: 87
High quality sequence stop: 543.
Location/Qualifiers
    Nash, W., Rabinowicz, P.D. and Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                       'organism="Brassica oleracea"
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                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 GCATAGTTAAGCCAGCCCCGACACCC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GCATAGTTAAGCCAGTATCTGCTCCC 88
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing Center."
                                                                       Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW409112
AW409112.1 GI:11999687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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AW409112
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Gaps . 0 9/

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/issue type="inflorescence meristem"
//issue type="inflorescence meristem"
//dow stage="about one week after bolting"
//lab_host="E. coli SCS-1/pSE111"
//clone lib="AtM1"
//clone lib="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CK120360 766 bp mRNA linear EST 01-JUN-2004
207104.pl ALM1 Arabidopsis thaliana cDNA clone MPMGp2011J04207
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clome_lib="AtM1"
/note="Vector: pQE-30NAST-attB (AY386205); Site_1: Sall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 TCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA
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Feilner, T., Immink, R.G.H., Cahill, D.J. and Kersten, B.
Generation of a cDDA expression library from Arabidopsis
inflorescence meristem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 761;
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/dev_stage="about one week after bolting"
/lab_host="E. coli SCS-1/pSE111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
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Contact: Birglt Kerret
Contact: Birglt Kerret
Max-Planck-Institute for Molecular Genetics
Thestr. 73 , D-14195 Berlin, Germany
Fax: +49(0)30/84131128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53.4; DB 7;
Pred. No. 5.6e-08;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Arabidopsis thaliana"
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Insert Length: 76 Std Error: 0.00
Plate: 207 row: J column: 4
Seg primer: pQE65.
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/clone="MPMGp2011J04207"
               clone="MPMGp2011009212"
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/ecotype="Columbia"
/db_xref="GABI:953059"
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Best Local Similarity 84.5%;
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 TCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 76
280 TTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                      Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 315)

10 (bases 1 to 145)

Hardelin,J.P., Weissenbach,J. and Petit,C.

A subtracted cDNA library from the zebrafish (Danio rerio)

Embryonic inner ear

Unpublished (2002)
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Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ilmestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
Fax: +49(0)30/84131128

    .761
    /organism="Arabidopsis thaliana"

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Insert Length: 761 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="inner ear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
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/ecotype="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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Seq primer: pQE65.
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CK119397
CK119397.1 GI:47829713
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SOURCE
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209p08.pl AtMl Arabidopsis thaliana cDNA clone MPMGp2011P08209
5-FMHMS, mRNA sequence.
Site 2: Not1, About 1 week after bolting, cDNA synthesis using SuperscriptTM-system (Invitrogen) with an oligo (df) -primer containing Not1 restriction site and a SalI adapter. The main library (plate numbers begin with 1) of 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at https://gabi.rzpd.de"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         679 TTCACACCGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 TCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /notes-Tvector: pQE-30NAST-attB (AY386205); Site 1: Sall; Site 2: NotI; About 1 week after bolting, cDNA synthesis using SuperscriptTM-system (Invitrogen) with an oligo(dT)-primer containing NotI restriction site and a Sall adapter. The main library (plate numbers begin with 1) of 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative
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                                                                                                                                                                                                                                                                                                                                                                                             53.4%; Score 53.4; DB 7; Length 766; llarity 84.5%; Pred. No. 5.6e-08; Conservative 0; Mismatches 11; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GABI:953578"
|db_xref="taxon:3702"
|clone="kpMg2011p08209"
|fissue_type="inflorescence meristem"
|dev_stage="about one week after bolting"
|deb_host="E. coli SCS-1/pSE111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inhestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
Fax: +49(0)30/84131128
Fax: +49(0)30/84131128
Enail: Kersten@molgon.mgg.de
Insert Length: 788 Std Error: 0.00
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Seq primer: pQE65.
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/ecotype="Columbia"
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Matches 60; Conserve
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CK117844/c
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REFERENCE

LOCUS

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FEATURES

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ISB1-118J17_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-118J17, pgenomic survey sequence.
expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at https://gabi.rzpd.de"
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                                                                                                                                                                                                                                                           514 TICACACGCATATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA 455
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
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/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
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                                                                                                                                                                                Gaps
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Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 4
High quality sequence stop: 742.
Location/Qualifiers
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ilarity 84.5%; Pred. No. 5.8e-08;
Conservative 0; Mismatches 11;
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/mol_type="genomic DNA"
/db_xref="taxon:8364"
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192 GTATACACTCC 182
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1SB1-118B12_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-118B12,
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(bases 1 to 1009)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                       Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 899)
Mremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
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Washington University School of Medicine
Bmail: submissions@wateno.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTATAAGG
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Washington University School of Medicine
Bmail: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTATAGGG
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Xenopus tropicalis
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/db_xref="taxon:8364"
/clone="ISB1-118B12"
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High quality sequence stop: 681.
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                                                                                                                                                                                                                                                                                                                     Contact: Richard K Wilson
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                        genomic survey sequence. CL140877
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Best Local
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryothyta; Magnoliaphyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

Ehrhartoideae; Oryzae; Oryza.

I (bases 1 to 814)

Ming.R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome

Lu Opublished (1998)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

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Tel: 864 656 4293

Email: rwing@clemson.edu

Seq primer: GGAAACRGCTATCACCATG
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/lab host="E. Coli PH10B"
/cloal lib="CUGI Rice BAC Library (EcoRI)"
/note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACIndigo; Site_1: EcoRI; Site_is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely moncoctyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 02-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 TICACACCGCATAIGGIGCACTCTCAGIACAAICTGCTCTGAIGCCGCAIAGITAAGCCA 193
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nbeb0049M21r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica
cultivar-group) genomic clone nbeb0049M21r, genomic survey
                                                                                                                                                                                                                                                                                         /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC Library Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 TCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                   1. .1009
/organism="Xenopus tropicalis"
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/clone="ISB1-84J15"
/clone_lib="ISB1"
Class: BAC ends
High quality sequence start: 167
High quality sequence stop: 324.
Location/Qualifiers
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High quality sequence stop: 361.
Location/Qualifiers
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AQ914559
AQ914559.1 GI:6511075
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Gaps .; 0

62

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Gaps
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                                                                     ;
0
                              53.2%; Score 53.2; DB 8; Length 814; 78.0%; Pred. No. 6.7e-08; tive 0; Mismatches 18; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
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Seg primer: -21UPpOT forward
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High quality sequence start: 29
High quality sequence stop: 94.
Location/Qualifiers
                                                                                                                                                                                                           339 AGTTAAGCCAGCCCGACACCC 360
                                                                                                                                                                           67 AGTTAAGCCAGTATCTGCTCCC 88
                                                                                                                                                                                                                                                                                                                                                                      BZ051815.1 GI:23652690
                                                                   64; Conservative
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Brassica oleracea
                              Query Match
Best Local Similarity
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53.0%; Score 53; DB 8; Length 675; 75.6%; Pred. No. 7.6e-08;

Query Match Best Local Similarity

ORIGIN

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53 CGGNACGATAGGTCCCTGGACTAGTTATGGTGCACTCTCAGTACAATCTGCTCTGATGCC 112
                                                                                         3 cegarceseagarerecegareeeerareerecegaeeeerecegaareee
                21; Indels
                0; Mismatches
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Job time : 957.146 secs
                65; Conservative
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Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the Sequencing Center.
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Sequence Sequence Sequence

AX342686

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X96612 Expression
X96610 Expression
X96610 Expression
BD134374 Peptide 1
AR428934 Sequence
AX513181 Sequence
AX513181 Sequence
AX513181 Sequence
AX513725 Sequence
AX207725 Sequence
AX207726 Sequence
AX207740 Sequence
AX207740 Sequence
AX207740 Sequence
                  AX211281 Sequence
AX343455 Sequence
BD168975 Method of
AX211283 Sequence
AX343459 Sequence
AX434364 Sequence
BD168966 Method of
AR01374 Sequence
BD009742 Compositi
                                                                                                                                                                                                                                                                                                                                                                                            cloning vector; expression vector; multiple cloning site; Plasmid. synthetic construct synthetic construct
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A new small sized high-level eukaryotic expression vector
Unpublished
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Submitted (07-AUG-1995). H. Peters, Inst. f. Immunologie, Michaelisstr.5, D- 24105 Kiel, FRG
Related sequences: M21295 and K03104.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 101; DB 12; Length 3986; Best Local Similarity 100.0%; Pred. No. 5.1e-15; Matches 101; Conservative 0; Mismatches 0; Indels 0;
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'note="cloning vector (pcDNA3). (Invitrogen)"
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BD134374
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EVPCMVPA3
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AX234391 Sequence
BA91754 Sequence
BD085110 Vertebrat
BD334590 Screening
AX026821 Sequence
BD195386 Compositi
AX119694 Sequence
AX311282 Sequence
AX202478 Sequence
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AX342685 Sequence
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                                                                  July 14, 2005, 04:39:07; Search time 756.618 Seconds (without alignments) 6468.225 Million cell updates/sec
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1 cggtctattcttttgattta.....acgcgaattaattctgtgga 101
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                      4708233 seqs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
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Sequence:

Run on:

Searched:

Score

Result Š. SYN 16-AUG-1995

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Gaps

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1 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGATTTTCGGCCTATTGGTTAAAAATG

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1693 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGATTTTCGGCCTATTGGTTAAAAAATG 1752
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Materials and methods involving hybrid vascular endothelial gr
factor dnas and proteins and screening methods for modulators
Patent: WO 0162942-A 130-AUG-2001;
LUDWIG INSTITUTE FOR CANCER RESERRCH (US) ; Licentia OY (FI)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="pCDNA3.1/GS vector by Invitrogen Corporation"
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                                    61 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 101
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100.0%; Pred. No. 4.8e-15;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                      other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                    Hyaluronic acid microspheres for sue
Patent: WO 0078358-A 3 28-DEC-2000;
The Collaborative Group, Ltd. (US)
Location/Qualifiers
1. .4597
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Sequence 3 from Patent WO0078358.
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C12N15/12,C12N5/10,C12N15/85,C07K14/435,C07K16/18,A61K38/17,
A61K49/00,
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JACQUES SIMON MAERTENS,
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Bogaert, T.A. and Deraeymaeker, M.

Patent: WO 9824810-A 10 11-JUN-1998;

BOGAERT THIERRY ANDRE OLIVIER (BE); DERAEYWAEKER MARC (BE)
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Vertebrate homologues of UNC-53 protein of C elegans.
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100.0%; Pred. No. 4.8e-15;
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/db_xref="taxon:32644"
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Sequence 10 from Patent WO9824810.
A91754
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BD085110.1 GI:22630720
JP 200152222-A/8.
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Composition and methods for administering Pneumococcal DNA.
BD195386
BD195386.1 GI:33065156
JP 2002514061-A/3.
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1 (bases 1 to 5446)

1 (bases 1 to 5446)

Exilae, D.E., Mcdaniel, L.S., and Curiel, D.T.

Composition and methods for administering Pneumococcal DNA Patent: JP 2002514061-A 3 14-MAY-2002;

UNIVERSITY OF ALABAMA AT BIRMINGHAM
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PN JP 202514061-A/3
PD 14-MAY-2002
PF 04-DEC-1996 US 08/759505
PR 04-DEC-1996 US 08/759505
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PR 04-DEC-1996 US 08/759505
PR 04-DEC-1997 JP 1998525895
PR 04-DEC-1997 JP 1998525895
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PR 04-DEC-1996 US 08/759505
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Pred. No. 4.7e-15;
; Mismatches 0;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Mutagen"
                                                                                                           DNA
                                                                                                                                                                                                                                                                             other sequences; artificial sequences
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HOECHST MARION ROUSSEL DE GMBH (DE)
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Sequence 9 from Patent DE19856261.
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    .5446
    /organism="unidentified"

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/db_xref="taxon:32644"
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C12Q1/02,G01N33/53
Strandedness: Double;
Topology: Circular;
Vertebrate homologues of UNC-53 protein of C elegans FH
Location/Qualifiers
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                                                                                                                                                   organism='Unidentified'
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100.0%; Score 101; DB 6;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 101; Conservative 0; Mismatches 0;
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1 (bases 1 to 5432)
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Patent: JP 2002531141-A 2 24-SEP-20
AVENTIS PHARMA DEDTSCHLAND GWBH
OS Artificial Sequence
PN JP 2002531141-A/2
PD 24-SEP-2002
PD 24-SEP-2002
PP 27-NOV-1999 JP 2000586944
PR 07-DEC-1998 DE 198 56 261.6
PI GISELA PERAUS
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Screening assay of Abeta-peptide.
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AUTHORS

REFERENCE

PAT 06-SEP-2001

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PRAWEPELNEAI PNDRSDTTWPVAMATTIRKLITGELLITASRQOLIDWMEADBVVRL
IRSALPAGWFIADKSGAGERGSRGIIAALGPDGKFSRIVVIYTTGSQATMDERNRQIA
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/note="Coding sequence for human FSH-beta"
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100.0%; Pred. No. 4.7e-15;
cive 0; Mismatches 0;
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AX349366.1 GI:18615329
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Direct Submission
Submitted (14-ocr-2003) Department of Biology, College of Natural
Sciences, Chungnam National University, 305-764, Daejeon 305-764,
                                                                                       1 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGATTTCGGCCTATTGGTTAAAAATG
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other sequences; artificial sequences; vectors.
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/mol_type="other DNA"
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ive 0; Mismatches 0;
   100.0%; Pred. No. 4.7e-15; ive 0; Mismatches 0;
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Chemicon International (US)
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Sequence 5 from Patent WO0181614.
AX319694
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Cell proliferation assay
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                             synthetic construct
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                                                                     Okkels,J.S., Jensen,A.D. and van den Hazel,B. Peptide extended glycosylated polypeptides
Patent: WO 0205597-A 4 10-JAN-2002;
Maxygen Aps (DK) ; Maxygen Holdings Ltd (KY)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.7e-15;
Matches 101; Conservative 0; Mismatches 0;
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iive 0; Mismatches 0;
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/db_xref="taxon:32630"
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1231. .1617
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Sequence 66 from Patent WO0152620.
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PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
YRGBYKCKYGNKALPAPIEKTISKAKGOPREPQYYTLPPSRDELTKNOVSLTCLVKGF
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ALHNHYTQKSLSLSGGK"
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                                           Thomassen-Wolf,E., Borges,E., Yayon,A. and Rom,E.
Antibodies that block receptor protein tyrosine kinase activation,
methods of screening for and uses thereof
Patent: WO 02102854-A 5 27-DEC-2002;
MorphoSys AG (DE); ProChon Biotech Ltd. (IL)
Location/Qualifiers
1. 5995
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/db xref="waxon:32630"
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Developpement, Campus de Luminy Case 907 F-13288 Marseille, 13288,
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398. .1652
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other sequences; artificial sequences.
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AJ575208
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134. .1776
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under control of CMV enhancer/chicken beta-actin promoter"
1782. .1996
/note="bovine growth hormone"
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Best Local Similarity 100.0%; Pred. No. 4.6e-15;
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2908. .3723
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under control of SV40 promoter"
3757. .3887
/note="late"
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ВР.

ADH11353 standard; DNA; 3482

RESULT 1 ADH11353

UNC-53 vertebrate protein homologue; UNC-53; Caenorhabditis elegans; cell shape regulator; cell motility regulator; cell migration; cell behaviour regulator; phenotype; signal transduction pathway; signal transducing protein; signal integrator protein, prevascularisation; revascularisation; wound healing; chronic neurodegenerative disease; acute traumatic injury; Verhasselt P; Vandekerckhove JS; Vertebrate UNC-53 protein homologue related nucleotide sequence. CM, Deraeymaeker M, Luyten W, Geerts H, 97WO-EP006956. 96GB-00025283 (first entry) fibrotic disease; gene; ds (JANC ) JANSSEN PHARM NV. 03-DEC-1997; 04-DEC-1996; 11-MAR-2004 Unidentified WO9824810-A2 11-JUN-1998. ADH11353; 

Platteeuw CJ, Buesa Arjol CM, Pujol NJR, Maertens LJS, Luyt Geysen J, Bogaert TAOE;

WPI; 1998-362411/31. P-PSDB; ADH11354.

Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.g. promoting neuronal regeneration, treating chronic neuro-degenerative diseases or acute traumatic injuries.

Disclosure; Page 414-417; 479pp; English.

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The present invention describes a vertebrate protein homologue of an UNC-
53 protein of Caenorhabditis elegans or a functional equivalent,
CC derivative or bioprecursor of UNC-53. Also described. (1) a CDNA sequence
cnooding a vertebrate homologue of the C. elegans UNC-53 protein; (2) a
cnucleic acid which hybridises to the CDNA of (1); (3) vector comprising
cc the CDNA as in (1); (4) a host cell containing the vector as in (3); (5)
ca transgenic cell, tissue or animal comprising the vector as in (3); (6)
ca compound identified as an enhancer or inhibitor of the regulation of
ccll shape, motility, or the direction of cell migration for use as a
thermagenic; (7) a method for determination of whether a protein is an
cinhibitor or enhancer of regulation of call behaviour, growth, shape or
complity or the direction of migration by contacting a host cell
complity or the direction of migration by contacting a host cell
complity or the direction of migration by contacting a host cell
complity or the direction of referemining a change of phenotype;
(8) a method for identification of vertebrate homologues of C. elegans
cunc-53 gene by hybridising a probe of 15-50 bp of the unc-53 sequence to
cc a DNA library; and (9) a method for identification of a protein which as
cc cc a DNA library; and (11) analysing such a complex to
cative in the signal transduction pathway of a cell of which a vertebrate
cc active in the signal transduction pathway of a cell of which a vertebrate
cc active in the signal integrator protein involved in controlling
cative in the directionality of cell migration and cell shape in C. elegans.
cc signal transducing or signal integrator protein involved in controlling
cdirectionality of cell migration and cell shape in C. elegans.
controllarisation or wound healing, to treat charge in electrory and controllarises of controllarises of controllarises of controllarises of controllarises of controllarises.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 101; DB 2; Length 3482; Best Local Similarity 100.0%; Pred. No. 4.1e-19; Matches 101; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3482 BP; 767 A; 956 C; 913 G; 846 T; 0 U; 0 Other;
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                                                                                                             The specification describes a microsphere comprising dihydrazide derivatised hyaluronic acid crosslinked to a nucleic acid (NA). The microspheres cause reduced inflammatory responses, and have increased safety and blodegradability. The microspheres are useful for transfecting a cell of a subject and for tracting a subject having myocardial ischemia, by increasing cardiac anglogenesis. They are also useful for treating heemophilia. The present sequence represents the plasmid pCDNA:1/Gs, into which is inserted a polynucleotide sequence which is crosslinked to hyaluronic acid. The polynucleotide sequence encodes a vascular endothelial growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant vector which comprises DNA, consisting of an insertion cassette contained between at least two insertion sites, that encodes a small nuclear (sn) RNA. The invention is used to identify snRNA modifications that inhibit expression of transcription products (and the identified snRNA are used to suppress expression) for delivering antisense sequences to the nucleus and to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant vector containing sequence for small nuclear RNA, useful e.g. for identifying variant snRNA that suppresses expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; recombinant vector; insertion cassette; small nuclear RNA; snRNA;
Hyaluronic acid micro spheres for use in gene therapy of myocardial ischemia and hemophilia, comprising dihydrazide derivatized hyaluronic acids crosslinked to nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGGATTTCGGCCTATTGGTTAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 4.3e-19;
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                                                                              Example 1; Page 36-38; 38pp; English
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ilarity 100.0%;
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Matches 101; Conserv
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                                                                                                                                                                                                                                                            The protein (RP) comprising: (1) an amino acid sequence of amyloid precursor protein (RP) comprising: (1) an amino acid sequence of amyloid precursor protein (APP), either the wild type, Swedish or NFEV versions; and (ii) a transcription factor (TF), fused in frame to the C-terminus of (i). Also described: (1) an expression vector containing (I); all ewarding (I); all ewarding (I); all ewarding (I); and (3) methods for identifying a compound (A) that inhibits processing of APP, using the cells of (2). (I) has nootropic and neuroprotective activities. (I) can be used to produce eukaryotic cells that express FP and are useful in secrening for agents that inhibit processing of Alzheimer's disease. Cells that express FP can screen for inhibitors of: (a) beta- and gamma-secretases, and (b) cytoplasmic/extracellular APP signaling in a single assay. Cell-based assays may be free of interference from alpha-secretase activity and are homogeneous (no chromatography, immunopracipitation or washing required) so well suited to high-throughput screening. The present invention.
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                                                                                                                                   1261 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGATTTCGGCCTATTGGTTAAAAATG 1320
                                                                                                                                                                                                                                                                                                                                                                                    nootropic; neuroprotective; APP inhibitor; anyloid precursor protein inhibitor; Alzheimer's disease; beta-secretase; gamma-secretase; human; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes a DNA molecule (I) that encodes a fusion
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                                                                                                          1 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGGATTTCGGCCCTATTGGTTAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding a fusion protein of amyloid precursor protein, useful in screening for anti-Alzheimer agents, comprises a fused transcription
                                                                                                                                                                                                                                                                                                                                                                      fusion protein; amyloid precursor protein; APP; transcription factor;
                                                                                  Gaps
 create transgenic animals. The present DNA sequence is human snRNA,
                                                                               ;
                         Sequence 4639 BP; 1067 A; 1198 C; 1243 G; 1131 T; 0 U; 0 Other;
                                                       Length 4639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inglese J;
                                                                            Indels
                                                                                                                                                                              1321 AGCTGATTTAACAAAAATTTAACGCGAATTAATTCTGTGGA 1361
                                                                                                                                                              61 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 101
                                                                                                                                                                                                                                                                                                                                             Expression vector nucleotide sequence SEQ ID NO:27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zuck
                                                    ; Score 101; DB 6;
; Pred. No. 4.3e-19;
0; Mismatches 0;
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Shi X, Simon AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 32B-F; 193pp; English.
                                                                                                                                                                                                                                                           ADB33528 standard; DNA; 5015 BP
                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 101; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-2003; 2003WO-US005458.
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                                                                                                                                                                                                                                                                                                                  (first entry)
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Miller MD, Register B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-689968/65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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ADB33528
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The present invention relates to polypeptides that bind cellular receptors for vascular endothelial growth factors (VEGFs), the polymucleotides encoding them, and their use for identifying agents that modulate interactions between VEGFs and their receptors. VEGFs and their receptors play an important role in vasculogenesis, the development of the embryonic vasculature from early differentiating endothelial cells and angiogenesis, the process of forming new blood vessels from premay be used to treat dysfunction of the endothelial cell regulatory system. Such disorders include cancers, abnormal angiogenesis, proliferative retinopathies, age-related macular degeneration, rheumatoid arthritis and psoriasis. The polypeptides of the invention exhibit unique receptor binding profiles compared to known naturally occurring VEGFs. The present DNA sequence for psecTagl vector is used to express VEGFs.
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                                                                                                                                                                                                                                                 1637 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGATTTTCGGCCTATTGGTTAAAAAATG 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, vascular endothelial growth factor; VEGF-A; vasculogenesis;
angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
age-related macular degeneration; rheumatoid arthritis; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides that bind cellular receptors for vascular endothelial growth
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                                                                                                                                                                                      CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGATTTTCGGCCTATTGGTTAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence of pSecTagI vector used to express VEGF-A/VEGF-C hybrids.
                                                                                                                       Gaps
0 U; 0 Other;
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                                                        Length 5015;
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                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                     1697 AGCTGATTTAACAAAAATTTAACGCGAATTAATTCTGTGGA 1737
                                                                                                                                                                                                                                                                                                                AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 101
Sequence 5015 BP; 1167 A; 1297 C; 1279 G; 1272 T;
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                                                           В
                                                                                      ; Pred. No. 4.3
0; Mismatches
                                                           Score 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factors, polynucleotides encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pSecTagI; cyclic; circular; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS12839 standard; DNA; 5070
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                                                           100.08;
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                                                                                            100.08;
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                                                                                         Local Similarity 100.
nes 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LICN ) LICENTIA OY.
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                                                        Query Match
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Matches
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a method for identification of vertebrate homologues of C. elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytomegalovirus
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07-OCT-2002
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Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                             1693 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGGATTTCGGCCTATTGGTTAAAAAATG 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Si protein of Caenorhabditis elegans or a functional equivalent, derivative or bioprecursor of UNC-53. Also described: (1) a cDNA sequence encoding a vertebrate homologue of the C. elegans UNC-53 protein; (2) a nucleic acid which hybridises to the CDNA of (1); (3) vector comprising the cDNA as in (1); (4) a host cell containing the vector as in (3); (5) a transgenic cell, tissue or animal comprising the vector as in (3); (6) a compound identified as an enhancer or inhibitor of the regulation of cell shape, motility, or the direction of cell migration for use as a therapeutic; (7) a method for determination of whether a protein is an inhibitor or enhancer of regulation of cell behaviour, growth, shape or motility or the direction of migration by contacting a host cell expressing a homologue of UNC-53 and determining a change of phenotype;
                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a vertebrate protein homologue of an UNC-
                                     1 CGGTCTATTCTTTTGATTTATAAGGGATTTTTGGGGATTTCGGCCTATTGGTTAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.g. promoting neuronal regeneration, treating chronic neuro-degenerative diseases or acute traumatic injuries.
              Gaps
                                                                                                                                                                                                                                                                             UNC-53 vertebrate protein homologue, UNC-53; Caenorhabditis elegans; cell shape regulator; cell motility regulator; cell migration; cell behaviour regulator; phenotype; signal transduction pathway; signal transducing protein; signal integrator protein; neuronal regeneration; revacularisation; wound healing; chronic neurodegeneration disease; acute traumatic injury;
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Vandekerckhove JS;
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              Indels
                                                                                                      101
                                                                                      61 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA
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   4.3e-19;
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en W, Geerts H,
             0; Mismatches
 Pred. No.
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Luyten W,
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1028. .2149
/*tag= a
                                                                                                                                                                                                                                                      Plasmid pCB201 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                         fibrotic disease; human; gene; ds.
                                                                                                                                                                              ADH11417 standard; DNA; 5082 BP
100.08;
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Pujol NJR, Maertens LJS,
Geysen J, Bogaert TAOE;
                                                                                                                                                                                                                             (first entry)
 Best Local Similarity 100.
Matches 101; Conservative
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P-PSDB; ADH11424.
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unc-53 gene by hybridising a probe of 15-50 bp of the unc-53 sequence to a DNA library; and (9) a method for identification of a protein which is active in the signal transduction pathway of a cell of which a vertebrate homologue of UNC-53 is a component comprising; (i) contacting an extract of a cell with an antibody to the UNC-53 homologue; (ii) identifying an antibody/homologue complex; and (iii) analysing such a complex to identify any non-antibody protein bound to the complex. UNC-53 is a signal transducing or signal integrator protein involved in controlling directionality of cell migration and cell shape in C. elegans Vertebrate homologues of UNC-53 can be used to promote neuronal regeneration, revascularisation or wound healing, to treat chronic neurodegenerative diseases or acute traumatic injuries or fibrotic diseases. The present sequence is used in the exemplification of the present invention.
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Temple GF;
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Byrd DRN,
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Cheo D, Hartley JL,
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2001US-0318902P.
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27-NOV-2001; 2001US-0333124P.
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Matches 101; Conservative
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28-SEP-2001; 2001US-0326092P
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                                                                            The INVENTION (a) consisted and all solutions sites; and (b) one or more comprising: (a) one or more recombination sites; and (b) one or more topoisomerases. Also included are a vector comprising the nucleic acid, a vector chosen from penNAGWDT(sc), pENTR-DT(sc), penNAB-DEST41, pENTRAD-TOPO, pENTR/BOD-TOPO, pENTR/BOD-TOPO, a host cell comprising the penNAGWDT(sc), pENTR-DT(sc), penNAB-DEST41, pENTRAD-TOPO, a host cell comprising the penNAGWDT acid or vectors and an in vitro method of cloning a nucleic acid molecule involving: (a) obtaining a first nucleic acid molecule to be cloned in vitro with a second nucleic acid molecule comprising at least a first recombination site, and at least a second topoisomerase recognition site flanked by at least a second recombination site, where the first and second comprising to site, where the first and second comprising to recombination sites do not recombine with each other, and at least one second nucleic acid molecule to be cloned is inserted into the second copisomerase; and (c) incubating the mixture under conditions such that the first nucleic acid molecule to be cloned between the first and second comprising crecombination sites, thereby producing a first product molecule comprising crecombination sites, thereby producing a first product molecule caid molecule to be cloned between the first and second crecombination sites, thereby producing a first product molecule caid molecule to be cloned between the first and second crecombination sites, thereby producing a first product molecule caid molecule to be cloned between the first and second crecombination sites, thereby producing a first product molecule caid molecule construction of gene targeting nucleic acid conclusions and second conclusions and second conclusions and second conclusions and second conclusions of gene targeting and fealures construction of gene targeting and fealures or targeting or mutating a sequence is the topoisomerase site-containing vector ponNAG-2/VS/GWD-CCTOPO. (Updated on 07-AUG-2003 to corr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1747 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGGATTTTCGGCCTATTGGTTAAAAATG 1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGGTCTATTCTTTTGATTTATAAGGGATTTTTGGGGGATTTCGGCCTATTGGTTAAAAAATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombination site; topoisomerase recognition site; topoisomerase; transfection; two-hybrid assay; ds; plasmid; cyclic; circular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5173 BP; 1247 A; 1338 C; 1274 G; 1305 T; 0 U; 9 Other;
                                                                  The invention relates to an isolated nucleic acid molecule (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 101; DB 6; Length 5173; 100.0%; Pred. No. 4.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1807 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 101
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0
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                   Disclosure; Fig 25B-25C; 324pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE83792 standard; DNA; 5173 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-2000; 2000US-0254510P.
11-DEC-2000; 2000US-00732914.
21-MAX-2001; 2001US-0291972P.
14-SEP-2001; 2001US-0318902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mest bocal Similarity 100.0%;
Matches 101; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-2001; 2001US-00005876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pcDNA6.2/V5/GWD-TOPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pcDNA6.2/V5/GWD-TOPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003186233-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE83792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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1747 CGGTCTATTCTTTTGATTTATAAGGGATTTTTGGGGGATTTCGGCCTATTGGTTAAAAAATG 1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an isolated nucleic acid molecule comprising at least one recombination site, and at least one topoisomerase recognition site and/or at least one topoisomerase. The isolated nucleic acid molecule is used as a vector in a host cell. It can be used directly for transfecting a cell, or as a template for performing amplification, e.g. PCR, a recombination reaction, an in vitro transcription reaction, or a coupled transcription/translation reaction. The invention allows several nucleic acid molecules to be covalently linked in a predetermined directional orientation. A functional product can be selected in vitro by performing an amplification reaction using primers specific for the termini of the desired covalently linked recombinant nucleic acid molecule. This sequence represents plasmid poDNA6.2/V5/GMD-TOPO
                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule useful as vector in host cell comprises at
least one recombination site, and at least one topoisomerase recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGGATTTCGGCCTATTGGTTAAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector; recombination site; topoisomerase recognition site; topoisomerase; in vitro cloning; recombinatorial cloning; plasmid; pcDNA6.2/V5/GWD-TOPO; ds.
                                                                                                                                                 Fan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chesnut JD, Carrino J, Leong L, Madden K, Gleeson M, Fan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5173 BP; 1247 A; 1338 C; 1274 G; 1305 T; 0 U; 9 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5173;
                                                                                                                                         Gleeson M,
Temple GF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 101; DB 12;
100.0%; Pred. No. 4.3e-19;
ive 0; Mismatches 0;
                                                                                                                                         Madden K,
Byrd DRN,
                                                                                                                                                                                                                                                                                                                                                                                                            site and/or at least one topoisomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 25B-C; 136pp; English.
                                                                                                                                                 ŗ,
                                                                                                                                         JD, Carrino J, Leong L, MA, Cheo D, Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AD006721 standard; DNA; 5173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-2002; 2002US-0385613P.
27-NOV-2001; 2001US-0333124P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2003; 2003WO-US018036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 101; Conservative
                                                                  (INVI-) INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INVI-) INVITROGEN CORP
                                                                                                                                                                                                                                                   WPI; 2004-031998/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003103600-A2
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09

Gaps

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0; Mismatches

BP.

Length 5218; Indels

100.0%; Score 101; DB 12; 100.0%; Pred. No. 4.3e-19;

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into the population of cells an isolated DNA construct comprising a promoter operatively linked to a targeting sequence. The method is useful in developing a sensor cell for determining the activity of a target gene in the cell. The sensor cell and the methods are useful in developing new and therapeutic drugs directed to the targets. The present sequence is a
                                                                                                                                                                               1 CGGTCTATTCTTTTGATTTATAAGGGATTTTTGGGGATTTTCGGCCTATTGGTTAAAAATG
                                                                                              Sequence 5218 BP; 1231 A; 1361 C; 1335 G; 1291 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of plasmid pcDNA6/Biotag(TM)-D-TOPO
                                                                                                                                                                                                                                                  4684 AGCTGATTTAACAAAAATTTAACGCGAATTAATTCTGTGGA 4724
                                                                                                                                                                                                                                    61 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinational cloning; recombination; topoisomerase;
                                                                     vector used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion protein production; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-2002; 2002US-0393756P.
19-JUL-2002; 2002US-0396627P.
10-OCT-2002; 2002US-0417172P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUL-2003; 2003WO-US021339.
                                                                                                                                                                                                                                                                                                                                  ADI34681 standard; DNA; 5302
                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2004 (first entry)
                                                                                                                      Query Match
Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INVI-) INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004005482-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bennett RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                             ADI34681;
                                                                                                                                                                                                          4624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins.
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                                                                                                                                                                                                                                                                                                                                              1747 CGGTCTATTCTTTTGATTTTTAAGGGATTTTTGGGGATTTTCGCCCTATTGGTTAAAAATG 1806
                                                                                                                                                    that contains one or more recombination sites, one ore more topoisomerase recognition sites, and/or one or more topoisomerases. The nucleic acid sequence of the invention is useful for in vitro cloning (e.g. recombinatorial cloning) of a nucleic acid molecule. The present DNA sequence represents a plasmid vector of the invention.
                                                                                                                                      The invention comprises an isolated nucleic acid sequence (e.g. a vector)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                target
                                                                                                                                                                                                                                                                                                                     1 CGGTCTATTCTTTTGATTTATAAGGGATTTTTGGGATTTTCGGCCTATTGGTTAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Developing a sensor cell, useful in determining the activity of a targene and in developing therapeutic drugs, comprises providing cells comprising a signal transduction detection system and introducing DNA
                                                                                                                                                                                                                                                                                          Gaps
                                                      Novel isolated nucleic acid molecule comprising recombination sites, topoisomerase recognition sites and/or topoisomerases, useful for in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme; sensor cell; signal transduction detection system; promoter;
                                                                                                                                                                                                                                    Sequence 5173 BP; 1247 A; 1337 C; 1274 G; 1305 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                              Length 5173;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                    AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 1847
  Temple GF;
                                                                                                                                                                                                                                                                                                                                                                          61 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 101
                                                                                                                                                                                                                                                               Score 101; DB 12;
Pred. No. 4.3e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  targeting sequence; targeted drug; ds; vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        & X UAS beta-lactamase vector SEQ ID NO: 64.
 Byrd DRN,
                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 231-234; 234pp; English.
                                                                                                            Claim 12; Fig 25; 369pp; English
 Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanders PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВР
                                                                                 vitro cloning of nucleic acid.
                                                                                                                                                                                                                                                               100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM97811 standard; DNA; 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-2003; 2003WO-US028078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                         Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        construct into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zeh K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-330208/30.
Cheo D,
                            WPI; 2004-090674/09
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004031415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
Unidentified.
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 Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                    1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM97811;
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM9781.
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The invention relates to an isolated nucleic acid molecule (I) comprising one or more recombination sites, and one or more nucleic acid sequences which encode an amino acid sequence tag. (I) can also comprise one or more topoisomerase recognition sites and/or one or more topoisomerases. The amino acid sequence tag is an amino acid sequence that is capable of being post-translationally modified, and is an amino acid sequence that is capable of being post-translationally modified, and is an amino acid sequence that is capable of attachment of flaving, and is an autachment of lipoic acid or attachment of flavins, and is an amino acid sequence that is capable of being biotinylated, wherein the amino acid sequence that is capable of being biotinylated is all or a portion of the Klebsiella pneumoniae oxalacetate decarboxylase a subunit, all or a portion of the Propionibacterium shermanii transcarboxylase 1.35 subunit, or all or a
                                                                                                                          New isolated nucleic acid molecules having one or more recombination sites and encoding an amino acid sequence tag, useful for recombinational and/or topoisomerase-mediated cloning methods for producing fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 11A-B; 135pp; English.
WPI; 2004-091356/09.
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The present invention relates to a method of developing a sensor cell, for determining the activity of a target gene in the cell, which comprises providing a homogeneous population of cells, where each of the cells comprises a signal transduction detection system and introducing

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                                                                                                                                                                                                                                                                                                                            1872 CGGTCTATTCTTTTGATTTTAAGGGATTTTGGGGATTTCGGCCTATTGGTTAAAAATG 1931
portion of the Escherichia coli biotin carboxyl carrier protein component of acetyl-CoA carboxylase. The methods and compositions of the present invention are useful for identifying, concentrating, purifying and/or producing fusion proteins that comprise an amino acid sequence tag. The nucleic acid molecules can also be used in recombinational cloning and/or topoisomerase-mediated cloning methods to produce polymucleotide constructs which encode the fusion proteins. The present sequence represents the nucleotide sequence of a plasmid pcDNA6/Biotag(TM)-D-TOPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 protein of Caenorhabditis elegans or a functional equivalent, derivative or bioprecursor of UNC-53. Also described: (1) a CDNA sequence encoding a vertebrate homologue of the C. elegans UNC-53 protein; (2) a nucleic acid which hybridises to the CDNA of (1); (3) vector comprising the CDNA as in (1); (4) a host cell containing the vector as in (3); (5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a vertebrate protein homologue of an UNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrate homologues of C. elegans UNC-53 protein - useful for, e.g. promoting neuronal regeneration, treating chronic neuro-degenerative diseases or acute traumatic injuries.
                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNC-53 vertebrate protein homologue, UNC-53; Caenorhabditis elegans; cell shape regulator; cell motility regulator; cell migration; cell behaviour regulator; phenotype, signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Verhasselt P;
Vandekerckhove JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrate UNC-53 protein homologue related nucleotide sequence.
                                                                                                                                                                        Sequence 5302 BP; 1254 A; 1361 C; 1349 G; 1338 T; 0 U; 0 Other;
                                                                                                                                                                                                                Length 5302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signal transducing protein; signal integrator protein;
neuronal regeneration; revascularisation; wound healing;
chronic neurodegenerative disease; acute traumatic injury;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                      1932 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 1972
                                                                                                                                                                                                                                                                                                                                                                   AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 101
                                                                                                                                                                                                            ; DB 12;
4.3e-19;
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Luyten W, Geerts H,
                                                                                                                                                                                                            ;; Score 101; DB
;; Pred. No. 4.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADH11233 standard; DNA; 5425 BP
                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 101; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-EP006956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrotic disease; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Buesa Arjol
Maertens LJS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platteeuw CJ, Buesa Arj
Pujol NJR, Maertens LJS
Geysen J, Bogaert TAOE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-362411/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ADH11234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-DEC-1997;
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a compound identified as an enhancer or inhibitor of the regulation of cell shape, motility, or the direction of cell migration for use as a therapear cell shape, motility, or the direction of cell migration for use as a that shape, motility or the direction of cell behaviour, growth, shape or inhibitor or enhancer of regulation of cell behaviour, growth, appe or expressing a homologue of UnC-33 and determining a change of phenotype; (8) a method for identification of vertebrate homologues of C. elegans unc-53 gene by hybridising a probe of 15-50 bp of the unc-53 sequence to a DNA library; and (9) a method for identification of a protein which is cell with an antibody to the UNC-53 homologue; (i) contacting an extract component comprising; (i) contacting an extract complex; and (iii) analysing such a complex; and (iii) analysing such a complex to attribody/homologue complex; and (iii) analysing such a complex to identify any non-antibody protein bound to the complex. UNC-53 is a signal transducing or signal integrator protein involved in controlling clirectionality of cell migration and cell shape in C. elegans. Vertebrate homologues of UNC-53 can be used to promote neuronal regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3664 CGGTCTATTCTTTTGATTTATAAGGGATTTTGGGGATTTCGGCCTATTGGTTAAAAATG 3723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           processing via the Major Histocompatibility Complex class I pathway and/or promotes activity of an antigen presenting cell, useful as vaccine
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  transgenic cell, tissue or animal comprising the vector as in (3); (6)
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                                                                                                                                                                                                                                                                                                                                                                                                   diseases or acute traumatic injuries or fibrotic diseases. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGTCTATTCTTTTGATTTATAAGGGATTTTTGGGGATTTTCGGCCTATTGGTTAAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5425 BP; 1250 A; 1463 C; 1420 G; 1292 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 2;
Pred. No. 4.3e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for cancer and viral infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
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The invention relates to a new nucleic acid molecule (I) encoding a fusion polypeptide useful as a vaccine composition. (I) comprises a first nucleic acid sequence encoding a first polypeptide or peptide that promotes processing via the Major Histocompatibility Complex (MHC) class I pathway (MHC-I-PP) and/or promotes development or activity of an infame to the first nucleic acid sequence is linked in frame to the first nucleic acid sequence or to a linker nucleic acid sequence and encodes an antigenic polypeptide or peptide. The methods and compositions of the present invention are useful as therapeutic vaccine compositions of the present invention are useful as therapeutic vaccine compositions of the present invention are useful as therapeutic vaccine cor cancer, that cause morbidity and mortality. They can also be used in treating animal diseases, such as equine herpesvirus, bovine viruses, Marek's disease, retroviral and lentiviral diseases and rabies, in the veterinary medicine context. The present sequence represents the veterinary medicine context. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1636 CGGTCTATTCTTTTGATTTATAAGGGATTTTTGGGGGATTTTCGGCCTATTGGTTAAAAATG 1695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a nucleic acid (I) encoding a chimeric fusion or fusion polypeptide comprising a first domain with a franslocation polypeptide, and a second domain comprising an antigen having at least one antigenic peptide. Also described: (I) an expression vector comprising (I) operatively linked to a promoter and optionally, to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chimeric fusion; translocation; antigenic; cytostatic; immunotherapy; gene therapy; cancer; tumour; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid vector pcDNA3 nucleotide sequence SEQ ID NO:8.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 6;
Pred. No. 4.3e-19;
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100.0%; Score 101; D
Best Local Similarity 100.0%; Pred. No. 4.3
Matches 101; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating cancer.
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1636 CGGTCTATTCTTTTTTTTTATAAGGGATTTTTGGGGATTTTCGCCCTATTGGTTAAAAATG 1695
                                                                                                                                           comprising (I), expression vector, particle, cell, cell of the particle, or the chimeric polypeptide; and a carrier or excipient; (6) inducing or enhancing an antigen specific immune response by administering the composition described above; (7) increasing the number of CDB + CTLS specific for a selected desired antigen in a subject by administering the composition described above; and (8) inhibiting the growth of a tumour in a subject by administering the composition described above. (I) has cytostatic activity, and can be used in immunotherapy, and gene therapy. The nucleic acids (I), compositions and methods are useful for treating cancer. The present sequence represents a plasmid vector nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel chimeric polypeptide e.g., Pseudomonas aeruginosa exotoxin A domain II/human papilloma virus-16 E7 peptide useful for inducing or enhancing antigen specific immune response, or for inhibiting growth of tumor in subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Translocation domain; bacterial toxin; exotoxin A domain II; ETA; major histocompatibility complex; MHC class I; vaccine; immune response; CD8+ cytotoxic I lymphocyte; CTL; tumour; E7 antigen; pcDNA3 plasmid; ds.
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one or more regulatory elements that enhance expression of the nucleic acid in a cell, (2) a particle comprising (1) or the expression vector; (3) a cell that has been modified to comprise (1) or the expression vector; (4) a chimeric polypeptide comprising a first domain with a translocation polypeptide, and a second domain comprising an antigen having at least one antigenic peptide; (5) a pharmaceutical composition capable of inducing or enhancing an antigen specific immune response.
                                                                                                                                                                                                                                                                                                                                                      sequence which is used in the exemplification of the present invention.
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Best Local Similarity 100.0%; Pred. No. 4.3e-19;
Matches 101; Conservative 0; Mismatches 0;
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09-FEB-2000; 2000US-00501097.
20-OCT-2000; 2000WO-US041422.
04-APR-2001; 2001US-0281003P.
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Disclosure; SEQ ID NO 8; 48pp; English.

The invention relates to nucleic acid encoding a chimeric polypeptide accomprising a translocation domain of a bacterial toxin and at least one antigenic peptide. The preferred translocation domain is domain II of Pseudomonas aeruginosa exotoxin A (ETR (dII)) and the preferred antigen is human papilloma virus type 16 (HPV-16) E7 which is a model tumour antigen. The antigenic peptide comprises an epitope that binds to and is presented on the cell surface by major histocompatibility complex (MHC) class I proteins. The nucleic acid of the invention is useful as vaccine composition for enhancing antigen specific immune response, increasing the number of CD8+ cytotoxic I lymphocytes (CTLs) and for inhibiting the growth of a tumour. The present sequence is pcDNA3 plasmid vector used in the invention.  $\overset{\alpha}{\times}\overset{\times}{\times}\overset{\circ}{\times}\overset{\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\overset$ 

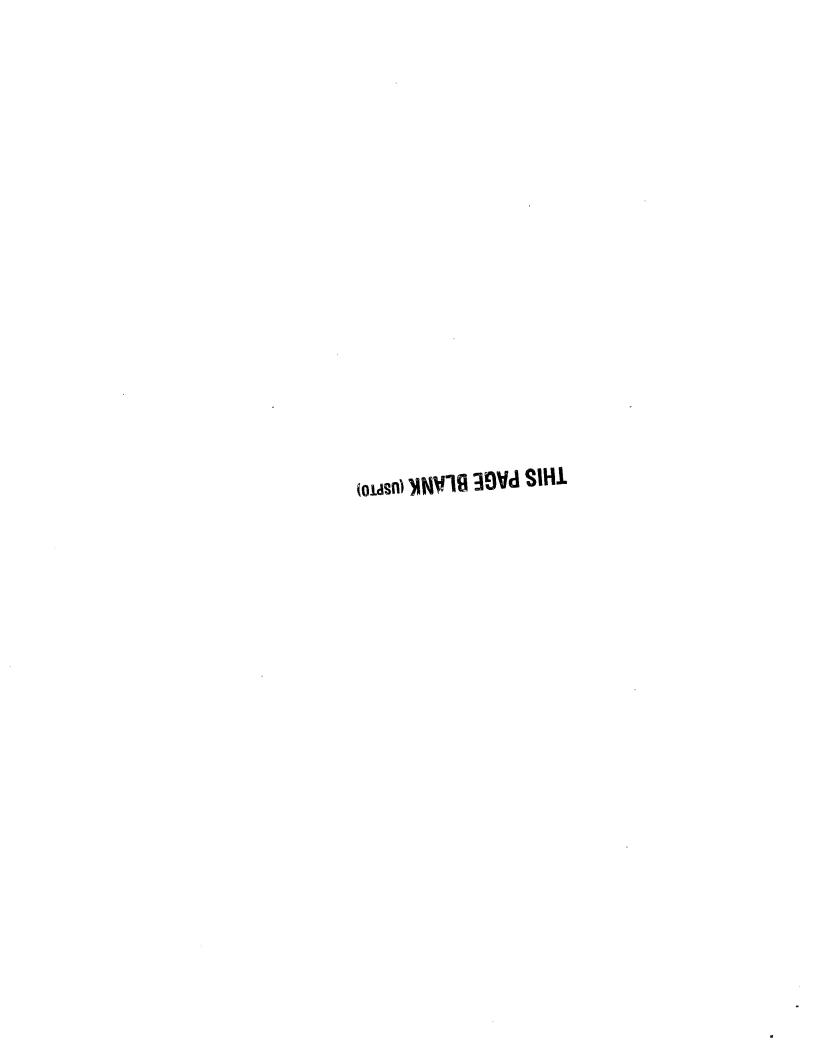
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1696 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 1736 61 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTGTGGA 101 ò g

Search completed: July 14, 2005, 07:01:25 Job time : 143.448 secs



OM nucleic

Run on:

Sequence:

Searched:

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827 bp mRNA linear EST 24-APR-2002
NF044H03LF1F1029 Developing leaf Medicago truncatula cDNA clone
NF044H03LF 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
       CD282765 G38937.16
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AQ014434 CIT-HSP-2
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BF9425 T3 PP11TR TA
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CD28039 G43699.50
CD280392 G43700.8
CN52145 GQ0113.B3
AJ409361 AJ409361
B60716 T18B54TR TAM
CD28039 G43699.82
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.5%; Score 88.4; DB 5; Length 827; 98.9%; Pred. No. 1.1e-13; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 224 6650
Fax: 580 224 6650
Email: gdmay@noble.org
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    .827
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Medicago truncatula
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CD280049
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Best Local Similarity 98.9
Matches 89; Conservative
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BQ145762 NP017H10G
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BU998405 HI10P066
BQ15417 NP104G07D
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                                                                        July 14, 2005, 05:15:57; Search time 961.667 Seconds (without alignments) 3997.736 Million cell updates/sec
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BM276444
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Compugen Ltd.
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101
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Maximum Match 100%
Listing first 45 summaries
                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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BU998405
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BQ145733/c
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/note="Vector: Lambda Zap; M. truncatula seeds were acid
/note="Vector: Lambda Zap; M. truncatula seeds were acid
/note="Vector: Lambda Zap; M. truncatula seeds were acid
treatment charvested at 0, 1, 2 and 3 days after acid
treatment. CDMA was prepared from polyA+ enriched, pooled
samples of equivalent amounts of total RNA from each time
point. The CDMA was directionally ligated into the
Uni-Zap XR vector (Stratagene) and packaged using the
Gigapack III Gold packaging extracts. Phagemids
containing cDMA inserts were in vivo excised from the
recombinant Uni-Zap XR vector using ExAssist helper phage
and the E. coli strain XII-Blue MRR' (Stratagene).
Excised plasmids were plated using SOLR cells."
                                                                                                                                                                                                                          805 bp mRNA linear EST 24-APR-2002 NF017H10GS1F1091 Germinating Seed Medicago truncatula cDNA clone NF017H10GS 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Torres-derez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula germinating seed library
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                       483 CGGTCTATTCTTTTATAAGGGATTTTGCCGCATTTTCGCCCTATTGGTTAAAAAAGG 424
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Pred. No. 1.3e-13;
0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: May Go
Teact: May Go
Teact: May Go
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 224 6692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: gdmay@noble.org
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                                                                                       61 AGCTGATTTAACAAAATTTAACGCGAATT 90
                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula (barrel medic)
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813 bp mRNA linear EST 24-APR-2002
NF017D06GS1F1057 Germinating Seed Medicago truncatula cDNA clone
NF017D06GS 5', mRNA sequence.
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula germinating seed library
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Contact: May GO
That Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 224 6650
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llarity 92.1%; Pred. No. 1.3e-13;
Conservative 0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: gdmay@noble.org
Insert Length: 813 Std Error: 0.00
Plate: 017 row: D column: 06
Seg primer: TCACACAGGAAACAGCTATGAC.
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/db_xref="taxon:3880"
/clone="NF017D06GS"
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1 (bases 1 to 813)
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Best Local Similarity 5
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Location/Qualifiers
1. .750
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93.8%;
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Matches 91; Conserv
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BQ154917/c
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   AUTHORS
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NF104G07DT1F1054 Drought Medicago truncatula cDNA clone NF104G07DT
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                                                                      Hordenm vulgare subsp. vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Sporideae; Triticeae; Hordeum.
1 (bases 1 to 585)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and annalysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="HI"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of CDNA); Site 2: XhoI (3'-end of CDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
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Medicago truncatula
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="female inflorescences"
dev_stage="female inflorescences (approx. 3 mm in size)"
lab_host="XI10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 CGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAATG 113
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                                                                                                                                                                                                                                      Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Hordeum vulgare subsp. vulgare"
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94.8%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GAB1:252269"
/db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                        Email: stein@ipk-gatersleben.de
Insert Length: 585 Std Error:
Plate: 10 row: P column: 6
                                                          Hordeum vulgare subsp. vulgare
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BQ144787
BQ144787.1 GI:20281846
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Best Local Similarity
 BU998405
BU998405.1
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BQ144787/c
                                   KEYWORDS
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AUTHORS
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Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 224 6692
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Medaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_staga="Pooled timepoints"
/clone_lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plantlets harvested in a series of days-post-watering
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NF074C04IR1F1034 Irradiated Medicago truncatula cDNA clone
NF074C04IR 5', mRNA sequence.
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 224 6650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AGCTGATTTAACAAAATTTAACGCGAATTAATTCTG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87.4; DB 5;
Pred. No. 2.1e-13;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Medicago truncatula"
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Insert Length: 750 Std Error: 0.00
Plate: 074 row: C column: 04
Seq primer: TCACAGGAAACAGGTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Email: gdmay@noble.org
Insert Length: 750 Std Brror: 0.00
Plate: 104 row: G column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF104G07DT"
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/note="Vector: Lambda Zap, Seedlings were exposed either to 100 gy gamma or 0.5, 1, 5, or 10 KJ/m2 Uv irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XII-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."
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/dev_stage="rrifoliate"
/dow_lb="phosphate starved leaf"
/note="Vector: lambda Zap; At the trifoliate stage, M.
truncatula plants were transplanted to phosphate-free sand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             768 bp mRNA linear EST 24-APR-2002 NF117H07PL1F1064 Phosphate starved leaf Medicago truncatula CDNA clone NF117H07PL 5', mRNA sequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 87.4; DB 5; Length 764; Pred. No. 2.1e-13; 0; Mismatches 6; Indels 0
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
TE1: 580 221 7328
Fax: 580 221 7380
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/mol_type="mRNA"
/db_xref="taxon:3880"
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Insert Lenghh: 768 Std Error: 0.00
Plate: 117 row: H column: 07
Seg primer: TCACACAGGAAACAGCTATGAC.
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Medicago truncatula
                      /dev_stage="seedling"
/clone_lib="Irradiated"
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ilarity 93.8%;
Conservative
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Best Local Similarity
Matches 91; Conserv
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                                                                                                                                           /dev stage="seedling"
/clone lib="Irradiated"
/clone lib kJ/m2 UV irradiation
/clone lib kJ/m2 UV irradiation
/clone after treatment. UV-irradiated samples were
/clone lib kJ hours post-treatment. OnNA was prepared from
/clone lib kNA from each sample. The cDNA was directionally
/clone lib kNA from each sample. The CDNA was directionally
/clone lib kNA from each sample. The CDNA was directionally
/clone lib kNA irradiated lib kNA inserts were in vivo excised
/clone the recombinant Uni-ZAP XR vector using ExAssist
/clone the recombinant Uni-ZAP XR vector using ExAssist
/clone lib kNA irradiated using SOLR
/clone lib kNA irradiated using SOLR
/clone lib."
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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|mol_type="mRNA"
|db_xref="taxon:3880"
|clone="NP085C081R"
                   organism="Medicago truncatula"
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Insert Length: 764 Std Error: 0.00
Plate: 085 row: C column: 08
Seg primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                      /clone="NF074C04IR"
/tissue_type="seedlings"
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                                                   /mol_type="mRNA"
/db_xref="taxon:3880"
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1 (bases 1 to 764)
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Fax: 580 224 6692
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Matches 91; Conserv
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BQ159352.1 GI:20296409
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BQ159157/c
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/dev_stage="trifoliate"
/dev_stage="trifoliate"
/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliate stage, M.
runcatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
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and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20wh potassium phosphate. RNA was prepared from above ground tissues."
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Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
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Plant Biology Division
The Samuel Roberts Noble Foundation
Tels Sam Vole Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
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larity 93.8%; Pred. No. 2.1e-13;
Conservative 0; Mismatches 6;
                                                                                                         86.5%; Score 87.4; DB 5; ilarity 93.8%; Pred. No. 2.1e-13; Conservative 0; Mismatches 6;
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Insert Length: 783 Std Error: 0.00
Plate: 070 row: H column: 02
Seq primer: TCACAGGAAACAGCTATGAC.
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/db_xref="taxon:3880"
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truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoadlands solution containing only 20um potessium phosphate. RNA was prepared from above ground tissues."
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NF050D02PL1F1014 Phosphate starved leaf Medicago truncatula cDNA
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clone NF114D02PL 5', mRNA sequence.
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/dev_stage="trifoliate"
/clome_lib="Phosphate starved leaf"
/note="vector: Lambda Zap; At the trifoliate stage, M.
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Tel: 580 221 7325
Fax: 580 221 7380
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Insert Length: 784 Std Error: 0.00
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Plant Biology Division
The Samuel Roberts Noble Foundation
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/note="Vector: Lambda Zap; At the trifoliate stage, M.
/note="Vector: Lambda Zap; At the trifoliate stage, M.
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
Unpublished (2001)
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larity 93.8%; Pred. No. 2.1e-13;
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 784 Std Error: 0.00
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/cloue_weetcr: Landaa Zap; Seedlings were exposed either /note="Vector: Landaa Zap; Seedlings were exposed either to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The CDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing CDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XII-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."
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NF014C09PH1F1070 Phoma-infected Medicago truncatula cDNA clone
NF014C09PH 5', mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Watson, B.S., Shin, H.S., Lopez-Weyer, M., Scott, A.D., Harris, A.R.,
Watson, B.S., Shin, H.S., Inman, J.T., Waugh, M.E., Sullivan, J.P.,
May, G.D. and Paiva, N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 224 6650
Fax: 580 224 6692
Email: gdmay@noble.org
Insert Length: 785 Std Error: 0.00
Plate: 094 row: D column: 10
Seq primer: TCACACAGGAAACAGCTATGAC.
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
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Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                   organism="Medicago truncatula"
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BST.
Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="NP094D10IR"
/tissue type="seedlings"
/dev_stage="seedling"
/clone_lib="Irradiated"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula
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/doce=10.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 |
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Flores,H.K., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula irradiated library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 CGCTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAATG 134
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Medaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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NF056D06IR1F1057 Irradiated Medicago truncatula cDNA clone
NF056D06IR 5', mRNA sequence.
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 224 6650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 AGCTGATTTAACAAAATTTAACGCGAATTCCTGCAG 97
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                                                                                                   1. 796
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/db xref="taxon:3880"
/clone="NP040H05IR"
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Insert Length: 798 Std Brror: 0.00
Plate: 056 row: D column: 06
Seg primer: TCACACAGGAAACAGCTATGAC.
       Plate: 040 row: H column: 05
Seg primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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                                                                                                                                                                                                                                                                          /tissue_type="seedlings"
/dev_stage="seedling"
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BQ154182.1 GI:20291241
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Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                              source
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BQ154182/c
LOCUS
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KEYWORDS
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                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                            /tissue_trye="leaf"
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/dev_stage="Pathogen-induced, young trifoliate leaves
/clone_lib="Phoma-infected"
/clone_lib="Phoma-infected"
/note="Wector: pBluescript SK(-); Young trifoliate leaves
of Medicago truncatula were excised and dip-inoculated in
a spore suspension of Phoma medicaginis, and incubated in
humid dishes. Pools of leaves were harvested at 0, 15, and
30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours,
and used to prepare total RNA. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the E. coli strain XLI-Blue MRF'
(Stratagene). Excised plasmids were plated using SOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
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                                                                                                                                                                                                                                                                             'organism="Medicago truncatula"
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Unpublished (2001)
Contact: May GD
Tel: 580 221 7317

Fax: 580 221 7380

Email: nlpaiva@noble.org
Insert Length: 796 Std Error: 0.00

Plate: 014 row: C column: 09

Seg primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                          'mol_type="mRNA"
'db_xref="taxon:3880"
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 clone="NF014C09PH"
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Insert Length: 796
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Best Local Similarity 93.8
Matches 91; Conservative
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Fax: 580 224 6692
Email: gdmay@noble
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EST 24-APR-2002

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Gaps

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/mol type="mcRNA"

/db_xref="taxon:3880"

/clone="NerOsings"

/tissue_type="seedlings"

/dev stage="seedlings"

/clone_lib="Irradiated"

/clone_lib="Tradiated"

/clone_lib="Tradiated"

/clone_lib="Tradiated"

/clone_lib="Vector: Lambda Zap; Seedlings were exposed either

/clone_gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.

Gamma-irradiated samples were harvested at 6, 12, 24 and

48 hours after treatment. UV-irradiated samples were

harvested 24 hours post-treatment. cDNA was prepared from

polyA+ enriched, pooled samples of equivalent amounts of

total RNA from each sample. The cDNA was directionally

ligated into the Uni-Zap Rx vector (Stratagene) and

packaged using the Gigapack III Gold packaging extracts.

Phagemids containing cDNA inserts were in vivo excised

from the recombinant Uni-ZAP XR vector using ExAssist

helper phage and the E. coli strain XII-Blue MRF'

(Stratagene). Excised plasmids were plated using SOLR

cells."
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Ouery Match 86.5%; Score 87.4; DB 5; Length 798; Best Local Similarity 93.8%; Pred. No. 2.1e-13; Matches 91; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 61 AGCTGATTTAACAAAATTTAACGCGAATTATTCG 97

 Db
 131 AGCTGATTTAACAAAAATTTAACGCGAATTCCTGCAG 95

Search completed: July 14, 2005, 23:22:30 Job time : 967.667 secs

CFAJ4121 AY589493 AY538698 AY538700 AY538701 AY538702

AY394610

AY392531

AY538699 Serratia
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AY628199

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AY243512

**AY628175** 

AY101764

AR371489 AX195443

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July 14, 2005, 04:39:07; Search time 756.618 Seconds (without alignments) 6468.225 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                       4708233 segs, 24227607955 residues
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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101
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Maximum Match 100%
Listing first 45 su
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seq length: 200000000
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gb htg: *
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Maximum DB
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ALIGNMENTS

PATN1PN2 PATN2PN1B

PATN3PN1A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

L18624 Human chrom BD195256 Nucleotid E00892 Synthetic D E01156 DNA fragmen E01274 DNA encodin E01302 DNA encodin AX260098 Sequence AX260150 Sequence A43586 Sequence 11 AR116755 Sequence AY559171 Pseudomon X97254 S.marcescen Z92776 Caenorhabdi AR356490 Sequence AR538046 Sequence E00019 DNA coding M10199 Plasmid pMM E00018 DNA coding I01644 Sequence 1 Description I01644 HUMUT5345 BD195256 AR116755 AY559171 SMTEMAQGE CEC11F10 E00019 PMMOENDO AX260098 AX260150 AR356490 E00892 E01156 E01274 E00018 A43586 6 6 11 Length Query Match 1 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 Score Result Š 0 0 0 0 0 0 0 00

AR356490 142 bp DNA linear PAT 17-AUG-2003 Sequence 2608 from patent US 6593114. AR356490 AR356490.1 GI:33762574	<pre>Unknown. Unknown. Unclassified. 1 (bases 1 to 142) Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and</pre>	Kosen, C.A. Staphylocc Patent: US	100 08. Carre 101. PB	Similarity 100.0%; Score 101; DB 0; 1; Conservative 0; Mismatches 0;	1 AGGGTTATTGTCTCATGAGCGGATACATATTGAATGTATTTAGAAAATAAACAAATAG 60 	61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101 	AR538046 142 bp DNA linear PAT 08-OCT-2004 Sequence 2608 from patent US 6737248. AR538046 AR538046.1 GI:53929263 Unknown.
RESULT 1 AR356490/c LOCUS DEFINITION ACCESSION VENESION	SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL FEATURES SOURCE	ORIGIN	Query Malch Best Local Matches 10	95 10	Oy Db	RESULT 2 AR538046/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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source
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Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and Sosen, C.A.

Stabbylococcus aureus polynucleotides and sequences

Patent: US 6737248-A 2608 18-MAY-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriales; Enterobacteriales; 1 (Dases 1 to 228)
Uorutaa, G. and Karen, T.
SYNTHESIS OF SELECTIVE AGED PROTEIN OR POLYPEPTIDE IN BACTERIA PATENTY HARVARD
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30-NOV-1981
09-APR-1981 JP 1981052488
11-APR-1980 US 80 139225
UORUTAA GIRUBAATO, KAREN TARUMATSUJI
CI2P21/00,CO7H21/00,CI2N1/00,CI2N15/00//CI2R1/19; CC
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/product='E.coli penicilinase'.
Location/Qualifiers
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DNA coding for Escherichia coli penicillinase.
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Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:562"
                                                                                                                                          /mol_type="genomic DNA"
                                                                                                    Location/Qualifiers
                                                                                                                   1. 142
/organism="unknown"
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anti-sense: No;
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JP 1981154999-A/2.
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Unclassified.
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PMMOENDO 240 bp DNA linear BCT 26-APR-1993
Plasmid pMM110 region of endo VII cleavage sites near cruciform
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                                                                                                                                                                                                                                                 other sequences; plasmids.

1 (bases 1 to 240)

Remper, B., Jensch, F., von Depka-Prondzynski, M., Fritz, H.J.,

Borgmeyer, U. and Mizunchi, K.

Resolution of Holliday structures by endonuclease VII as observed
in interactions with cruciform DNA

Cold Spring Harb. Symp. Quant. Biol. 49, 815-825 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriales; Enterobacteriales; It (bases 1 to 251)
Uorutaa,G. and Karen,T.
SynTHERIS OF SELECTIVE AGED PROTEIN OR POLYPEPTIDE IN BACTERIA Patent: JP 1981154999-A 1 30-NOV-1981; UNIV HARVARD
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GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 75
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DNA coding for Escherichia coli penicillinase.
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/mol_type="genomic DNA"
/db_xref="taxon:2599"
/plasmid="Plasmid pMM110"
Unreported.
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JP 1981154999-A/1
30-NOV-198
09-APR-1981 JP 1981052488
11-APR-1980 US 80 139225
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JP 1981154999-A/1.
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Plasmid pMM110
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BD195256.1 GI:33005021
JP 2002513277-A/43.
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20sec
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                                                                                                                                                                                                                                                                                       Annealing: 60C
Extension: 72C
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primer_bind
ORIGIN
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ACCESSION
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ORGANISM
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                               TITLE
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                                                                                                                                                                                                                                                                                175 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 116
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1 (bases 1 to 344)
Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L18624.1 GI:308338
STS; PCR primer; STS sequence; microsatellite marker;
microsatellite repeat; repeat polymorphism; sequence tagged site.
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Patent: US 4338397-A 1 06-JUL-1982;
President and Fellows of Harvard College; Cambridge, MA
                                               /product='E.coli penicilinase' FT
                                                                                                                                                                                       Query Match
100.0%; Score 101; DB 6; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.7e-20;
Matches 101; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 6; Length 251; 100.0%; Pred. No. 8.7e-20; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                        61 GGGTTCCGCGCACATTTCCCCGGAAAGTGCCACCTGACGTC 101
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 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     101644 251 bp ss-DNA Sequence 1 from Patent US 4338397.
                                                                                                         Organism="Escherichia coli"
(mol_type="genomic DNA"
(db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unknown"
/wol_type="unassigned DNA"
                                 210. .>252
                                                              al 190. .196.
Location/Qualifiers
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Gilbert, W. and Talmadge, K.
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Homo sapiens
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Best Local Similarity
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                                                              TATA_signal
 Key
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EELL
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HUMUT5345
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I01644/c
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OS Unidentified
PN JP 2002513277-A/43
PD 08-MAY-2002
PF 21-NOV-1997 JP 1998523916
PR 22-NOV-1996 US 60/031626,14-OCT-1997 US 60/061953 PI
PATRICK J DILLON, GIL H CHOI, RODNEY A WELCH
C C12N15/11, C12N15/63, C07K16/12, G01N33/569, G06F17/30, G11B7/00 CC
Strandedness: Double,
C Topology: Linear;
C Topology: Linear;
C Topology: Linear;
C Nucleotide sequence of Escherichia coli pathogenicity islands
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Ballard, L., Melis, R., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Rodriguez, P., Albertsen, H., Lalouel, J.-M. and White, R. Benetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome Unpublished (1993)
                                                                                                                                                              Original source text: Homo sapiens DNA.
Submitted by: Utah Center for Human Genome Research University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTTTAGAAAAATAAACAAATAG
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Dillon,P.J., Choi,G.H. and Welch,R.A.
Nucleotide sequence of Becherichia coli pathogenicity islands
Patent: JP 200251327-A 43 08-MAY-2002;
HUMAN GENOME SCIENCES INC, WISCONSIN ALUMNI RESEARCH FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BD195256 400 bp DNA linear PAT 17-JUI
Nucleotide sequence of Bacherichia coli pathogenicity islands.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                    Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 . 224
/standard_name="STS UT5345"
                                                                                                                                                                                                                                                                                                                                              Primer A: GAGCAAAAACAGGGCAAAATGC
Primer B: TTCGGGGAAATGTGCGCGGAACC
32P-label: B Primer
PCR Profile:
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Corganism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
/map="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Denaturation: 94C 300sec
                                                                                                                                                                                                                                                                                                                             e-mail: sts@corona.med.utah.edu
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complement(202. .224)
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61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
  /db xref="taxon:32630"
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hypothetical: No;
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JP 1987083890-A/1.
synthetic construct
synthetic construct
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mat_peptide
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Matches 101; Conserv
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E01156/c
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Ojida,K. and Mateunshiro,A.
DOLYPEPTIDE SECRETION DEVELOPMENT VECTOR, MICROORGANISM PROLYPEPTIDE SECRETION DEVELOPMENT VECTOR, MICROORGANISM PATCH: JP 1986149089-A 1 07-JUL-1986;
BARTH CHEM CORP LID
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1986149089-A/1
PN JP 1986149089-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E00892 456 bp DNA linear PAT 29-SEP-1997 Synthetic DNA encoding fused polypeptide between E coli beta-lactamase and human beta-urogastrone.
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                                                                                                                                                                                                                                                                                                                                                                                         1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-1984 JP 1984271206
OKAI HIDBO, MOMOTA YUTAKA, KUMAKURA TAKESHI,
TOCHIFUSA NORIYUKI,
KITAZAWA TOSHIKI, OJIDA KAZUHIDE, MATSUSHIRO AIZO PC
15/00,C12N1/20,C12P21/00,(C12N1/20,C12R1:19),(C12P21/00, PC
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                           100.0%; Score 101; DB 6; Length 400; larity 100.0%; Pred. No. 8.7e-20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACTGACGTC 65

    .400
    /organism='Unidentified'.

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*source: clone=pVG201;
Feature is identified by experimental;
Key Location/Qualifiers
Location/Qualifiers
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.
1 (bases 1 to 456)
                                                                                                1. .400
/organism="unidentified"
                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                      Location/Qualifiers
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OC Artificial sequence; Gen
DC JUL-1986
DF 1986149089-A/1
DF 07-10H-1986
DF 1-DEC-1984 JP 1942712
DF OKAI HIDEO, MOMOTA YUTA
DF TOCHIFUSA NORIVEL,
DF KITAZAWA TOSHIKI, OJIDA
C12N15/00, C12N1/20, C12P21/00
C12R1:19),
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: Double;
CC strandedness: No;
CC ant.-sense: No;
CC ant.-sense: No;
CC strandedness: No;
CC stranded
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JP 1986149089-A/1.
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synthetic construct
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  Key
source
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Matches 101;
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  표보단
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DEFINITION
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VERSION
KEYWORDS
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E00892/c
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                                                                                                                                                                                                                                                                                                                                           PAT 29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other sequences; artificial sequences.

1 (bases 1 to 456)
Yoshikawa,K., Momota,Y., Kajifusa,N., Koide,T. and Okai,H.
POLYPEPTIDE SECRETION EXPRESSION VECTOR, MICROORGANISM TRANSFORMED
BY SAID VECTOR AND PRODUCTION OF POLYPEPTIDE USING SAID
PATENT: JP 1997/083890-A 1 17-APR-1987;
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C12N15/00,C12N1/20,C12P21/00,(C12N1/20,C12R1:19),(C12N1/20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                           1 AGGGTTATTGTCTCATGAGCGGATACATATTTTGAATGTATTTAGAAAAATAAACAAATAG
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09-OCT-1985 JP 1985225393
YOSHIKAWA KAZUTOSHI, MOMOTA YUTAKA, KAJIFUSA NORIYUKI,
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  Length 456;
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/note='beta lactamase promoter'
                                                                                                                                                                                                                                                                                                                                              linear
                                                 Indels
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/product='beta urogastrone'
209. .277
278. .486
/product='beta urogastrone'
                                                                                                                                                                                  61 GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                          113 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                              E01156 456 bp DNA 1:
DNA fragment which secrets beta urogastrone.
100.0%; Score 101; DB 6;
llarity 100.0%; Pred. No. 8.7e-20;
Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Artificial sequence; Genes.
JP 1987083890-A/1
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*source: clone=pUG201;
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anti-sense: No;
 synthetic construct
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mat_peptide
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                                                                                                                                                                                                                                 C12R1:19);
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AX260098/c
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KEYWORDS
SOURCE
ORGANISM
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ACCESSION
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AUTHORS
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DNA encoding beta-urogastron fused with DNA encoding a promoter and signal peptide of beta-lactamase.
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31-JAM-1986 JP 1986021032
OKAI HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, ADACHI SHOJI, MATSUBARA AKIMASA, OJIDA KAZUHIDE, YANO MAKI, MIHARA SHIGERU, MATSUSHIRO AIZO, YANAIHARA NOBORU CI2P21/00,CI2R1591);
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                                                                                                                                                                                                             Ojida,K., Yano,M., Mihara,S., Matsushiro,A. and Yanaihara,N., PRODUCTION OF BETA-URCASTRONE
Patent: JP 1987179398-A 1 06-AUG-1987;
EARTH CHEM CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E01302 456 bp DNA linear PAT 29-5 DNA encoding human beta-urogastrone fused with DNA encoding promoter and signal peptide of beta-lactamase.
                                                                                                                                      JP 1987179398-A/I.
synthetic construct
synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 456)
Okai, H., Kumakura, T., Kawamoto, S., Adachi, S., Matsubara, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jepcide 278. .436
/product='beta-urogastron'
209. .439
/product='beta-urogastron'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
113 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 73
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                   Artificial gene
Artificial sequence, Genes.
Homo sapiens
JP 1987179398-A/1
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hypothetical: No;
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E01302.1 GI:2169561
JP 1987190083-A/1.
synthetic construct
                                                                                                                              E01274.1 GI:2169533
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Matches 101; Conservative
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                                                                                       DEFINITION
                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                               TITLE
JOURNAL
                                                   RESULT 11
E01274/c
                                                                                                                 ACCESSION
                                                                                                                             VERSION
KEYWORDS
SOURCE
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KEYWORDS
SOURCE
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MOMOTA YUTAKA
C12N15/00,C07H21/04,C12N1/00,C12P21/02,(C12N1/00,C12R1:19), PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                    14-FEB-1986 JP 1986031415
OKAI HIDEO, KUMAKURA TAKESHI, KAWAMOTO SHOICHI, KOIDE TAKAO,
                                                 Okai, H., Kumakura, T., Kawamoto, S., Koide, T. and Momota, Y. POLYPEPTIDE-EXPRESSION VECTOR, HOST TRANSFORMED WITH SAID VECTOR MD PRODUCTION OF POLYPEPTIDE USING SAID HOST PAtent: JP 1981190083-A 1 20-AUG-1987;
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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    466
/organism="Drosophila melanogaster"
/mol_type="unassigned DNA"

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100.0%; Score 101; DB 6;
Best Local Similarity 100.0%; Pred. No. 8.7e-20;
Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
other sequences; artificial sequences.
1 (bases 1 to 456)
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Patent: WO 0172774-A 60 04-OCT-2001;
Cyclacel Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 60 from Patent WO0172774.
                                                                                                                                                                               Artificial gene
Artificial sequence; Genes.
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200. .203
209. .277
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topology: Linear;
hypothetical: No;
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JP 1987190083-A/1
20-AUG-1987
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Other publication AU 7615494 950327.
Location/Qualifiers
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                                      source
                  FEATURES
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; Myrtales; Lythaceae; Cuphea.

Toepfer, K., Bautor, J., Bothmann, H., Filsak, E.,
Hoericke-Grandpierre, C., Klein, B., Martini, N., Mueller, A.,
Schulte, W., Voetz, M., Walek, J. and Schell, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAAATAAACAAATAG 221
                                                                                                                       1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                               100.0%; Score 101; DB 6; Length 466; 100.0%; Pred. No. 8.7e-20; 1.ve 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 101; DB 6; 100.0%; Pred. No. 8.8e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deak, P., Glover, D.M. and Midgley, C.
Cell cycle progression proteins
Patent: WO 0172774-A 112 04-OCT-2001;
Cyclacel Limited (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 9507357-A 11 16-MAR-1995;
MAX PLANCK GESELLSCHAFT (DE)
Other publication CA 2169093 950316
                                                                                                                                                                                                                                                                                                            Sequence 112 from Patent W00172774. AX260150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Sequence 11 from Patent WO9507357.
A43586
A43586.1 GI:2298779
/db xref="taxon:7227"
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Best Local Similarity 100.
Matches 101; Conservative
                                                                                      Conservative
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                                                                 al Similarity
101; Conserv
                                                   Query Match
                                                                     Best Local
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KEYWORDS
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ACCESSION
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AX260150/c
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AUTHORS
TITLE
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A43586
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AUTHORS
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JOURNAL
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SOURCE
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                                                                                                                                            Length 693;
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                                                                                                                                                                                                                                                                                                                               GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 692
/organism="Cuphea lanceolata"
/mol_type="unassigned DNA"
/d_xref="taxon:3930"
/clone="CikkASIG8"
/clone_lib="Genomic Lambda Fix II"
                                                                                                                                          Query Match

100.0%; Score 101; DB 6;
Best Local Similarity 100.0%; Pred. No. 8.8e-20;
Matches 101; Conservative 0; Mismatches 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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July 14, 2005, 04:35:42; Search time 142.398 Seconds (without alignments) 4198.742 Million cell updates/sec Run on:

US-09-482-682-8\_COPY\_7369\_7469 101

1 agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101 Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters:

8780412

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2004as:\* geneseqn2003as:\* geneseqn2003bs:\* N\_Geneseq\_16Dec04:\* .: geneseqn1980s:\* : geneseqn1990s:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:

## SUMMARIES

	ion	Staphyloc	Sequence		E. coli J		Sequence		Sequence		Polynucle		Drosophil	Adh58311 Electroph	DNA encod	DNA encod	Genomic s	Human rep	Human rep	Human rep	Human rep
	Description	Aav76919	Aan10032	Aan10031	Aav31229	Aan60624	Aan71080	Aan70833	Aan81765	Aba90413	Aax21173	Aax21149	Aba90456	Adh5831	Aas30560	Aas27819	Abk42984	Aa107344	Aa103229	Aa106588	Aa107340
	TD 01	AAV76919	AAN10032	AAN10031	AAV31229	AAN60624	AAN71080	AAN70833	AAN81765	ABA90413	AAX21173	AAX21149	ABA90456	ADH58311	AAS30560	AAS27819	ABK42984	AAL07344	AAL03229	AAL06588	AAL07340
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de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Abal4573 Human ner	Aas34681 Human DNA	Ada41574 Human sec	Acc50905 Human sec	Abz71508 Secreted	Adb91869 Human sec	Adb61140 Connectiv	Adb94622 Novel hum	Adc74663 Human sec	Adas7709 BAC fragm	Adn41551 Novel hum	Aas30559 DNA encod	Aas27818 DNA encod	Abk42983 Genomic s	Aas41807 Genomic s	Aas41855 Genomic s	Aak85485 Human imm	Aak85434 Human imm	Aal07343 Human rep	Aal06587 Human rep	Aal07339 Human rep	Aal03228 Human rep	Abal4572 Human ner	Aas34680 Human DNA	Adb61139 Connectiv	
ABA14573	AAS34681	ADA41574	ACC50905	ABZ71508	ADB91869	ADB61140	ADB94622	ADC74663	ADA57709	ADN41551	AAS30559	AAS27818	ABK42983	AAS41807	AAS41855	AAK85485	AAK85434	AAL07343	AAL06587	AAL07339	AAL03228	ABA14572	AAS34680	ADB61139	
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176	176	176	116	116	176	176	116	176	116	176	845	845	845	845	845	845	845	845	845	845	845	845	845	845	
100.0	100.0	100.0	100.0	0.001	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	
c 21	c 22	c 23	c 24	c 25	c 26	c 27	c 28	c 29	c 30	c 31	c 35	c 33	C 34	c 35	c 36	c 37	c 38	c 39	c 40	c 41	c 42	c 43	C .44	c 45	

## ALIGNMENTS

Staphylococcus aureus contig SEQ ID #2608. 踞 AAV76919/c ID AAV76919 standard; DNA; 142 (first entry) 16-MAR-1999 AAV76919; 

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;

toxic shock syndrome; ds

Staphylococcus aureus

EP786519-A2.

30-JUL-1997

97EP-00100117. 07-JAN-1997; 96US-0009861P. 05-JAN-1996; (HUMA-) HUMAN GENOME SCI INC.

Rosen CA; Fannon MR, Dillon PJ, Barash SC, Choi GH, WPI; 1997-374922/35. Kunsch CA,

Staphylococcus aureus -in the production of anti-Polynucleotide(s) and proteins derived from stored on computer readable medium and used S.aureus vaccines

Claim 1; Page 2287; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or

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          likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer
industrial importance can be obtained. Specifically, sequences which are
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                                                                                                                                                                                                                                                                                                           The closest identifiable promoter for the penicilinase gene in pKT241 (AAN10031) is located in the region 14 to 20 nucleotides before its
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthesis of mature protein or polypeptide – by using bacterial host transformed by cloned vehicle contg. DNA fragment etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning vehicle; bacterial vector; transformed host; penicillinase; insulin; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of the pKT218 EcoRI-PstI penicillinase gene fragment.
                                                                                                                                                                                                                        Length 142;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                          Sequence 142 BP; 45 A; 25 C; 26 G; 45 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                           GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                   47 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 7
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                                                                                                                                                                                                                     ; Score 101; DB 2;
; Pred. No. 2.1e-21;
0; Mismatches 0;
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/*tag= a
/label= sticky end
225. .228
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ID AAN10032 standard; DNA; 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                  101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1981-80125D/44.
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAP10039
                                                                                                                                                              readable medium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-1980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1992
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                                                                                                                                                                                                                                                                                                            107
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Best Local
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translational start signal. In the examples, the 3' end of pKT241 was stached to the signal DNA sequence of the DNA fragment (19) for rat preproingulin (see AAN10033). The closest identifiable promoter for the penicillinase gene in pKT218 (AAN10032) is located in the region 14 to 20 mucleotides before its translational start signal. In the examples, the 3' end of pKT218 was attached to the signal DNA sequence of the DNA fragment (CB6) for rat preproinsulin (see AAN10034)
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                                                                                                                                                                                                                            1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthesis of mature protein or polypeptide - by using bacterial host transformed by cloned vehicle contg. DNA fragment etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning vehicle; bacterial vector; transformed host; penicillinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of the pXT241 EcoRI-PstI penicillinase gene fragment.
                                                                                                                                                            100.0%; Score 101; DB 1; Length 228; 100.0%; Pred. No. 2.3e-21;
                                                                                                                                                                                            Indels
                                                                                                                              Sequence 228 BP; 72 A; 37 C; 46 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                             GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                            0; Mismatches
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/label= sticky end
248. .251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 101; Conservative
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P-PSDB; AAP10038.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39-APR-1981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc feature
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Query Match

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RESULT 4 AAV31229/c

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165 AGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The plasmid produces secreted beta-urogastrone in a transformed expression system. Similar plasmids may be constructed where the seceretion signal may be coupled with eg. somatostatin, insulin, growth hormone, interferon, IL-2, gastric inhibitory peptide, influenza B SA, epidermal growth factor and thymosine-beta4. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant vector for polypeptide secretion - contains signal peptide sequence directly bonded to peptide-coding sequence.
                     1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 101; DB 1; Length 456; 100.0%; Pred. No. 2.6e-21; tive 0; Mismatches 0; Indels (
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                                                                                             GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= d
/label= Beta-lactamase signal peptide
                                                                                                                 105 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                               Plasmid pUG201 sequence encoding beta-urogastrone.
                                                                                                                                                                                                                                                                                                                                                                                                   Beta-lactamase signal peptide; pGH54; pGH55; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kajifusa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
/label= Beta-urogastrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Table 4; 79pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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AAN60624/c
ID AAN60624 standard; DNA; 456
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(first entry)
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209. .439
/*tag= c
209. .277
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Matches 101; Conservative
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200. .20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1986-182911/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EART ) EARTH CH
(OHGA/) OHGAI H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAP60678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1985;
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29-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                  AAN60624;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a E. coli strain J96 contig containing pathogenicity island (PAI) sequences, and represents a nucleic acid molecule of the invention. PAIs are large fragments of DNA which comprise pathogenicity determinants. The sequences of the invention are taken from PAI IV and PAI V. PAI IV is located at approximately 64 min (near pheV) on the E. coli chromosome and is greater than 170 kb. PAI V is located at approximately 94 min (at pheR) on the E. coli chromosome and is approximately 160 kb in size. Antibodies specific to the proteins encoded by the PAI open reading frames of the invention can be used in kits to detect uropathogenic E. coli. The proteins are used in vaccines to elicit strain J96
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                                                                                                                                                                                        PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; vaccine; protective immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to elicit an immune
                                                                                                                                                                    9
                                                                                                                                                                  1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
3' end of pKT218 was attached to the signal DNA sequence of the DNA fragment (CB6) for rat preproinsulin (see AAN10034)
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                                                                                       100.0%; Score 101; DB 1; Length 251; 100.0%; Pred. No. 2.3e-21;
                                                                                                                               0; Indels
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                                                                                                                                                                                                                                            61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                   Sequence 251 BP; 74 A; 45 C; 50 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                    115 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 75
                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. coli J96 pathogenicity island contig #43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Page 140-141; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon PJ, Choi GH, Welch RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response to pathogenic E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0061953P.
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AAV31229 standard; DNA; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                             Best Local Similarity 100.1
Matches 101; Conservative
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Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                           Local Similarity
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Gaps

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Oshiden

Kitazawa T,

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Location/Qualifiers
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            AAN70833 standard; DNA; 456
                                                                                                                                             Tumour; inosine; DNA probe;
                                                                                                                                                                                                                                                  /*tag= c
209. .439
/*tag= a
209. .277
                                                                                          (first entry)
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200. .204
                                                                                                                   Beta-urogastrone sequence.
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                                                                (revised)
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                                                                                                                                                                     Unidentified
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                                     AAN70833;
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                                                                                                                                                                                                            promoter
AAN70833/c
                                                                                                                                                                                                                                     RBS
                                                                                                                                                                                                Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression vector contg. multiple information units is used to transform host all for increased prodn. of polypeptides.
 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 101; DB 1; Length 456; 100.0%; Pred. No. 2.6e-21; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                   61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/transl_except= (pos:434. .436,aa:Arg)
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                                                                          113 GGGTTCCGCGCACATTCCCCGGAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 553; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                 Sequence encoding beta-urogastrone.
                                                                                                                             AAN71080/c
ID AAN71080 standard; DNA; 456 BP.
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                                                                                                                                                                                              (revised)
(revised)
(first entry)
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.439
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Best Local Similarity 100.
Matches 101; Conservative
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209. .43
                                                                                                                                                                                                                                                                         pUGT 150s; beta-UG; ds
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                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                            25-MAR-2003
10-MAR-2003
13-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-1986;
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                                                                                                                                                                     AAN71080;
                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                  RESULT 6
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                                                                                                                                                                         An example of a sequence detected by a probe consisting of polyinosine, polydeoxyinosine, oligoinosine and/or oligodeoxyinosine is labeled. The sens and probe are hybridized and the existence of DNA in the product is detected. It can be used to detect the presence of malignant tumour. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of DNA and/or RNA - by converting to single strand form and using probe contg. labelled inosine deriv.
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                  Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GGGTTCCGCGCACATTTCCCCGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 73
                                                                                                                                                                                                                                                                                                                                                                              ; Score 101; DB 1;
; Pred. No. 2.6e-21;
0; Mismatches 0;
                                                                                                                                    Disclosure; Page 11; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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(first entry)
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Best Local Similarity 100.0
Matches 101; Conservative
                                                                                                                                                                                                                                                                                          to correct PA field.)
WPI; 1987-339045/48.
P-PSDB; AAP70505.
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13-DEC-1990
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AAN81765/c
ID AAN8:
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AC AAN8:
XC
DT 25-M:
DT 13-D:
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RESULT

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Synthetic

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The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90360-ABA90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting mitosis and/or meiosis. They can also be used in a method for inhibiting mitosis and/or meiosis. They can also be used in a method for tracting a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomopathy), autoimmune disorders such as (glomerulonephritis and rheumatoid arthritis), dermatological disorders (such as psoriasis), antiinflammatory, antifungal and antiparasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                 Polynucleotides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide sequence from the genome of Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 466 BP; 135 A; 87 C; 93 G; 150 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 101; DB 6;
100.0%; Pred. No. 2.6e-21;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 99; 213pp; English.
                                                                                                                                                                                                 Glover DM, Midgley C;
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                                                                                                                 24-MAR-2000; 2000GB-00007268
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                                                                             23-MAR-2001; 2001WO-GB001297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders (such as malaria)
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Matches 101; Conservative
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                                                                                                                                                         (CYCL-) CYCLACEL
WO200172774-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1997;
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                                       04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
          Sequence of HB101 (pGH201) encoding new beta-urogastrone deriv. Met(21), Arg (53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-urogastrone deriv. - has gastric acid secretion inhibition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tic enzymes such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The deriv. has various biological activities such as gastric acid secretion inhibiting action, or cell proliferation promoting action. T deriv. has the same biological or pharmacological activities as betaurogastrone. It is not susceptible to denaturation by oxidn. and is chemically stable. Deriv. has resistance to proteolytic enzymes such a protease. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila cell cycle progression protein coding sequence #48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 101; DB 1; Length 456; 100.0%; Pred. No. 2.6e-21; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 456 BP; 115 A; 86 C; 104 G; 151 T; 0 U; 0 Other;
                                                                             фв.
                                                                                                                                                                                                                                                            /product= "New beta-urogastrone deriv."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTTCCGCGCACATTCCCCCGAAAAGTGCCACCTGACGTC 73
                                                                             secretion; cell proliferation; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 685; 76pp; Japanese.
                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation promotion activity.
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ABA90413 standard; DNA; 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAP81349
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                                                                       Gastric acid
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Query Match

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Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                               158
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                             New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                                                                                                                                                                              AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis,
                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pallidum infection; syphilis; Borrelia infection; animal; duction; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                               Length 487;
                                                                                                                                                                                                                                               Sequence 487 BP; 125 A; 127 C; 113 G; 121 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTTCCGCGCACATTTCCCCGAAAGTGCCCACCTGACGTC 223
                                                                                                                                                                                                                                                                              100.0%; Score 101; DB 2; 100.0%; Pred. No. 2.6e-21;
                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                biosynthetic products such as enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1093; 1150pp; English.
                                                                                              Claim 1; Page 1106; 1150pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0050667P
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                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-081273/07.
WPI; 1999-081273/07
                                                                                                                                                                                                                                                                                           Local Similarity
hes 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX21149
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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Sequence 535 BP; 145 A; 108 C; 122 G; 155 T; 0 U; 5 Other;

biosynthetic products such as enzymes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; antipsoriatic; dermatological; antifungal; mitosis; antiparasitic; antimalarial; antirheumatic; antiarthritic; cell division; cell cycle progression protein; tumour; proliferative disorder; cardiovascular; autoimmune; dermatological disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 AGGGTTATTGTCTCATGACGCGTACATATTTGAATGTATTTAGAAAAAATAACAAATAG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to Drosophila cell cycle progression proteins (AAM47572-AAM47608) and their coding sequences (ABA90366-ABA90520). The coding sequences and proteins are useful for identifying a substance capable of affecting the function of the corresponding gene, a substance capable of inhibiting the cell division cycle, or capable of inhibiting a tumour or proliferative disorder, cardiovascular disorders (such as restenosis and cardiomyopathy), autoimmune disorders such as (glomeralonephritis and rheumatoid arthritis), dermatological disorders (such as psoriasis), antiinflammatory, antifungal and antiparasitic
                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                  1 AGGGTTATTGTCTCATGAGGGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                                                                                         AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rolynuclectides encoding cell cycle progression proteins, useful for treating a tumor or a proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antiproliferative; cytostatic; cardiant; immunosuppressive; meiosis;
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                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                               61 GGGTTCCGCGCACATTTCCCCGGAAAGTGCCACCTGACGTC 101
                                                                                                                                                                                                                                                                                  GGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGACGTC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Score 101; DB 2;
Pred. No. 2.7e-21;
                                                         0; Mismatches
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   100.0%;
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Best Local Similarity 100.0%;
Matches 101; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA90456 standard; DNA; 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing the affinity of an extendable oligonucleotide (EO) for a target nucleic acid, for providing primers having improved specificity, comprises hybridization of the EO to a template oligonucleotide (TO) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electropherogram of a DNA sequencing reaction using E154 & T422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC 101
                                         295 GGGTTCCGCGCACATTCCCCGAAAAGTGCCACCTGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 10; Fig 23; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   medical research; pUC19 plasmid
                                                                                                                                                                                                                                                ADH58311 standard; DNA; 605 BP.
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61
                                                                                                                                                                         RESULT 13
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GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 359

61 GGGTTCCGCGCACATTTCCCCGGAAAGTGCCACCTGACGTC 101

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antianaemic; dermatological; immunosuppressive, antiinflammatory; antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic; antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic; prosteoglakic; prostaticis, adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostete neoplastic disorder; skin ading; reproductive system disorder; autoimmune disorder; skin ading; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative; ds.
                                                                                              Human; nootropic; neuroprotective; cytostatic; antiparkinsonian;
                                                                     DNA encoding novel prostate gland antigen, Seq ID No 418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-025267P.
2000US-025268P.
2000US-025270P.
2000US-0255447P.
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2000US-0186350P.
2000US-0189874P.
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2000US-0215135P.
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2000US-0217496P.
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2000US-0225266P.
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2000US-0226868P.
2000US-0227182P.
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05-SEP-2000;
06-SEP-2000;
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The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prevention, and/or treatment of diseases and/or disorders of prognosis, prevention, and/or treatment of diseases and/or disorders of prognations, gaute mon-bacterial prostatitis, chronic non-bacterial prostatitis, prostatodystonia, prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic non-bacterial prostatitis, benign prostatic non-bacterial prostatitis, benign prostatic non-bacterial prostations, benign prostatic non-bacterial prostations, benign prostatic non-bacterial prostations, disorders (squamous cell carcinomas, II, (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anaemia), hyperproliferative disorders, urinary system disorders (almenton-pahritis), cardiovascular disorders (alsorders (arrhythmias), respiratory disorders (alsorders), neural activity and neurological disorders (Alzheimer's disease and Parkinson's disease), condocrine disorders (Alzheimer's disease and Parkinson's disease), condocrine disorders (Alzheimer's diseases at the cellular level, condocrine disorders), liver disorders (biliary liver cirrhosis), condocreatic and gall bladder disorders (diseases at the cellular level, and wound healing and epithelial cell proliferation. (I) or (II) is cuseful to prevent skin aging, for preventing hair loss, to maintain organis before transplantation, and as food additive or preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
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2000US-0254097P
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Matches 101; Conservative
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RESULT 15 AAS27819/c ID AAS27819 standard; DNA; 776 BP. 2000US-0232081P. 2000US-023298P. 2000US-0232398P. 2000US-0232398P. 2000US-0232399P. 2000US-0232399P.

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2000US-0246478P

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26-SEP-2000;
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          AAS27819;
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2000US-0249207P

2000US-0246538P. 2000US-0246532P. 2000US-0246609P.

2000US-0246527P

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The invention relates to novel isolated polypeptides (I), and definition relates to novel isolated polypeptides (I), and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases (e.g. pepartiis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders (e.g. disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (c.g. Alzheimer's disease, Parkinson's (e.g. stroke), renal disorders (e.g. arrythmia), respiratory disorders, dermatological disorders (e.g. Andrison's epithelial cell proliferation, endocrine disorders (e.g. Addison's copithelial cell proliferation, endocrine disorders (cirrhosis), as stimulators of inflammatory disorders), liver disorders (cirrhosis), as stimulators of thigher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS), AAS26976-AAS27850 represent novel signal transduction pathway protein coding sequences and PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
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Job time : 147.448 secs

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OM nucleic

Run on:

Sequence:

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Hebeloma cylindrosporum
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
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(bases 1 to 300)

Whyf. D., Benjdia, M., Tegeder, M. and Frommer, W.B.

Construction of a functional cDNA library from the ectomycorrhizal fungus Hebeloma cylindrosporum

Unpublished (2001)
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Tel: 49 7071 2976160
Fax: 49 7071 293287
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ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hebeloma cylindrosporum"
/mol_type="mRNA"
/strain="H1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: daniel.wipf@zmbp.uni-tuebingen.de
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SYGNARD: pDR196 5' primer (PMA 5')
High quality sequence stop: 300
POLYA=No.
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CC818423
AL694813
AL694813
CC817633
CC81788
CC817788
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CC816929
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AUTHORS
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COMMENT
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                                                                    July 14, 2005, 05:15:57; Search time 961.667 Seconds (without alignments) 3997.736 Million cell updates/sec
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                                                                                                                                      1 agggttattgtctcatgagc......gaaaagtgccacctgacgtc 101
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                           34239544 segs, 19032134700 residues
                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                  nucleic search, using sw model
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seq length: 200000000
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990_est2:;

990_est4:;

990_est6:;

990_est6:;

900_gss1:;

900_gss2:;
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Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning Genome Res. 9 (10), 960-971 (1999)
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Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
Direct Submission
Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
Centre Hinnston, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
V_type: phagemid
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GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontidea; Tetradontidae; Tetradontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FR0009140 309 bp DNA linear GSS 25-FEB-200 F.rubripes GSS sequence, clone 010H20aC4, genomic survey sequence.
                                                                                          A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis
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Agaricales; Cortinariaceae; Hebeloma.
1 (bases 1 to 300)
Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and
Frommer, W.B.
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Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Mycelia"
/lab_host="E. coli XL1-Blue"
/clone_lib="Hebeloma cylindrosporum functional cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 101; DB 5; Length 300; 100.0%; Pred. No. 8.1e-19; ive 0; Mismatches 0; Indels (
                                                                                                                                                                           Context: Wipf D
ZMBP - Center for Molecular Biology of Plants
University of Tuebingen
Mid der Morgenstelle 1, 72076 Tuebingen, Germany
Tel: 49 7071 2976160
Fax: 49 7071 293287
Email: daniel wipf@zmbp.uni-tuebingen.de
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                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Hebeloma cylindrosporum"
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/strain="H1"
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1 (bases 1 to 300)

Wipf, D., Benjdia, M., Rikirsch, E., Zimmermann, S., Tegeder, M. and
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Hebeloma cylindrosporum
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
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A Hebeloma cylindrosporum expression cDNA library for suppression cloning in yeast mutants, complementation of a yeast his4 mutant and EST analysis Unpublished (2002)
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SON bp mRNA linear EST 13-NOV-EST88 Hebeloma cylindrosporum functional cDNA library Hebeloma cylindrosporum cDNA, mRNA sequence.
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|mol_type="mRNA"
|strain="H1"
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/tissue_type="Mycelia"
/lab_host="E. coli XL1-Blue"
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BU963956.1 GI:24204753
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DKFZp313J1611_r1 313 (вулолут: hlcc2) Homo sapiens cDNA clone
DKFZp313J1611_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dKz- heidelberg-de, sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
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Koehrer, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S. EST (Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DH10B"
/clome_lib="313 (synonym: hlcc2)"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
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No s1 sequence available.
This clone (DKFZp313J611) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
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PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
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Matches 101; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                             Length 309;
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This is the 5' sequence of the clone insert
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llarity 100.0%; Pred. No. 8.2e-19;
Conservative 0; Mismatches 0;
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/organism="Takifugu rubripes"
/mol type="genomic DNA"
/db_xref="taxon:31033"
/clone="0.10H20ac4"
/clone_lib="cosmid 010H20"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313J1611"
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1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 60

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CC819240 17-JUL-2003 100005D19R Oxytricha plasmid UUGCIO library Sterkiella histriomuscorum genomic clone UUGC100005D19 R, genomic survey
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228 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 287
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Sterkiella histriomuscorum
Eukaryota; Alvoclata; Ciliophora; Spirotrichea; Stichotrichia;
Stichotrichida; Oxytrichidae; Sterkiella.
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Paired end reads from plasmid inserts of Oxytricha trifallax
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                                                           288 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACTGACGTC 328
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                                     61 GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC
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Matches 101; Conservative 0; Mismatches
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Plate: 0005 row: D column: 19
Seg primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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Fax: 801 585 7177
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100006J13R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC10006J13 R, genomic survey
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                                       BJ684174 BJ684174 HCEST library Haplochromis chilotes cDNA clone no90c12,
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Haplochromis chilotes
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes,
Labroidei, Cichlidae, Haplochromis.
Haplochromis.
Watanabe,M., Kobayashi,N., Shin-i,T., Kohara,Y. and Okada,N.
Orf sequences of cichlid in Lake Victoria are essentially same
Unpublished (2004)
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
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Sterkiella histriomuscorum
Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella.
1 (bases 1 to 491)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
macronuclear chromosomes
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                        Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Haplochromis chilotes"
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/dev_stage="varied"
/clone_lib="HCEST_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bmail: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="no90c12"
                                                                                                                     BJ684174.1 GI:46527295
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-559-81-6856
Fax: 81-559-81-6855
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/olone="UUGCIO000613" /
/lab_host="UUGCIO000613" /
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone="UuCctor: PWD42nv; Purifided macronuclear chromosomal
/note="Vector: PWD42nv; Purifided macronuclear chromosomal
/note="Vector: PWD42nv; Purifided macronuclear chromosomal
/note="Vector: PWD42nv; Purifided macronuclear chromosomal
/note="Vector respective were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished (2001)
Bioinfomatics and Gene Network Research Group
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S035A01 Stem library from Oryza sativa (3-5 leaf stage) Oryza
sativa cDNA clone S035A01, mRNA sequence.
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Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Exa: 0086-571-8681525
Email: webmaster@estarray.org, URL: http://www.estarray.org
Seg primer: M13 forward primer.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:94289"
Email: ddunn@genetics.utah.edu
Plate: 0006 row: J column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 491.
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/mol_type="mRNA"
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Fax: 801 585 7177
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84112, US
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Sterkiella histriomuscorum
Bukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella
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                           /dev stāge="3-5 leaf stage"
/clone_lib="Stem library from Oryza sativa (3-5 leaf
stage)"
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Paired end reads from plasmid inserts of Oxytricha trifallax
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University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
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mol_type="genomic DNA"
'db_xref="taxon:94289"
                                                                                                                                                                                              100.0%; Score 101; DB 4;
Similarity 100.0%; Pred. No. 8.4e-19;
01; Conservative 0; Mismatches 0;
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                 /note="Vector: pSport2"
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Location/Qualifiers
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   /tissue_type="Stem"
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC818374.1 GI:32897661
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Fax: 801 585 7177
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Best Local 9
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KEYWORDS
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100.0%; Score 101; DB 9; Length 495;

Query Match

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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Coxytricha plasmid UUGCIO library"
/clone lib="Coxytricha plasmid UUGCIO library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polynucleotide kinase. Adaptor
oligonucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli Xili0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                892 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAATAAACAAATAG 333
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                                                                                              1 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG
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1 (bases 1 to 496)

Dunn, D., Doak, T., Herrick, G. and Weiss, R.

Paired end reads from plasmid inserts of Oxytricha trifallax unpublished (2003)
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                                 Indels
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                                                                                                                                                                                                                                                              332 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 292
                                                                                                                                                                                                                        61 GGGTTCCGCGCACATTTCCCCCGAAAGTGCCACCTGACGTC 101
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|mol type="genomic DNA"
|db xref="taxon:94289"
|clone="UUGC100004L13"
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Pred. No. 8.4e-19; ; Mismatches 0;
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Plate: 0004 row: L column: 13
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/lab hose="E. Col; strain XL10-Gold, T1-resistant, F-"
/lab hose="E. Col; strain XL10-Gold, T1-resistant, F-"
/clone lib="Coyytricha plasmid UUGC10 library"
/note="Vector: PWD42nv; Purified macronuclear chromosomal
DNA from Oxytricha trifallax was blunt end-repaired with
T4 DNA polymerase and T4 polymucleotide kinase. Adaptor
oligomucleotides were ligated to the blunt ends in high
molar excess. Vector DNA was prepared from a derivative of
pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible
derivative of plasmid R1. The vector was ligated with
adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. Coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases 1 to 515)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes
Unpublished (2003)
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Sterkiella histriomuscorum
Bukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
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100002D21R Oxytricha plasmid UUGC10 library Sterkiella
histriomuscorum genomic clone UUGC100002D21 R, genomic survey
         histriomuscorum genomic clone UUGC100003C16 R, genomic survey
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                                                                                                                                                                  Sterkiella histriomuscorum (Oxytricha trifallax)
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/mol_type="genomic DNA"
/db_xref="taxon:94289"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Plate: 0003 row: C column: 16
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                                                                                                                                                                                                    Sterkiella histriomuscorum
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CC817128.1 GI:32896415
GSS.
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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CC817128/c
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AUTHORS
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LOCUS CC817752 515 bp DNA linear GSS 17-JUL-2003
DEFINITION 100003C16R Oxytricha plasmid UUGC10 library Sterkiella
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Sterkiella histriomuscorum
Eukaryota, Alvoclata, Ciliophora, Spirotrichea, Stichotrichida,
Stichotrichida, Oxytrichidae; Sterkiella.
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Paired end reads from plasmid inserts of Oxytricha trifallax
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Plate: 0006 row: N column: 08
Seg primer: CACACAGGAAACAGCTATGACC
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Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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CC819854.1 GI:32900533
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Eukaryota, Alveolata, Ciliophora, Spirotrichea, Stichotrichia,
Stichotrichida, Oxytrichidae, Sterkiella.
1 (bases 1 to 519)
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Stichotrichida, Oxytrichidae, Sterkiella.
1 (Dases I to 518)
Dunn, D., Doak, T., Herrick, G. and Weiss, R.
Paired end reads from plasmid inserts of Oxytricha trifallax
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Paired end reads from plasmid inserts of Oxytricha trifallax macronuclear chromosomes
Unpublished (2003)
Contact: Robert B. Weiss
University of Utah Genome Center
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Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah
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'db_xref="taxon:94289"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                  macronuclear chromosomes
Unpublished (2003)
                                                                                                                                                                                                              Contact: Robert B. Weiss
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Best Local Similarity 100.
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/orde="Vector: PMAJIVA; purified macronuclear chromosomal note="Vector: pWaJIVA; purified macronuclear chromosomal DNA from Oxytricha trifallax was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli Xill0-Gold (Stratagene) cells and selected for ampicillin resistance."
Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@enetics.utah.edu
Plate: 0002 row: J column: 19
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